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GAM3539 DKFZp564I1922 3' TAAAATATATATATATATAT 80150 T

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GAM3539 DKFZP566M114 3' TATATATATATATATATA 80053

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GAM3539 DKFZp761D112 3' AATATATATATATATATAT 80108

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GAM3539 DKFZp761D112 3' ATATATATATATGTATCATATA 80151

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GAM3539 DNAJC5 3' ATATATACATATACACATAT 80152

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GAM3539 DNCLI1 3' CATATATATATATATATAT 80114

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GAM3539 ELF2 3' TATATATATATATATATATAT 79979

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GAM3539 ELF2 3' TATATATATATATATATA 80053

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GAM3539 ELF2 3' ATATATATATATATATATATAT 79978

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GAM3539 ELF2 3' TATATATATATATATATAT 79980

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GAM3539	ELF2	3'	ATATATATGTATGTATATATAT	80158	A	A
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GAM3539	ELF2	3'	ATATGTATGTATATATATATAT	80156	A	A
			ATAT TAT TATATATATATAT			
			TATA ATA ATATATATATATA			
			C C			
GAM3539	ELF2	3'	ATATATGTATGTATATATATAT	80157	A	A
			ATATAT TAT TATATATATAT			
			TATATA ATA ATATATATATA			
			C C			
GAM3539	ELF2	3'	TATGTATATATATATATAT	80155	A	
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GAM3539	ELF2	3'	TATGTATATATATATATAT	80153	A	
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			ATA ATATATATATATATA			
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GAM3539	ELF2	3'	ATATATATATGTATGTATATAT	80154	A	A
			ATATATATAT TAT TATATAT			
			TATATATATA ATA ATATATA			
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GAM3539	EPB41L1	3'	TATATATCTATATATATAT	80159	A	
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			ATATATA ATATATATATA			
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GAM3539	ERAP140	3'	ATATATATGTATATGTACATAT	80161	A	A
			ATATATAT TATAT TATATAT			
			TATATATA ATATA ATGTATA			
			C C			
GAM3539	ERAP140	3'	ATACACTCATATATATGTATAT	80160	A	A
			ATATAT TATATATAT TATAT			
			TATGTG GTATATATA ATATA			
			A C			
GAM3539	EVI5	3'	ATATATATATATATATATATAT	79978		
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GAM3539 EVI5 3' AATATATATATATATATATATA 79989 III
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GAM3539 EVI5 3' ATATATATATATATATACATAT 80162
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GAM3539 FBXO9 3' ATATATATATATATATATATAT 79978
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GAM3539 FBXO9 3' ATATATATATATATATATATAT 79978
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GAM3539 FBXO9 3' ATATATATATATATATATATAT 79978
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GAM3539 FBXO9 3' ATATATATATATATATATATAT 79978
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GAM3539 FBXO9 3' ATATATATATATATATATATAT 79978
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GAM3539 FLJ10477 3' TACATATGTATATATATAT 80163 A
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GAM3539 FLJ10482 3' TATATATATATGTATATAT 80034 A
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GAM3539 FLJ10482 3' TATATATATATGTATATATAT 80036 A
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GAM3539 FLJ10620 3' TATATACATACATATATAT 80164
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GAM3539	FLJ10782	3'	TATTTATATATATATATAT	80069	A
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GAM3539	FLJ10782	3'	TATATATATATATATATA	80053	
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GAM3539	FLJ11127	3'	ATATGTATATATACACACATAT	80165	A
			ATAT TATATATATATATATAT		
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GAM3539	FLJ11342	3'	TAACATATATATTATATTATAT	80166	— A
	AT		TAATATATATAT ATAT TATATAT		
			ATTGTATATATA TATA ATATATA		
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GAM3539	FLJ12078	5'	ATATATATATATTTATATATAT	80167	A
			ATATATATATAT TATATATAT		
			TATATATATATA ATATATATA		
			A		
GAM3539	FLJ12987	3'	ATATATCCATATATATATATAT	80170	A
			ATATAT TATATATATATATAT		
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GAM3539	FLJ12987	3'	ATATGTATATATACATATAT	80168	A
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GAM3539	FLJ12987	3'	TATATATATACATATATAT	80070	
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			ATATATATATGTATATATA		
GAM3539	FLJ12987	3'	ATATATATCCATATATATATAT	80179	A
			ATATATAT TATATATATATAT		
			TATATATA GTATATATATATA		
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GAM3539	FLJ12987	3'	ATATATATATATCCATATATAT	80180	A
			ATATATATATAT TATATATAT		

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GAM3539	FLJ12987 3'	ATATATGTATATATACATATAT 80173	A
		ATATAT TATATATATATATAT	
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GAM3539	FLJ12987 3'	ATATACATATATATGTATATAT 80172	A
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GAM3539	FLJ12987 3'	ATATATATATCCATATATATAT 80178	A
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GAM3539	FLJ12987 3'	ATATATATATATATATATATAT 80064	III
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GAM3539	FLJ12987 3'	TATATATATCCATATATATAT 80176	A
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GAM3539	FLJ12987 3'	ATATATATATATATCCATATAT 80177	A
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GAM3539	FLJ12987 3'	TATATATATCCATATATAT 80169	A
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		ATATATATA GTATATATA	
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GAM3539	FLJ12987 3'	TATATATATATACATATATAT 80175	
		TATATATATATATATATATAT	
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GAM3539	FLJ12987 3'	ATATCCATATATATATATATAT 80174	A
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GAM3539	FLJ12987 3'	TATGTATATATACATATAT 80171	A
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GAM3539 FLJ20079 3'	TATATATATGTATATATATAT 80183	A
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GAM3539 FLJ20079 3'	TATATATATGTATATATAT 80081	A
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GAM3539 FLJ20079 3'	ATACATACATATGTGTATATAT 80181	A__
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	CAC	
GAM3539 FLJ20079 3'	ATATGTATATATATATACACAT 80182	A
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GAM3539 FLJ20079 3'	ATACATACATATGTGTATATAT 80181	A__
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	CAC	
GAM3539 FLJ20079 3'	ATACATACATATGTGTATATAT 80181	A__
AT	ATATATATATAT TATATATAT	
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	CAC	
GAM3539 FLJ21791 3'	TACATATATATATACATATAT 80044	
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GAM3539 FLJ22060 3'	ATATATATCATATATATATATA 80184	_
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GAM3539 FLJ22393 3'	AATATATATATATGTATGTATA 80185	A A III
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GAM3539 FLJ22393 3'	ATATATATATGTATGTATATAT 80154	A A
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GAM3539	FLJ22393 3'	ATATATATGTATGTATATATAT 80158	A	A
		ATATATAT TAT TATATATAT		
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GAM3539	FLJ23047 3'	ACATATATATATATATATAT 80186		
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GAM3539	FLJ23259 3'	ATATATATGTAATATATATATA 80187	___	III
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GAM3539	FLJ23259 3'	ATATGTATATTACATATATATA 80188	A	_
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GAM3539	FLJ23259 3'	ATATATATATTTACATATATAT 80083	A	
		ATATATATAT TATATATATAT		
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GAM3539	FLJ23259 3'	ATATGTATATTACATATATATA 80189	A	_
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GAM3539	FLJ23259 3'	ATATATATATTTACATATATAT 80083	A	
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GAM3539	GAPCENA 3'	ATATATATATATATATATATAT 79978		
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GAM3539	GAPCENA 3'	ATATATATATATATATATATAT 79978		
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GAM3539	GAPCENA 3'	ATATATATATATATATATATAT 79978		
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GAM3539 GAPCENA 3' ATATATATATATATATATATAT 79978
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GAM3539 GAPCENA 3' TATATATATATATATACAT 80190
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GAM3539 GAPCENA 3' TATATATATATATATATATAT 79979
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GAM3539 GAPCENA 3' ATATTTATATATATATATAT 80191 A
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GAM3539 GAPCENA 3' ATATATATATATATATATAT 79973
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GAM3539 GFR 3' TACATATATATTATATATA 80192 A
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GAM3539 GRID1 3' AATATATATATATATATAT 80108
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GAM3539 GRID1 3' ATATATATATATATATAAACAT 80193 T
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GAM3539 GTPBP2 3' ATACATATGTATATATATATAT 80194 A III
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GAM3539 GTPBP2 3' ACATATGTATATATATATATAT 80195 A
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GAM3539 HNRPA3 3' ATATGTATATACATATATATAT 80205 A
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GAM3539	HNRPA3	3'	ATATATATATATATATGTATAT 80204	A	III
	A		ATATATATATATATAT TATAT	A	
			TATATATATATATATA ATATA	T	
			C	III	
GAM3539	HNRPA3	3'	ATATATATGTATATATGTATAT 80198	A	A
			ATATATAT TATATAT TATAT		
			TATATATA ATATATA ATATA		
			C	C	
GAM3539	HNRPA3	3'	ATATATATATATATGTATATAT 79990	A	
			ATATATATATATAT TATATAT		
			TATATATATATATA ATATATA		
			C		
GAM3539	HNRPA3	3'	ATATATGTATATACATATATAT 80202	A	
			ATATAT TATATATATATATAT		
			TATATA ATATATGTATATATA		
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GAM3539	HNRPA3	3'	TATATATCCATATATATATAT 80203	A	
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GAM3539	HNRPA3	3'	ATATATATATATATGTATATAT 79990	A	
			ATATATATATATAT TATATAT		
			TATATATATATATA ATATATA		
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GAM3539	HNRPA3	3'	ATATATATATATGTATATAT 80207	A	
			ATATATATATAT TATATAT		
			TATATATATATA ATATATA		
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GAM3539	HNRPA3	3'	ATATATCCATATATATATATAT 80170	A	
			ATATAT TATATATATATATAT		
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GAM3539	HNRPA3	3'	TATATATCCATATATATATAT 80206	A	
			TATATAT TATATATATAT		
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GAM3539	HNRPA3	3'	ATATATATATATATATGTATAT 80204	A	III
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GAM3539	HNRPA3	3' TATATATATCTATATATAT	80201	A
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GAM3539	HNRPA3	3' TATATACATATATATATAT	80200	
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GAM3539	HNRPA3	3' ATATATATATATATGTATATAT	79990	A
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GAM3539	HNRPA3	3' ATATATACCTGTATATATATAT	80197	A__
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GAM3539	HNRPA3	3' TATATATGTATATACATATAT	80199	A
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GAM3539	HNRPA3	3' ATATCCATATATATATATATAT	80174	A
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GAM3539	HNRPA3	3' ATATCCATATATATATATATAT	80174	A
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GAM3539	HNRPA3	3' TATATATATATATAAAATAT	80196	TAT
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GAM3539	HRIHFB2436	3' ATATATATATATATATATAT	79973	
		ATATATATATATATATATAT		
		TATATATATATATATATATA		
GAM3539	HRIHFB2436	3' TATATATATATATATATA	80053	
		TATATATATATATATATA		

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GAM3539 IL1RAPL1 3' TATATATATATGTATATATATA 80209 A III
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GAM3539 IL1RAPL1 3' TATATATATATGTATATATAA 80208 A ATIII
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GAM3539 IL1RAPL1 3' ATATATATATGTATATATATAT 79998 A
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GAM3539 KIAA0022 3' TATATATATATATATAGCAC 80210 —
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GAM3539 KIAA0100 3' TATATATAATATATATATA 80212 T
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GAM3539 KIAA0100 3' TAATATATATATATTTATATAT 80211 A
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GAM3539 KIAA0103 3' TATATATATACATGTATAT 80140 A
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GAM3539 KIAA0189 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0189 3' ATATATATACACACATATATAT 80214 III
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GAM3539 KIAA0189 3' ATATATATACACACATATATAT 80215
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GAM3539 KIAA0189 3' ATATATACACACATATATAT 80213
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GAM3539 KIAA0189 3' ATATATATACACACATATATAT 80215
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GAM3539 KIAA0189 3' ACACATATATATATATATATAT 80216
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GAM3539 KIAA0189 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0189 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0189 3' ATATATATACACACATATATAT 80215
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GAM3539 KIAA0189 3' TATATACACACATATATAT 80217
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GAM3539 KIAA0189 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0222 3' AATATATATATATATATATATA 80074 ATIII
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GAM3539 KIAA0222 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0222 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0222 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0222 3' AATATATATATATATATATATA 79989 III
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GAM3539 KIAA0222 3' TATATATATATATATATA 80053
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GAM3539 KIAA0295 3' ATATATATTTATATATATATAT 80218 A III
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GAM3539 KIAA0377 3' AATAAATATATATATATATAT 80148 T
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GAM3539 KIAA0391 3' TAATATATACATATAGCTAT 80219 TA
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GAM3539 KIAA0443 3' AATATATATATATATACA 80220
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GAM3539 KIAA0545 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0545 3' AATATATATATATATATATATA 79989 III
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GAM3539 KIAA0545 3' AATAAATATATATATATATATA 80221 T III
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GAM3539 KIAA0545 3' AATATATATATATATATATATA 80074 ATIII
A AATATATATATATATATATAT A

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GAM3539 KIAA0546 3' AATATATATATATATATATATA 80074 ATIII
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GAM3539 KIAA0546 3' TATATATATATATATATA 80053

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GAM3539 KIAA0546 3' AATATATATATATATATATATA 79989 III
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GAM3539 KIAA0650 3' ATATATTTATATATATATATATAT 80222 A III
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GAM3539 KIAA0650 3' ATATTTATATATATATATATATAT 79966 A III
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GAM3539 KIAA0650 3' TATATATATATATATATATAA 79967 ATIII

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GAM3539 KIAA0660 3' TATATATATATATATATAT 79980

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GAM3539 KIAA0716 3' ACATATATATGTATATATATAT 80224 A III
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GAM3539 KIAA0716 3' CACATATATATGTATATATATA 80223 A III
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GAM3539 KIAA0731 3' ATATATATATATGTATATATAA 80225 A ATIII
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GAM3539 KIAA0731 3' ATATATATATATGTATATATAT 80226 A III
A ATATATATATAT TATATATAT A
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GAM3539 KIAA0731 3' ATATATATATGTATATATATAT 79998 A
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 80064 III
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0757 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA0828 3' ATATAGATATATATATATATAT 80227 T
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GAM3539	KIAA0828	3' ATATAGATATATATATATAT 80227	T	
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GAM3539	KIAA0828	3' ATATATATATATATGTATATAT 79990	A	
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GAM3539	KIAA0844	3' ATATATATGTATATATGTATAT 80198	A	A
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GAM3539	KIAA0844	3' ATATATGTATATATGTATATAT 80228	A	A
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GAM3539	KIAA0848	3' TAATATTATATATATATAT 80229	A	
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GAM3539	KIAA0872	3' TATATATATATATACACATAT 80233		
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GAM3539	KIAA0872	3' ACACATATGTATATGTATATAT 80230	A	A
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GAM3539	KIAA0872	3' ATATACATATATATATATATAT 80080		
		ATATATATATATATATATATAT		
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GAM3539	KIAA0872	3' ATATATACACATATATATATAT 80234		III
	A	ATATATATATATATATATATAT	A	
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GAM3539	KIAA0872	3' ATATATATACACATATATATAT 80232		III
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GAM3539 KIAA0872	3' ATATACACATATATATATAT	80231	III
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GAM3539 KIAA0895	3' TATATATATACAAGTATAT	80235	TA
	TATATATATATA	TATAT	
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GAM3539 KIAA0937	3' CATATATATATATATATATAT	80110	
	TATATATATATATATATATAT		
	GTATATATATATATATATATA		
GAM3539 KIAA0937	3' CATATATATATATATATATAA	80238	ATIII
	TATATATATATATATATAT	A	
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GAM3539 KIAA0937	3' TATATATATATATATATAC	80237	
	TATATATATATATATATAT		
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GAM3539 KIAA0937	3' AATATATATGCATATATATATA	80236	A
T	AATATATAT	TATATATATATAT	
	TTATATATA	GTATATATATATA	
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GAM3539 KIAA0976	5' TACATATATATACACATAT	80239	
	TATATATATATATATATAT		
	ATGTATATATATGTGTATA		
GAM3539 KIAA0993	3' TAATATATATTATATATATATA	80240	—
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GAM3539 KIAA0993	3' TAATATATATTATATATATATA	80240	—
TAT	TAATATATAT	ATATATATATATAT	
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GAM3539 KIAA0993	3' TATATATATATATATGTACAT	80241	A
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GAM3539 KIAA0997	3' TAATATATATATGTGCACATAT 80242	_____	III
	ATATATA TATATAT ATATATATATAT A		
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GAM3539 KIAA1096	3' TATATATATATATGTATATAA 80244	A	ATIII
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GAM3539 KIAA1096	3' ATATATATATATGTATATATAT 80015	A	
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GAM3539 KIAA1096	3' ATATATATATGTATATATATAT 79998	A	
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GAM3539 KIAA1096	3' ATATATATATATATATTTATAT 80243	A	
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GAM3539 KIAA1096	3' TATATATATATATGTATATATA 80011	A	III
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GAM3539 KIAA1096	3' ATATATGTATATATATATATAT 80000	A	
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GAM3539 KIAA1096	3' ATATGTATATATATATATATAT 79996	A	
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GAM3539 KIAA1128	3' TAATATATATATAAATACA 80245	T	
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GAM3539	KIAA1196	3'	AATATATATGTATATATATATA 80246	A	ATIII
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GAM3539	KIAA1198	3'	AATATATATAAATATATAT 80247	T	
			AATATATATA ATATATAT		
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GAM3539	KIAA1260	3'	TATATATATATATATTTTATAT 80248	A	
			TATATATATATATAT TATAT		
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GAM3539	KIAA1281	3'	TATATTTATATATATATATAT 80251	A	
			TATAT TATATATATATATAT		
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GAM3539	KIAA1281	3'	ATATGTATACGTATATATATAT 80250	A	TA
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GAM3539	KIAA1281	3'	TATATATATGTATATATACA 80249	A	
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GAM3539	KIAA1281	3'	TATATATATATATATGTATATA 80061	A	III
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GAM3539	KIAA1281	3'	ATATATATATATATGTATATAT 79990	A	
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GAM3539	KIAA1321	3'	ATATATATATATGTATATATAT 80015	A	
			ATATATATATAT TATATATAT		
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GAM3539	KIAA1321	3'	TATATATATATATATATATAA 79967		ATIII
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GAM3539 KIAA1321	3' TATATATATATATTTGTATATA	80252	A__
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GAM3539 KIAA1321	3' ATATATATATATATGTATATAT	79990	A
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GAM3539 KIAA1321	3' ATATATATGTATATATATATAT	79999	A
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GAM3539 KIAA1321	3' TATATATATATATATGTATATA	80061	A III
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GAM3539 KIAA1321	3' ATATATATATGTATATATATAT	79998	A
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GAM3539 KIAA1332	3' TAATATATATATATATATTTAT	80253	A
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GAM3539 KIAA1332	3' TATATAATATATATATATATAT	80254	_
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GAM3539 KIAA1361	3' TATATATATGTACACACAT	80255	A
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GAM3539 KIAA1384	3' ACATATATTTATATATATATAT	80256	A
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GAM3539 KIAA1430	3' ATATATAAAACATATATATATA	80257	T_
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GAM3539 KIAA1464 3' TAATATATATATTTTTATATAT 80258 _____
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GAM3539 KIAA1522 3' TATATATGTATATATATAC 80050 A
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GAM3539 KIAA1522 3' AATATATATATGTATATATAT 80259 A
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GAM3539 KIAA1546 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA1546 3' ATATATATATATATATATATAT 79978
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GAM3539 KIAA1577 3' TACATATATATATGTATACAT 80261 A
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GAM3539 KIAA1577 3' TATACATATATATATGTAT 80260 A
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GAM3539 KIAA1615 3' TATATATATATATATATAT 79980
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GAM3539 KIAA1615 3' TATATATATATATATATA 80053
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GAM3539 KIAA1681 3' TACATATATGTATACATATAT 80262 A
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GAM3539 KIAA1691 3' TATATATATATATATTATATAT 80263 —
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GAM3539 KIAA1726 3' TAATATATATATACTGTAACAC 80264 ATAT
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GAM3539 KIAA1856	3'	TATATATATATTTATATATAT	80265	A
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GAM3539 KIAA1866	3'	CATATATACATATATATAT	80266	
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		GTATATATGTATATATATA		
GAM3539 KIAA1972	3'	ATATATTTATATATATATATAT	80267	A
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GAM3539 MAN1	3'	TATATATATACATCTATATATA	80268	A III
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GAM3539 MCAM	3'	ATATATATATATTTTCATATAT	80271	III
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GAM3539 MCAM	3'	ATATATATATTTTCATATATAT	80269	III
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GAM3539 MCAM	3'	ATATATATATACATACATATAT	80270	
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GAM3539 MEGF11	3'	ATATATATATATATCAGCTATA	80273	ATA_
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GAM3539 MEGF11	3'	ATAAATATATATATATATAT	80272	T
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GAM3539 METAP1	3'	ACATATATATTTCCATATATAT	80274	ATA
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GAM3539	MGC10992	3' TATATATATATATAAAACAT	80275 TAT
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GAM3539	MGC29937	3' AATATATACATATATATAT	80276
		AATATATATATATATATAT	
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GAM3539	MGC9912	3' ACATATATATCTATATGTATAT	80277 A A
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GAM3539	MKP-7	3' AATATATATGTATGTACATATA	80278 A_____
		TATAT AATATATAT TATATATATATAT	
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		CATAC	
GAM3539	NFAT5	3' TATATATATGTATATATAT	80081 A
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GAM3539	NMT1	3' ATATATATATAATATATATATA	80279 _
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GAM3539	P66	3' AATATATCTTTATATATATATA	80280 A__
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GAM3539	PARG1	3' TATATATATATATATATAT	79980
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GAM3539	PCDH20	3' AATATATATATGTATGTATATA	80281 A A III
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		TTATATATATA ATA ATATATA T	
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GAM3539	PELI1	5' AATATATATATATATATGTAT	80282 A
		AATATATATATATATAT TAT	

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GAM3539	PLAC3	3' TAATATATATAATATATTTATA 80283	T	A
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GAM3539	PPP1R1A	3' CATATATATATATATAT 80114		
		TATATATATATATATATAT		
		GTATATATATATATATATA		
GAM3539	PRO0365	5' TATATATATACACGTATATAT 80284	TA	
		TATATATATATA TATATAT		
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GAM3539	PRO0365	5' TATATATATACACGTATAT 80286	TA	
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GAM3539	PRO0365	5' ATATATACACACGTATATAT 80285	TA	
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GAM3539	PRO0971	3' AATATATATATATATATAT 80108		
		AATATATATATATATATAT		
		TTATATATATATATATATA		
GAM3539	PRO2032	5' TACATATATATACTATATA 80287	A	
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GAM3539	RAI1	3' ATATGTATATGTATACATATAT 80290	A	A
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GAM3539	RAI1	3' ATATATATTATATATATGTATA 80288	—	A
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GAM3539	RAI1	3' TATATGTATACATATATAT 80289	A	
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GAM3539 RDC1 3' TATATATATTTATATATATAT 80005 A

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GAM3539 SCAMP5 3' ATATACATATATATATATATAT 80080

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GAM3539 SCYA11 3' TATATATATATATATATA 80053

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GAM3539 SCYA11 3' AATATATATATATATATAT 80108

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GAM3539 SDFR1 3' ATATATATATATATATTTATAT 80243 A

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GAM3539 SDFR1 3' ATAAATATATATATATATATAT 80291 T

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GAM3539 SDFR1 3' ATATATATATATATATTTATAT 80243 A

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GAM3539 SEMA3E 3' TACATATATATGTACATAT 80292 A

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GAM3539 SENP3 3' ATATATATATATATATATATAT 79978

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GAM3539 SENP3 3' TATATATATATATATATATAA 79967 ATIII
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GAM3539 SENP3 3' TATATATATATATATATA 80053
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GAM3539 SENP3 3' ATATATATATATATATATATAT 79978
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GAM3539 SENP3 3' TATATATATATATATATATATA 80003 III
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GAM3539 SENP3 3' ATATATATATATATATATATAT 79978
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GAM3539 SHARP 3' TATATATATTTATATATAT 80078 A
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GAM3539 SLK 3' ATATATGTATATATATTTATAT 80293 A A
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GAM3539	SLK	3'	TAATATGTATATATGTATATAT 80294	A A	III
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GAM3539	SNRK	3'	TATATATATATACACACAT 80295		
			TATATATATATATATATAT		
			ATATATATATATGTGTGTA		
GAM3539	SPIN	3'	TATATATGTATACACACATAT 80296	A	
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			ATATATA ATATGTGTGTATA		
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GAM3539	SPRY4	3'	CAATATATATTTATATATAT 80297	A	
			TAATATATAT TATATATAT		
			GTTATATATA ATATATATA		
			A		
GAM3539	STRIN	3'	CATACACACATATGTGTATATA 80298	A__	
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			GTATGTGTGTATA ATATATA		
			CAC		
GAM3539	TIMM10	3'	ATATATATATATATATATATAT 79978		
			ATATATATATATATATATATAT		
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GAM3539	TIMM10	3'	ATATATATATATATATATATAT 79978		
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GAM3539	TIMM10	3'	ATATATATATATATATATATAT 79978		
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GAM3539	TIMM10	3'	ATATATATATATATATACACAT 80299		
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GAM3539	TIMM10	3'	TATATATATATATATATATATA	80003	III
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GAM3539	TIMM10	3'	ATATATATATATATATATATAT	79978	
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GAM3539	TIMM10	3'	ATATATATATATATATATATAT	79978	
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GAM3539	TRIM2	3'	TATATATATATATATATA	80053	
			TATATATATATATATATA		
			ATATATATATATATATAT		
GAM3539	TRIM2	3'	TATATATATATATATATAT	79980	
			TATATATATATATATATAT		
			ATATATATATATATATATA		
GAM3539	TSPAN-2	3'	TATATACATACATGTATATAT	80301	A
			TATATATATATAT TATATAT		
			ATATATGTATGTA ATATATA		
			C		
GAM3539	TSPAN-2	3'	ACAGATATATATATATATATAT	80300	T
			ATA ATATATATATATATATAT		
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			C		
GAM3539	ZDHHC5	3'	ATATATATATATATATTATAT	80303	—
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			A		
GAM3539	ZDHHC5	3'	TAATATATATATATATATAT	80302	
			TAATATATATATATATATAT		
			ATTATATATATATATATATA		
GAM3539	ZF	3'	ATATATATATATGTATATATAT	80015	A
			ATATATATATAT TATATATAT		

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GAM3539	ZF	3' ATATATATATATATGTATATAT 79990	A	
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GAM3539	ZF	3' TATATATATATATATAT 79980		
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GAM3539	ZF	3' ATATATATGTATATATATATAT 79999	A	
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GAM3539	ZF	3' TATATATATATATATATAT 79980		
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GAM3539	ZF	3' ATATATATATGTATATATATAT 79998	A	
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GAM3539	ZF	3' ATATATATATATATATGTATAT 79991	A	
		ATATATATATATATAT TATAT		
		TATATATATATATATA ATATA		
		C		
GAM3539	ZNF238	3' ATATATATGTATATATATATAT 79999	A	
		ATATATAT TATATATATATAT		
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GAM3539	ZNF238	3' ATATATATATATATTATTTATA 80304		III
		TATATA ATATATATA TATATATAT	A	
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GAM3539	ZNF238	3' ATATATGTATATATATATATAT 80000	A	
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GAM3539	ZNF238	3' TATATATATGTATATATATATA 80021	A	III
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GAM3539	ZNF238	3'	ATATATATATATTATTTATATA 80305	_____
			TATAT ATATATATATA TATATATATAT	
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GAM3539	ZNF384	3'	TATATATATATATTTATATAT 80307	A
			TATATATATATAT TATATAT	
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			A	
GAM3539	ZNF384	3'	TAATATATTTATATATATATAT 80306	A
			TAATATAT TATATATATATAT	
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GAM3539	ZYG	3'	AATATATATATATAATATATAT 80308	—
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GAM3539	ZYG	3'	ATATATATATAATATATATATA 80279	—
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GAM3539	LOC113251	3'	ATATATATATATATATTTATAT 80243	A
			ATATATATATATATAT TATAT	
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			A	
GAM3539	LOC124801	3'	TAATATATATTTTCATATATAT 80309	ATA
	AT		TAATATATAT TATATATATAT	
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			AAA	
GAM3539	LOC125434	3'	ATATATATATATATTTATATAT 79976	A
			ATATATATATATAT TATATAT	
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			A	
GAM3539	LOC145474	5'	TACATAAATTATATATATATAT 80310	TA_
			TATATA TATATATATATAT	
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GAM3539	LOC145868	5'	AATATATATATGTATATATATA 80316	A III
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GAM3539	LOC145868 5'	ATATATATGTATATATATATAT 79999	A
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GAM3539	LOC145868 5'	ATATATATATATATAGTATATA 80313	—
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GAM3539	LOC145868 5'	ATATATATATATATATAGTATA 80314	—
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GAM3539	LOC145868 5'	ATATGTATATATATATATATAT 79996	A
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GAM3539	LOC145868 5'	TAATATATATAACATTTATATA 80315	T A
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GAM3539	LOC145868 5'	TAACATATATAACATTTATATA 80312	T A
	T	TAATATATATA ATAT TATATAT	
		ATTGTATATAT TGTA ATATATA	
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GAM3539	LOC145868 5'	TAATACATAACATTTATATATA 80311	T A
	T	TAATATATA ATAT TATATATAT	
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GAM3539	LOC145868 5'	TAACATATATAACATTTATATA 80312	T A
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GAM3539	LOC145868 5'	ATATATGTATATATATATATAT 80000	A
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GAM3539	LOC145868 5'	TATATATATATATATATAT 79980	
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GAM3539 LOC146176 5' AATATATATATTATATATAT 80317 A
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GAM3539 LOC146909 3' TATATATCTATATATATAT 80159 A
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GAM3539 LOC148195 5' TATATATATGTATACATAC 80319 A
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GAM3539 LOC148195 5' ATATACGTATATATATATATAT 80001 TA
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GAM3539 LOC148195 5' TATATACGTATATATATATAT 80318 TA
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GAM3539 LOC148195 5' TATATACGTATATATATAT 80323 TA
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GAM3539 LOC148195 5' TATATACATACATATGTATAT 80322 A
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GAM3539 LOC148195 5' AATATATATGTGTATATATATA 80320 ATA III
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GAM3539 LOC148195 5' TATATATATATGTATACAT 80321 A
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GAM3539 LOC149267 3' TATATATATATATATATA 80053
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GAM3539 LOC149267 3' TATATATATATATATAT 79980
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GAM3539 LOC151273 3' TATATATGCATATATATAT 80325 A
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GAM3539 LOC151273 3' TATATATGCATATATATATAT 80324 A
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GAM3539 LOC151521 3' CATAAATATATATATATATAT 80327 T
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GAM3539 LOC151521 3' ATATATATATATATAATAT 80326 T
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GAM3539 LOC153196 5' ATATACACATTATATATATATA 80332 —
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GAM3539 LOC153196 5' AATATATATATATACACAT 80331
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GAM3539 LOC153196 5' ATATATATATATATATATATAT 79978
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GAM3539 LOC153196 5' ATATATACACATTATATATATA 80330 —
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GAM3539 LOC153196 5'	AATATATATATATACACAT 80331	
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GAM3539 LOC153196 5'	TATATATATATATATATATATA 80003	III
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GAM3539 LOC153222 3'	ATATATATATATATATATATAT 79978	
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GAM3539 LOC153222 3'	ATATATATATATTTTATATATAT 80167	A
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	A	
GAM3539 LOC153222 3'	ATATATATATATATTTTATATAT 79976	A
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GAM3539 LOC153222 3'	TATATATATATATATATAT 79980	
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GAM3539 LOC153222 3'	TATATATATATATATATATAT 79979	
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GAM3539 LOC153387 5' ATATATATATATGTGTATATAT 80342 A__
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GAM3539 LOC153387 5' ATATATATATATATATATAT 79973
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GAM3539 LOC153387 5' ATATATATATATATATAT 80072
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GAM3539 LOC153387 5' ATATATATGTATATACATATAT 80334 A
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GAM3539 LOC153387 5' TATATGTATATACATATAT 80336 A
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GAM3539 LOC153387 5' TATATATATATATATATATATA 80003 III
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GAM3539 LOC153387 5' TATATATATATATATAT 79980
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GAM3539 LOC153387 5' ATATATATATGTGTATATATAT 80343 A__
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GAM3539 LOC153387 5' ATATATATGCACATATATATAT 80338 A
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GAM3539 LOC153387 5' ATATATATGCACATATATATAT 80341 A III
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GAM3539 LOC153387 5' ATATATGTATATACATATAT 80337 A
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GAM3539 LOC153387 5' ATATATATGTATATACATATAT 80334 A
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GAM3539 LOC153387 5' TATATACATATATGTATATAT 80340 A
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GAM3539 LOC153387 5' TATATATATATATATATATAT 79979
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GAM3539 LOC153387 5' ATATATATATATATGTGTATAT 80335 A__
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GAM3539 LOC153387 5' ATATATATATATATATATATAT 79978
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GAM3539 LOC153387 5' ATATATATATATATATATAT 79973
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GAM3539 LOC153387 5' ATATACATATATGTATATATAT 80339 A
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GAM3539 LOC153387 5'	ATATATATGCACATATATATAT 80338	A	
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GAM3539 LOC153396 3'	TAATATATAATATATATACA 80344	T	
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GAM3539 LOC153454 3'	TATATATATGTATATATACA 80249	A	
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GAM3539 LOC153454 3'	CATATATATATATGTGTATATA 80345	A__	III
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GAM3539 LOC153454 3'	ACACGTATATATATGTATATAT 80346	TA	A
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GAM3539 LOC153454 3'	ATATATGTGTATATATACATAT 80347	A__	
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GAM3539 LOC153727 5'	ATATATACCCATATATATATAT 80348	A	
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GAM3539 LOC157285 3'	TATATATATATTTATATAT 80020	A
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GAM3539 LOC158160 3'	ACATATATATTAAATATATATA 80349	AT_
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GAM3539 LOC158629 5'	ATATATATATATATGTATAT 80350	A
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GAM3539 LOC158629 5'	ATATATATATGTATATGTATAT 80351	A A
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GAM3539 LOC158629 5'	TATATATATATATATATATAT 79979	
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GAM3539 LOC161742 3' ATATATATATATATATAT 80072
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GAM3539 LOC168667 3' TATATATATATACACATATAT 80352
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GAM3539 LOC196411 3' TATATATGTATACATATAT 80353 A
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GAM3539 LOC196411 3' ATATATATATGTATACATATAT 80359 A
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GAM3539 LOC196411 3' TATATATGTATACATATAT 80353 A
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GAM3539 LOC196411 3' TATATATGTATACATATAT 80353 A
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GAM3539 LOC196411 3' ATATATATGTATACATATAT 80357 A
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GAM3539 LOC196411 3' ATATATATGTGTATATATATAT 80358 A__
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GAM3539 LOC196411 3' ATACATACATATATGTGTATAT 80354 A__ III
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GAM3539 LOC196411 3' TATATATGTATACATATAT 80353 A
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GAM3539 LOC196411 3'	TATATATGTATACATATAT 80353	A	
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GAM3539 LOC196411 3'	ATACATATATATGTGTATATAT 80356	_____	III
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GAM3539 LOC196411 3'	TATATATGTATACATATAT 80353	A	
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GAM3539 LOC196411 3'	ATATATGTGTATATATATATAT 80355	A__	
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GAM3539 LOC196411 3'	TATATATGTATACATATAT 80353	A	
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GAM3539 LOC196411 3'	TATATATGTATACATATAT 80353	A	
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GAM3539 LOC196989 3'	AATATATATATATATATATATA 80360		III
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GAM3539 LOC196989 3'	ATATATATATATATATATATAT 79978		
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GAM3539 LOC199907 3' ATATATATATATATGGAGATAT 80361 _____ III
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GAM3539 LOC201626 3' TATATATATATTACATATAT 80362 A
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GAM3539 LOC203078 3' ATATGTATATATATATATATAT 79996 A
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GAM3539 LOC203078 3' ATATATGTATATATATATATAT 80000 A
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GAM3539 LOC203078 3' ATATATATGTATATATATATAT 79999 A
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GAM3539 LOC203078 3' TATATATATGTATATATATATA 80021 A III
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GAM3539 LOC220477 5' TAATATATATTTATATATAT 80006 A
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GAM3539 LOC221087 3' ATATATATATATGTACACACAT 80363 A
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GAM3539	LOC221312 3'	ACATTTATATATGTATATATAT 80364	A	A
		ATAT TATATAT TATATATAT		
		TGTA ATATATA ATATATATA		
		A C		
GAM3539	LOC245806 3'	ATATGCATACATATATATATAT 80365	A	III
	A	ATAT TATATATATATATATAT A		
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GAM3539	LOC254228 3'	ATATATATATATATATATATAT 79978		
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GAM3539	LOC254228 3'	ATATATATATATATATATATAT 79978		
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GAM3539	LOC254228 3'	ATATATATATATATATATATAT 79978		
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GAM3539	LOC254228 3'	ATATATATATATATATATATAT 79978		
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GAM3539	LOC254228 3'	ATATATATATATATATATATAT 79978		
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GAM3539	LOC254228 3'	TATATATATATATATATATAT 79979		
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GAM3539	LOC254228 3'	ATATATATATATATATATATAT 79978		
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GAM3539 LOC254228 3' TATATATATATATATATAT 79980
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GAM3539 LOC254228 3' ATATATATATATATATATAT 79978
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GAM3539 LOC254228 3' ATATATATATATATATATAT 79978
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GAM3539 LOC254228 3' ATATATATATATATATATAT 79978
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GAM3539 LOC254228 3' ATATATATATATATATATAT 79978
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GAM3539 LOC255646 3' ATATATATATATATGGAGATAT 80361 _____ III
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GAM3539 LOC255647 3' ATATATATATATATGGAGATAT 80361 _____ III
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GAM3539	LOC255798 3'	ATATATATATTTATATATATAT 80367	A	
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		TATATATATA ATATATATATA		
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GAM3539	LOC255798 3'	ATATATATTTATATATATATAT 80366	A	
		ATATATAT TATATATATATAT		
		TATATATA ATATATATATATA		
		A		
GAM3539	LOC91907 3'	CAATATATTCATATATATAT 80368	A	
		TAATATAT TATATATATAT		
		GTTATATA GTATATATATA		
		A		
GAM3539	LOC92218 3'	ACATATATACACACATATAT 80369		
		ATATATATATATATATATAT		
		TGTATATATGTGTGTATATA		
GAM3540	ELAVL2 3'	TGACTTACAAAGACATTTACTA 80372	CGTAG TT__	
	A	TGAC GCG CATTTACTAA		
		ACTG TGT GTAAATGATT		
		AA__ TTCT		
GAM3540	LOC154222 3'	TGGCCGTAGGCTCACCC 80373	A GT	
		TG CCGTAGGC TCATTT		
		AC GGCATCCG AGTGGG		
		C _		
GAM3541	B4GALT4 5'	TATTACGTGAATAATATCTAT 80376	C A	
		TAT ATGTGAATAATAT CTGT		
		ATA TGCACCTTATTATA GATA		
		A _		
GAM3541	GJA1 3'	TGTGAGTTTATACTGTAT 80377	ATAA	
		TGTGA TATACTGTAT		
		ACACT ATATGACATA		
		CAA_		
GAM3541	KCNH5 3'	ATATGTATATACTGTA 80378	AATA	
		ATGTG ATATACTGTA		
		TATAC TATATGACAT		
		A__		
GAM3541	SORCS3 3'	ATATGTACATATACTGTA 80379	AATA	
		ATGTG ATATACTGTA		

		TATAC TATATGACAT		
		ATG_		
GAM3541	DKFZp566H0824	5' TGCAAACTAATATACTGT	80380	TG __
		TG AA TAATATACTGT		
		AC TT ATTATATGACA		
		GT TG		
GAM3541	FAM8A1	3' ATGTGAATATGCTGTAT	80381	ATATA
		ATGTGAATA CTGTAT		
		TACACTTAT GACATA		
		AC__		
GAM3541	FLJ23142	3' TGCAGAACTAATATACTGTAT	80382	_ _
		TGT GAAT AATATACTGTAT		
		ACG CTTG TTATATGACATA		
		T A		
GAM3541	KIAA0865	3' ATATGTCCCGTATACTGTAT	80383	AATAA
		ATGTG TATACTGTAT		
		TATAC ATATGACATA		
		AGGGC		
GAM3541	KIAA1223	3' ATGTAAATGTACTGTA	80384	AATA
		ATGTGAAT TACTGTA		
		TACATTTA ATGACAT		
		C__		
GAM3541	KRTAP17-1	3' TCATGTGAATAAGTAAAGTAT	80385	TATACT
		TCATGTGAATAA GTAT		
		AGTACACTTATT CATA		
		CATT_		
GAM3541	MGC10520	3' CATCGTGTGGATAATACA	80386	A A
		TATC TGTG ATAATATA		
		GTAG ACAC TATTATGT		
		C C		
GAM3541	LOC149301	3' TGTTGAATACACACTGTAT	80387	_ A
		TGT GAATA TATACTGTAT		
		ACA CTTAT GTGTGACATA		
		A _		
GAM3541	LOC158696	3' ATGTGTTATATACTGTA	80388	AATA
		ATGTG ATATACTGTA		
		TACAC TATATGACAT		
		AA__		
GAM3541	LOC201695	5' ATGTGAAGTGTGTACTGTAT	80389	TAATA
		ATGTGAA TACTGTAT		

			TACACTT	ATGACATA		
			CACAC			
GAM3542	DGKG	3'	TTGAAACAGAATGTA	80392	TATAC	
			TTGAAACAGA	ATGTA		
			AACTTTGTCT	TACAT		
GAM3542	PPP6C	3'	CTGGGACAGGTATACATA	80393	AA	A
			TTG ACAG	TATACATG		
			GAC TGTC	ATATGTAT		
			CC	C		
GAM3542	FLJ20666	5'	TTGAAGCAAATATACCCAGC	80394	A	AT_
			TTGAA CAGATATAC	GT		
			AACTT GTTTATATG	CG		
			C	GGT		
GAM3542	KIAA1695	3'	TTGAAACATGGTGTACATGTA	80395	GATA_	
			TTGAAACA	TACATGTA		
			AACTTTGT	ATGTACAT		
			ACCAC			
GAM3542	LOC155376	5'	TTGAAAAAAAACACATGTAAC	80396	C	T
			TTGAAA AGA	ATACATGTAAC		
			AACTTT TTT	TGTGTACATTG		
			_	T		
GAM3542	LOC222233	5'	TTGAAAAAAAACACATGTAAC	80396	C	T
			TTGAAA AGA	ATACATGTAAC		
			AACTTT TTT	TGTGTACATTG		
			_	T		
GAM3542	LOC253532	5'	TTGAAAAAAAACACATGTAAC	80396	C	T
			TTGAAA AGA	ATACATGTAAC		
			AACTTT TTT	TGTGTACATTG		
			_	T		
GAM3542	LOC254875	5'	TTGAAAAAAAACACATGTAAC	80396	C	T
			TTGAAA AGA	ATACATGTAAC		
			AACTTT TTT	TGTGTACATTG		
			_	T		
GAM3543	MLLT3	3'	AGGTGGCTATTTGGTCCCCCA	80399	A_	G TG
	G		AGGTGGTTATTTG	TC T G		
			TCCACCGATAAAC	GG G C		
			CAG	G GT		
GAM3543	PFN2	3'	AGATGGTTATGTTGGG	80400	TTGATC	
			AGGTGGTTAT	GTTGGG		

			TCTACCAATA	CAACCC		
GAM3543	PFN2	3'	AGATGGTTATGTTGGG	80400	TTGATC	
			AGGTGGTTAT	GTTGGG		
			TCTACCAATA	CAACCC		
GAM3543	FLJ10971	3'	AGGGGTTATTTTGGG	80401	T	GATCGT
			AGG GGTTATTT	TGGG		
			TCC CCAATAAA	ACCC		
GAM3543	MGC4638	3'	AGGTGGTTGTTGGGTTGGG	80402	AT	ATC
			AGGTGGTT TTG	GTTGGG		
			TCCACCAA AAC	CAACCC		
			C_ C_			
GAM3543	PRO1048	3'	AGGTGGTTGTTTATAGGA	80403	A	ATCGT
			AGGTGGTT TTTG	TGGGA		
			TCCACCAA AAAT	ATCCT		
			C			
GAM3543	LOC221876	5'	AGGAGGTGTCGTTGGG	80404	T	TATTT A
			AGG GGT	G TCGTTGGG		
			TCC CCA	C AGCAACCC		
			T			
GAM3544	PLAGL1	3'	TCTAAAAACATAAGACA	80407	T	T
			TCTA AAACATAAG	ATA		
			AGAT TTTGTATTC	TGT		
			T			
GAM3544	BANP	5'	TCCATAAACTATATATAAT	80408	ATAA	
			TCTATAAAC	GTATATAAT		
			AGGTATTTG	TATATATTA		
			A			
GAM3544	KIAA1579	3'	TCCATGGATATAAGTATACAAT	80409	AAAC	
	AA		TCTAT	ATAAGTATATAATAA		
			AGGTA	TATTCATATGTTATT		
			CCTA			
GAM3544	KIAA1755	3'	TCTCTAAACATAAAATACAAT	80410	A	T
			TCT TAAACATAAG	ATATAAT		
			AGA ATTTGTATTT	TATGTTA		
			G			
GAM3544	USP25	3'	TACAAACAGCATCATATAATA	80411	TAAG	
			TATAAACA	TATATAATA		

		ATGTTTGT GTATATTAT	
		CGTA	
GAM3545 BCL11A	3'	AACAAGGGGTTGGGGACTCA 80414	T A A A C
		AACA GG GG TTG GGAC CA	
		TTGT CC CC AAC CCTG GT	
		T _ _ C A	
GAM3545 BCL11A	3'	AACAAGGGGTTGGGGACTCA 80414	T A A A C
		AACA GG GG TTG GGAC CA	
		TTGT CC CC AAC CCTG GT	
		T _ _ C A	
GAM3545 COG6	3'	TGGTTGGATTTAGGACCCA 80415	A_ G
		TGG GGATT AGGACCCA	
		ACC CCTAA TCCTGGGT	
		AA A	
GAM3545 CPSF4	3'	TGATGTCGACTGCAGGGACCCA 80416	C GAG A__
C		A ATG GATTG GGACCCAC	
		A TAC CTGAC CCTGGGTG	
		C AG_ GTC	
GAM3545 FGF1	3'	CATGGAGGGACTCAGCC 80417	_ G GAC
		CATGGAGG ATT AG CC	
		GTACCTCC TGA TC GG	
		C G _	
GAM3545 FGF1	3'	CATGGAGGGACTCAGCC 80417	_ G GAC
		CATGGAGG ATT AG CC	
		GTACCTCC TGA TC GG	
		C G _	
GAM3545 FGF1	3'	CATGGAGGGACTCAGCC 80417	_ G GAC
		CATGGAGG ATT AG CC	
		GTACCTCC TGA TC GG	
		C G _	
GAM3545 GNGT2	3'	ATGGAGGGACAGGACCCAC 80418	ATTG
		ATGGAGG AGGACCCAC	
		TACCTCC TCCTGGGTG	
		CTG_	
GAM3545 KCNA7	3'	CAACATGGCCCTAGGGGACCCA 80419	AGGA A_
C		TAACATGG TTG GGACCCAC	
		GTTGTACC GAT CCTGGGTG	
		GG_ CC	
GAM3545 PAK4	3'	AACATGGGGGAGGGCC 80420	A ATT A
		AACATGG GG GAGG CC	

TTGTACC CC CTCC GG
 — — C
 GAM3545 PPP2CA 3' ATGCAGGAAGAACCCAC 80421 G TTG
 ATG AGGA AGGACCCAC
 ||| ||| |||||
 TAC TCCT TCTTGGGTG
 G —
 GAM3545 SLC21A9 3' CATGGAGGGCAGCCTGGCCCCAC 80422 ATTGA__ A
 CATGGAGG GG CCCAC
 ||||| || |||||
 GTACCTCC CC GGGTG
 CGTCGGA _
 GAM3545 ARNTL2 5' CATGGAGGAGCCCCGGGCC 80423 _ GA A
 CATGGAGGA TT GG CCC
 ||||| || || |||
 GTACCTCCT GG CC GGG
 C GG C
 GAM3545 C20orf27 3' TGGGGAGTGGGGGACCCAC 80424 A T A_
 TGG GGA TG GGACCCAC
 ||| ||| || |||||
 ACC CCT AC CCTGGGTG
 _ C CC
 GAM3545 DKFZP566K1924 3' ACATGGGAGGACCCA 80425 AGGATT
 ACATGG GAGGACCCA
 ||||| |||||
 TGTACC CTCCTGGGT
 —————
 GAM3545 FLJ12568 3' TAACATGGAAGGTACACC 80426 GGATTG _ _
 TAACATGGA AGG AC CC
 ||||| ||| || ||
 ATTGTACCT TCC TG GG
 ————— A T
 GAM3545 KIAA0478 3' CAGGAGGATTGCGTGAGCCC 80427 T AG_ _
 CA GGAGGATTG GA CCC
 || ||||| || |||
 GT CCTCCTAAC CT GGG
 _ GCA C
 GAM3545 KIAA1396 3' CATGGGGGTCAGGGACCCAC 80428 A A GA
 CATGG GG TT GGACCCAC
 |||| || || |||||
 GTACC CC AG CCTGGGTG
 _ C TC
 GAM3545 MGC10715 3' ACAGAAAATTGAGGATTCAC 80429 CC
 ATGGAGGATTGAGGA CAC
 ||||| ||||| |||
 TGTCTTTTAACTCCT GTG
 AA
 GAM3545 MGC16142 5' ACATGGAAGTAGGGCCTAC 80430 ATTG A C
 ACATGGAGG AGG CC AC
 ||||| ||| || ||

TGTACCTTC TCC GG TG
 A__ C A
 GAM3545 MGC27382 5' ACGTGGACAGACAGGACCCA 80431 A _ TG
 AC TGGG GGAT AGGACCCA
 || ||| ||| |||||
 TG ACCT TCTG TCCTGGGT
 C G _
 GAM3545 MMD 3' CAACATGAATGAGGACC 80432 GGAT
 TAACATGGA TGAGGACC
 ||||| |||||
 GTTGTACTT ACTCCTGG

 GAM3545 NPC1L1 3' ACTTGAAACTGGGGACCCAC 80433 A G A
 AC TGGAG ATTG GGACCCAC
 || ||| ||| |||||
 TG ACCTT TGAC CCTGGGTG
 A _ C
 GAM3545 SCYA16 3' TAACATGGGAGGTAGAGA 80434 _ ATT
 TAACATGG AGG GAGG
 ||||| ||| |||
 ATTGTACC TCC CTCT
 C AT_
 GAM3545 SH3GLB1 3' TAACATGGAAGATACTTAACC 80435 TGAG
 TAACATGGAGGAT GACC
 ||||| ||| |||
 ATTGTACCTTCTA TTGG
 TGAA
 GAM3545 TEX27 3' TAACATGGGGCAACCAGGCCCA 80436 A ATTG_ A
 C TAACATGG GG AGG CCCAC
 ||||| || ||| |||||
 ATTGTACC CC TCC GGGTG
 _ GTTGG _
 GAM3545 TIP120B 3' CATGGAAGATGCCCA 80437 T AGGA
 CATGGAGGAT G CCCA
 ||||| ||| |||
 GTACCTTCTA C GGGT

 GAM3545 LOC124460 3' ATGGGTAGGGGGGGGACCCAC 80438 _ ATTGA
 ATGG AGG GGACCCAC
 ||| ||| |||||
 TACC TCC CCTGGGTG
 CA CCC_
 GAM3545 LOC255004 3' TAACATGGTGACCTGGGCCTAC 80439 AG GA A C
 TAACATGG GATT GG CC AC
 ||||| ||| ||| |||
 ATTGTACC CTGG CC GG TG
 A_ AC _ A
 GAM3545 LOC90120 5' TGGGGACTCAGGACCCAC 80440 A G
 TGG GGATT AGGACCCAC
 ||| ||| |||||

ACC CCTGA TCCTGGGTG
 _ G
 GAM3545 LOC90288 3' GGAGGCCTTGGACCCAC 80441 A GA
 GGAGG TT GGACCCAC
 ||||| || |||||
 CCTCC GG CCTGGGTG
 _ AA
 GAM3546 BCL9 3' CGTCTTACGCATGGGAGGGGG 80444 CCATC _
 CGTC TGTGCG GGGAGGGGG
 ||| ||||| |||||
 GCAG ATGCGT CCCTCCCC
 A _ A
 GAM3546 DRIL1 5' GCCCCTGCGGGGAGGGG 80445 ATCTG
 GTCCC TCGGGGAGGGG
 |||| |||||
 CGGGG ACGCCCTCCCC
 _
 GAM3546 KLHL2 5' CGTTCCATCCGCCCCGGAGGGG 80446 C GCGG
 G CGT CCATCTGT GGAGGGGG
 || ||||| |||||
 GCA GGTAGGCG CCTCCCC
 A GGG_
 GAM3546 LPIN2 3' TCCCTTGCTGTGGGAGGGGG 80447 AT_ GC
 TCCC CTGT GGGGAGGGGG
 ||| ||| |||||
 AGGG GACA CCCCTCCCC
 AAC _
 GAM3546 MNT 3' GTCCAGGTGGGAGGGGG 80448 CATCT GC
 GTCC GT GGGGAGGGGG
 ||| || |||||
 CAGG CA CCCCTCCCC
 TC _ _
 GAM3546 PAX7 5' CGTCCAGAAGCTGGGAGGGGG 80449 CATCT GC
 CGTCC GT GGGGAGGGGG
 |||| || |||||
 GCAGG CG CCCCTCCCC
 TCTT_ A_
 GAM3546 PAX7 5' CGTCCAGAAGCTGGGAGGGGG 80449 CATCT GC
 CGTCC GT GGGGAGGGGG
 |||| || |||||
 GCAGG CG CCCCTCCCC
 TCTT_ A_
 GAM3546 PPP2R5B 5' GTCCGGCCTTTGGGGGGGGG 80450 CA G C A
 GTCC TCT TG GGGG GGGG
 ||| ||| || |||||
 CAGG GGA AC CCCC CCCC
 CC A _ _
 GAM3546 RABL2B 3' TCTGCCTGCGGGGAGGGGG 80451 _
 TCTGT GCGGGGAGGGGG
 |||| |||||

AGACG CGCCCCTCCCC
 GA
 GAM3546 AIG-1 3' GTCCTCATTGGGGGAGGGGG 80452 _ CTG C
 GTCC CAT TG GGGGAGGGGG
 ||| ||| || |||||
 CAGG GTA AC CCCCTCCCC
 A _ _
 GAM3546 AKAP6 3' TCATGCTTGGGGAGGGGG 80453 T _
 TC GTGC GGGGAGGGGG
 || ||| |||||
 AG TACG CCCCTCCCC
 _ AA
 GAM3546 C14orf4 5' GCCCAGGGCGTGGGGAGGGGG 80454 T TCT C
 G CCCA GTG GGGGAGGGGG
 | ||| ||| |||||
 C GGGT CGC CCCCTCCCC
 _ CC_ A
 GAM3546 C5orf3 3' GTGTCATCCTGGGGAGGGGG 80455 CC GTGC
 GT CATCT GGGGAGGGGG
 || ||| |||||
 CA GTAGG CCCCTCCCC
 CA A_
 GAM3546 DKFZp547A023 3' GTCTTATTTGGCAGAGGGGG 80456 CC C T A
 GTC AT TG GCGGGG GGGG
 ||| ||| |||||
 CAG TA AC CGTCTC CCCC
 AA A _ _
 GAM3546 FLJ10829 3' CCTCCCTGGCGGGGAGGGGG 80457 G ATC T
 C TCCC TG GCGGGGAGGGGG
 | ||| ||| |||||
 G AGGG AC CGCCCCTCCCC
 G _ _
 GAM3546 FLJ14768 3' CATTCCACAGTCGGGGAGGGGG 80458 C CT G
 CGT CCAT GT CGGGGAGGGGG
 ||| ||| ||| |||||
 GTA GGTG CA GCCCCTCCCC
 A T_ _
 GAM3546 FLJ20195 3' CGCCCCGTCGAGGGAGGGGG 80459 ATCT G _
 CGTCCC GT CG GGGAGGGG
 ||||| ||| |||||
 GCGGGG CA GC CCCTCCCC
 _ _ T
 GAM3546 GMEB2 3' CGCCTCGTCTGTGCGGCCCTG 80460 CCA GGAG_
 GG CGTC TCTGTGCGG GGG
 ||| ||||| |||
 GCGG AGACACGCC CCC
 AGC GGGGA
 GAM3546 HSPC195 5' CCCGAGGCGGGGAGGGGG 80461 T_
 TCTG GCGGGGAGGGGG
 ||| |||||

GGGC CGCCCCTCCCCC
TC
GAM3546 NOVA2 3' TCCGGGCTGGGGAGGGGG 80462 T _
TCTG GC GGGGAGGGGG
||||| || |||||
AGGC CG CCCCTCCCCC
C A
GAM3546 PTRF 3' TCCTGGAGGTGTGGGGAGGGGG 80463 CATCT C
TCC GTG GGGGAGGGGG
||| ||| |||||
AGG CAC CCCCTCCCCC
ACCTC A
GAM3546 RAB3IL1 3' TCTGGGGACTGGGGAGGGGG 80464 T__ _
TCTG GC GGGGAGGGGG
||||| || |||||
AGAC TG CCCCTCCCCC
CCC A
GAM3546 SLC2A11 5' TCTCATCTGTGCGTCCTGGG 80465 C GGGAG
TC CATCTGTGCG GGG
|| ||||| |||
AG GTAGACACGC CCC
A AGGA_
GAM3546 THTPA 3' GTCTCAACACGGGGGCGGGGAG 80466 C TC_ T__
GGGG GTC CA TG GCGGGGAGGGGG
||||| || |||||
CAG GT GC CGCCCCTCCCCC
A TGT CCC
GAM3546 LOC148696 5' GTCTCACGTTTGTGGGGAGGGGG 80467 C CTG C
G GTC CAT TG GGGGAGGGGG
||| ||| || |||||
CAG GTG AC CCCCTCCCCC
A CAA A
GAM3546 LOC152765 5' CTCCCCAAAGTGGGGAGGGGG 80468 GT TCT GC
C CCCA GT GGGGAGGGGG
| ||| || |||||
G GGGT CA CCCCTCCCCC
AG TT_ _
GAM3546 LOC197003 3' ATCTGTGGAAGGGGG 80469 GCG
ATCTGT GGGAGGGGG
||||| |||||
TAGACA CCTTCCCCC

GAM3547 APPBP2 3' AGTAACCTAACATTTCCAT 80472 ____
AGTAACCTAACA CCAT
||||||| |||
TCATTGGATTGT GGTA
AAA
GAM3547 CDY1 3' AAAGTAACCTAAATCTGCACA 80473 CAC__
AAAGTAACCTAA CATA
||||||| |||

		TTTCATTGGATT GTGT		
		TAGAC		
GAM3547	CDY1	3' AAAGTAACCTAAATCTGCACA 80473	CAC__	
		AAAGTAACCTAA CATA		
		TTTCATTGGATT GTGT		
		TAGAC		
GAM3547	RGS2	3' AGTTTTCAACACCATAGCACT 80474	AACC	A
		AGT TAACACCATA CACT		
		TCA GTTGTGGTAT GTGA		
		AAA_ C		
GAM3547	DKFZP761I2123	3' AGGAACCTGACACCACACAC 80475	T	A A
		AG AACCT ACACCATA CAC		
		TC TTGGA TGTGGTGT GTG		
		C C _		
GAM3547	EPSIN	5' AAGGAACCTAACAGCCCCACT 80476	T	_ ATAA
		AAG AACCTAACA CC CACT		
		TTC TTGGATTGT GG GTGA		
		C C G__		
GAM3547	KIAA1191	3' AAAGTAAGTTAACACCAC 80477	CC	
		AAAGTAA TAACACCAT		
		TTTCATT ATTGTGGTG		
		CA		
GAM3547	KIAA1486	5' GGAGTAATCCAGCACCAT 80478	A	C A
		A AGTAA CTA CACCAT		
		C TCATT GGT GTGGTA		
		C A C		
GAM3547	KIAA1546	3' AAATAACCTGCATTTCATAACA 80479	AACAC	
		AAGTAACCT CATAACA		
		TTTATTGGA GTATTGT		
		CGTAA		
GAM3547	KPNB3	3' AAATAACTTTAGCCATAACACT 80480	CTAACA	
		AAGTAAC CCATAACACT		
		TTTATTG GGTATTGTGA		
		AAATC_		
GAM3547	SDCCAG33	3' AGCTTAACACCAAAAACA 80481	AACC	T_
		AGT TAACACCA AACA		
		TCG ATTGTGGT TTGT		
		A__ TT		
GAM3547	LOC152245	3' AAAGTAATTTAAACCACAACAC 80482	CC	C
		AAAGTAA TAA ACCATAACACT		

T

		TTTCATT ATT TGGTGTGTGA		
		AA _		
GAM3547	LOC203611 3'	AAAGTAACCTAAATCTGCACA 80473		CAC__
		AAAGTAACCTAA CATA		
		TTTCATTGGATT GTGT		
		TAGAC		
GAM3547	LOC255465 5'	AAAGTGACCCAACATCAC 80483	A	C
		AAAGT ACCTAACA CAT		
		TTTCA TGGGTTGT GTG		
		C A		
GAM3547	LOC91291 5'	AAAGTAACTAACTGCCATA 80484	C	A_
		AAAGTAAC TAAC CCATA		
		TTTCATTG ATTG GGTAT		
		_ AC		
GAM3547	LOC93587 3'	GTAACCTACCATACAC 80485	AAC	A
		GTAACCT ACCATA CAC		
		CATTGGA TGGTAT GTG		
		— —		
GAM3548	ALDOB 3'	TTGGTTGCAGCTATCTCCTTC 80488	AA	CATTA
		TTGGTTGCA TATT CTTC		
		AACCAACGT ATAG GAAG		
		CG AG__		
GAM3548	SH3BP2 3'	TGGTTGCAGATCGTTTACTTC 80489	A	ATTCA
		TGGTTGCA AT TTA CTTC		
		ACCAACGT TA AATGAAG		
		C GCA__		
GAM3548	CARD6 3'	TTGGTTGTTAATTCATTATTTTC 80490	CAAAT	C
		TTGGTTG ATTCA TTA TTC		
		AACCAAC TAAGTAAT AAG		
		AAT__ A		
GAM3548	KIAA1332 3'	TTGGCTGCATAAACATTATTTTC 80491	AA TT	C
		TTGGTTGCA TA CATTA TTC		
		AACCGACGT AT GTAAT AAG		
		_ TT A		
GAM3548	LOC116437 3'	TTGGTTGCACCATGT TACTT 80492	AATATTCA	
		TTGGTTGCA T TACTT		
		AACCAACGT AATGAA		
		GGTAC__		
GAM3548	LOC222001 5'	TTGCTTGCAAATTACT 80493	G	ATTCAT
		TTG TTGCAAAT TACT		

		AAC AACGTTTA ATGA	
		G _____	
GAM3549	FLJ11021	3' TTAATGGAAGTGGGTTTA 80496	ATAG C
		TTAATGGAA GG GTTTG	
		AATTACCTT CC CAAAT	
		CA__ _	
GAM3549	KIAA1371	3' TTAATGAAGGTGGCACAATGTT 80497	AATAG TT_
		TTAATGGA GGCG TGTT	
		AATTACTT CCGT ACAA	
		CCA__ GTT	
GAM3549	PTRF	3' TTAGTAGAGATGGGGTGTTTG 80498	A A A C
		TTA TGGA AT GGG GTTTG	
		AAT ATCT TA CCC CAAAC	
		C C C A	
GAM3549	SMBP	3' TCAATGGAAATAGATGTT 80499	GC
		TTAATGGAAATAGG GTT	
		AGTTACCTTTATCT CAA	
		A_	
GAM3549	ZFD25	3' TTAATAGAGATGGGGTTT 80500	A A C
		TTAATGGA AT GGG GTTT	
		AATTATCT TA CCC CAAA	
		C _ _	
GAM3549	LOC122830	3' TTAATGGAGGTAGGGTTTTTA 80501	AA CG
		TTAATGGA TAGGG TTTG	
		AATTACCT ATCCC AAAT	
		CC AA	
GAM3549	LOC127003	3' TTAATGGAAGTGGGCCGCAGT 80502	ATA _ TT
		TTAATGGAA GGGC GT GT	
		AATTACCTT CCCG CG CA	
		CA_ G T_	
GAM3549	LOC93097	5' TTAATGGAAGGGTGTT 80503	AAT C
		TTAATGGA AGGG GTT	
		AATTACCT TCCC CAA	
		_ A	
GAM3550	ABCB4	5' CTTTCCCATGTACCAGCTGTCT 80506	CGT _ CA
		CTTTCCCA TGTAT GC TCT	
		GAAAGGGT ACATG CG AGA	
		_ GT AC	
GAM3550	ABCB4	5' CTTTCCCATGTACCAGCTGTCT 80506	CGT _ CA
		CTTTCCCA TGTAT GC TCT	

			GAAAGGGT ACATG CG AGA	
			___ GT AC	
GAM3550	BACH1	3'	TCTTTTATAATCAGTATGCCAT 80507	CCCACGTT
	CT		TCTTT GTATGCCATCT	
			AGAAA CATACGGTAGA	
			ATATTAGT	
GAM3550	GIPR	3'	TTCCCCACTCAGTTGTCATCT 80508	GTT A C
			TTTCCCAC GT TG CATCT	
			AAGGGGTG CA AC GTAGA	
			AGT _ A	
GAM3550	GTF2H1	3'	TCTTTTCAAAGCACATGCCATC 80509	CC CGTTG
	T		TCTTT CA TATGCCATCT	
			AGAAA GT GTACGGTAGA	
			A_ TTCGT	
GAM3550	IL1F5	3'	TCTTCCCCGCGTCTCCTCT 80510	A GTATG A
			TCTTTCCC CGTT CC TCT	
			AGAAGGGG GCAG GG AGA	
			C A___ _	
GAM3550	KL	3'	TCTCTCCTGTATCTGCCATCT 80511	CACGT _
			TCTTTCC TGTA TGCCATCT	
			AGAGAGG ACAT ACGGTAGA	
			___ AG	
GAM3550	PCDH9	5'	TTTCCCCACTGTCTTCATCT 80512	GT ATGC
			TTTCCCAC TGT CATCT	
			AAAGGGTG ACA GTAGA	
			_ GAA_	
GAM3550	C20orf150	3'	TCTGTCCCACACACCTGCCATC 80513	T TTGTA
	T		TCT TCCCACG TGCCATCT	
			AGA AGGGTGT ACGGTAGA	
			C GTGG_	
GAM3550	DKFZP434F1735	5'	TCTTTCCCATTCTCTACATCT 80514	CG GTA C
			TCTTTCCCA TT TGC ATCT	
			AGAAAGGGT AG ATG TAGA	
			AA AG_ _	
GAM3550	DKFZp566O084	3'	TCTTTCCCACCTTGTGAGACAAA 80515	G AT_ C_
	TCT		TCTTTCCCAC TTGT GC ATCT	
			AGAAAGGGTG AACA TG TAGA	
			_ CTC TT	
GAM3550	DMTF1	5'	TCTCTCCCATGTTCTATC 80516	C GTATG _
			TCTTTCCCA GTT CC ATC	

		AGAGAGGGT CAA GG TAG	
		A ____ A	
GAM3550	FLJ10648	3' TCCTTCCCGTGTGGAGCC 80517	AC TAT
		TCTTTCCC GTTG GCC	
		AGGAAGGG CAAC CGG	
		CA CT_	
GAM3550	FLJ12619	3' TCTTTCCCATGGTTGTAT 80518	C_
		TCTTTCCCA GTTGTAT	
		AGAAAGGGT CAACATA	
		AC	
GAM3550	H2BFB	3' TTTCAGACGTCCTGCCATCT 80519	CC GTA
		TTTC ACGTT TGCCATCT	
		AAAG TGCAG ACGGTAGA	
		TC G_	
GAM3550	KIAA0565	5' TCTTTTTCACGTTATGC 80520	CC TG
		TCTTT CACGT TATGC	
		AGAAA GTGCA ATACG	
		AA _	
GAM3550	KIAA1272	3' TCTTTTCCTGCTGTCATC 80521	C AC ATGC
		TCTTT CC GTTGT CATC	
		AGAAA GG CGACA GTAG	
		A A_ _	
GAM3550	KIAA1546	3' TCTTTTCCTAGATGCCATC 80522	C ACGT T
		TCTTT CC TG ATGCCATC	
		AGAAA GG AT TACGGTAG	
		A _ C	
GAM3550	PRO1598	3' TCTTTCCCACTGTGGTTGT 80523	_____
		TCTTTCCCAC GTTGT	
		AGAAAGGGTG CAACA	
		ACAC	
GAM3550	SPRY4	3' CTTTCCACGTGTGCCATC 80524	C TGTA
		CTTTCC ACGT TGCCATC	
		GAAAGG TGCA ACGGTAG	
		_ C_	
GAM3550	TIMM22	3' TCTTTCCCTTCAGATGTTATCT 80525	ACG GT CC
		TCTTTCCC TT ATG ATCT	
		AGAAAGGG AG TAC TAGA	
		A_ TC AA	
GAM3550	LOC112448	3' TCTTTCCCCTGTGTGAGTTATC 80526	AC T ATGCC
	T	TCTTTCCC GT GT ATCT	

		AGAAAGGG CA CA TAGA	
		GA _ CTCAA	
GAM3550	LOC143916 3'	TCTTTCCCAAGTTCAT 80527	C GTATGC
		TCTTTCCCA GTT CAT	
		AGAAAGGGT CAA GTA	
		— ———	
GAM3550	LOC145663 3'	TCTTTCCACCATGCCATC 80528	C GTTG
		TCTTTCC AC TATGCCATC	
		AGAAAGG TG GTACGGTAG	
		— ———	
GAM3550	LOC150622 3'	CTTTCCCATATGCCAT 80529	CGTTG
		CTTTCCCA TATGCCAT	
		GAAAGGGT ATACGGTA	
		—————	
GAM3550	LOC201287 5'	TCTTTTTCACGTTATGC 80520	CC TG
		TCTTT CACGT TATGC	
		AGAAA GTGCA ATACG	
		AA —	
GAM3550	LOC203504 5'	TCTCTCCTGTCTGCCATC 80530	CACGT A
		TCTTTCC TGT TGCCATC	
		AGAGAGG ACA ACGGTAG	
		————— G	
GAM3550	LOC256207 5'	TCTTTTTCACGTTATGC 80520	CC TG
		TCTTT CACGT TATGC	
		AGAAA GTGCA ATACG	
		AA —	
GAM3550	LOC91145 5'	TCTTTCCAGTCTATGCCAT 80531	CAC G
		TCTTTCC GTT TATGCCAT	
		AGAAAGG CAG ATACGGTA	
		T — —	
GAM3551	MAP3K7IP2 3'	TGACATGAGGGGAAAAAGGTA 80534	AAAAATA TT
		TGACGTGA GA AGGTA	
		ACTGTACT TT TCCAT	
		CCCC — TT	
GAM3551	MMP1 3'	TGACTGAGAAAATAGAC 80535	G A
		TGAC TGA AAAATAGAT	
		ACTG ACT TTTTATCTG	
		— C	
GAM3551	LOC144866 5'	TGATTGAAAAAGCACTAGGTA 80536	CG ATAG
		TGA TGAAAAA ATTAGGTA	

			ACT ACTTTTT TGATCCAT			
			A_ CG__			
GAM3552	NR2E3	3'	TGAGGTCACCTGCCGGTTGTC	80539	AC	TCC C
			TGA TCATTGCC GG TGTC			
			ACT AGTGACGG CC ACAG			
			CC ____ A			
GAM3552	PML	3'	TGGA CTCACTGCTGCTGT	80540	A	CTCCG
			TG ACTCATTGC GCTGT			
			AC TGAGTGACG CGACA			
			C A____			
GAM3552	SIP	3'	GAATTCATTGCCTTTACT	80541	C	CCG
			GAA TCATTGCCT GCT			
			CTT AGTAACGGA TGA			
			A AA_			
GAM3552	TMEM2	3'	TGTACTCATTGCCAGTGT	80542	A	TCC C
			TG ACTCATTGCC GG TGT			
			AC TGAGTAACGG TC ACA			
			A ____ _			
GAM3552	CHDH	3'	TCACTGCCCAGTACTTGTC	80543	CCG	_
			TCATTGCCT GCT GTC			
			AGTGACGGG TGA CAG			
			TCA A			
GAM3552	FLJ14103	5'	TGGGCTCCAGCTGCAGCCTCTG	80544	ATT_____	C
			GCTGTGC TC GCCTC GGCTGTC		G	
			AG CGGAG CCGACAG C			
			GTCGACGT A			
GAM3552	KIAA1046	3'	TGAACTCATGTCCAAAATGTC	80545	TGCC	C_
			TGAACTCAT TCCGG TGTC			
			ACTTGAGTA AGGTT ACAG			
			C____ TT			
GAM3552	SCYA14	5'	TGGGCTCACTGCTTCCTGGCT	80546	AA	C _
			TG CTCATTGC TCC GGCT			
			AC GAGTGACG AGG CCGA			
			CC A A			
GAM3552	SCYA14	5'	TGGGCTCACTGCTTCCTGGCT	80546	AA	C _
			TG CTCATTGC TCC GGCT			
			AC GAGTGACG AGG CCGA			
			CC A A			
GAM3552	SCYA15	5'	TGGGCTCACTGCTTCCTGGCT	80546	AA	C _
			TG CTCATTGC TCC GGCT			

		AC GAGTGACG AGG CCGA		
		CC A A		
GAM3552	SCYA23	5' TGGGCTCACTGCTTCCTGGCT	80546	AA C _
		TG CTCATTGC TCC GGCT		
		AC GAGTGACG AGG CCGA		
		CC A A		
GAM3552	TXNL2	3' TGAACATCATGGCTTCTGA	80547	T C C
		TGAACATCAT GC TC GG		
		ACTTGAGTA CG AG CT		
		C A A		
GAM3552	WIT-1	5' ACTGCCTCTCCTTCGGCTGTC	80548	_____
		ATTGCCTC CGGCTGTC		
		TGACGGAG GCCGACAG		
		AGGAA		
GAM3552	ZFP95	3' TGAACATCATGAAGCTGT	80549	TGCCTCC
		TGAACATCAT GGCTGT		
		ACTTGAGTA TCGACA		
		CT_____		
GAM3552	ZFP95	3' TGAACATCATGAAGCTGT	80549	TGCCTCC
		TGAACATCAT GGCTGT		
		ACTTGAGTA TCGACA		
		CT_____		
GAM3552	LOC134957	3' TGACTTATTGCCTCTGC	80550	A C CG
		TGA CT ATTGCCTC GC		
		ACT GA TAACGGAG CG		
		_ A A_		
GAM3552	LOC145371	3' TGGACTCCAGCCCTGGCTGT	80551	A ATT CC
		TG ACTC GCCT GGCTGT		
		AC TGAG CGGG CCGACA		
		C GT_ A_		
GAM3552	LOC151176	3' TCAGCAGGCCCGGCTGTC	80552	TT C__
		TCA GC TCCGGCTGTC		
		AGT CG GGGCCGACAG		
		_ TCC		
GAM3552	LOC152897	3' TGGACTCATTAGTCTCTGCT	80553	A C_ CG
		TG ACTCATTG CTC GCT		
		AC TGAGTAAT GAG CGA		
		C CA A_		
GAM3552	LOC153338	3' GAACTCATTGCTGCCCTGTC	80554	CT GG
		GAACTCATTGC CC CTGTC		

		CTTGAGTAACG GG GACAG		
		AC _		
GAM3552	LOC201689	3' TCACTGCCAGTACTTGTC	80543	CCG _
		TCATTGCCT GCT GTC		
		AGTGACGGG TGA CAG		
		TCA A		
GAM3553	MYH13	5' TTCCCAAGTGACAGTCAG	80557	ACGAG TA
		TTCCCGA GACA GTCAG		
		AAGGGTT CTGT CAGTC		
		CA_ _		
GAM3553	NFATC1	3' CTCCTGGGCGAGGACACGTCGG	80558	CGAA A A
	C	TTCC CGAGGACAT GTC GC		
		GAGG GCTCCTGTG CAG CG		
		ACCC _ C		
GAM3553	PRLR	5' TTCCTGCACGAGGACATGAAGC	80559	CGA AGTC
		TTCC ACGAGGACAT AGC		
		AAGG TGCTCCTGTA TCG		
		ACG CT_		
GAM3553	TACR1	3' TTCCTGGATGGTGATAATCAGC	80560	CGAAC _ AC
		TTCC GA GG ATAGTCAGC		
		AAGG CT CC TATTAGTCG		
		AC_ A AC		
GAM3553	FLJ13725	5' TTCCCGAAGTGAGGGTGTGTC	80561	C_ ACATA
		TTCCCGAA GAGG GTC		
		AAGGGCTT CTCC CAG		
		CA CACA_		
GAM3553	NUDE1	3' TTCTCCAACGAGGAGACA	80562	_ G C
		TTC CC AACGAGGA ATA		
		AAG GG TTGCTCCT TGT		
		A _ C		
GAM3553	NUDT9	5' TTCCCGAACGGGAGTAGC	80563	A CA
		TTCCCGAACG GGA TAGT		
		AAGGGCTTGC CCT ATCG		
		_ C_		
GAM3553	LOC135043	3' CTCCGGATGAGGACACCCAGC	80564	C AC AG
		TTCC GA GAGGACAT TCAGC		
		GAGG CT CTCCTGTG GGTCG		
		C A_ _		
GAM3554	CAPN5	3' TTAGCAGTGGTGACAGTT	80567	AATAA
		TTAGTAGT GATAGTT		

AATCGTCA CTGTCAA
 CCA__
 GAM3554 CYB5 3' TAGTAGTGATAAGAGTTT 80568 A TA
 TAGTAGT ATAAGA GTTT
 ||||| ||||| ||||
 ATCATCA TATTCT CAAA
 C _
 GAM3554 VPS26 3' TAGTAGTAAAACAGGTTTAAA 80569 TAA _
 TAGTAGTAA GATAG TTTAAA
 ||||| ||||| |||||
 ATCATCATT TTGTC AAATTT
 _ C
 GAM3554 ARTS-1 3' AGTCAATAAGATAGTTTAA 80570 _
 AGT AATAAGATAGTTTAA
 || ||||| |||||
 TCA TTATTCTATCAAATT
 G
 GAM3554 KIAA0268 3' GTGACCAGATAGTTTAAA 80571 A A
 GT AT AGATAGTTTAAA
 || || ||||| |||||
 CA TG TCTATCAAATTT
 C G
 GAM3554 LATS1 3' TTAGCAGCATCAGATGGTTTA 80572 ATA A
 TTAGTAGTA AGAT GTTTA
 ||||| ||||| |||||
 AATCGTCGT TCTA CAAAT
 AG_ C
 GAM3554 LOC153606 5' TAGTACTAAATAGTTTAA 80573 ATA
 TAGTA AGATAGTTTAA
 ||||| ||||| |||||
 ATCAT TTTATCAAATT
 GA_
 GAM3555 RSP3 5' TTTGCAGGGCTGGTGTGGCG 80576 CCAGT GAC_ _
 TTTGCAGG GC GTTG CG
 ||||| || |||||
 AAACGTCC CG CAAC GC
 _ ACCA C
 GAM3555 LOC91035 5' TTTGCAGGCCAGGTGGGCGCAA 80577 T_____ ACGT
 CGTCG GCAGGCCAG GCG TG
 ||||| ||||| |||||
 CGTCCGGTC CGT GC
 CACCCIIIG TGCA
 GAM3556 KIAA0442 3' ATTTTATTTTCATACATATATTT 80580 TT_
 TA ATTTTATTTTAT TATATTTTA
 ||||| ||||| |||||
 TAAAATAAAGTA ATATAAAAT
 TGT
 GAM3556 PAPPA 5' TATTTTCATTTTATTTTATA 80581
 TATTTTATTTTATTTTATA
 ||||| ||||| |||||

ATAAAGTAAAATAAAATAT

GAM3556 PCDHB9 3' TTTTAAGTTATTTTATATTTTA 80582 TT
TTTTA TTATTTTATATTTTA
||||| |||||||||
AAAAT AATAAAATATAAAAT
TC

GAM3556 PCDHB9 3' TATTTTATTTTATTTTAT 80583
TATTTTATTTTATTTTAT
||||| |||||||||
ATAAAATAAAATAAAATA

GAM3556 PLA2G2D 3' TATTTTATTTTATTTTATTTT 80584 A
T TATTTTATTTTATTTTAT TTTT
||||| ||||||||| |||
ATAAAATAAAATAAAATA AAAA
A

GAM3556 PLA2G2D 3' TATTTTATTTTATTTTAT 80583
TATTTTATTTTATTTTAT
||||| |||||||||
ATAAAATAAAATAAAATA

GAM3556 PLA2G2D 3' TATTTTATTTTATTTTAT 80583
TATTTTATTTTATTTTAT
||||| |||||||||
ATAAAATAAAATAAAATA

GAM3556 PLA2G2D 3' TATTTTATTTTATTTTAT 80583
TATTTTATTTTATTTTAT
||||| |||||||||
ATAAAATAAAATAAAATA

GAM3556 PLA2G2D 3' TATTTTATTTTATTTTAT 80583
TATTTTATTTTATTTTAT
||||| |||||||||
ATAAAATAAAATAAAATA

GAM3556 ALS2CR3 3' TTTTATTTTATTTTACATT 80585
TTTTATTTTATTTTATATT
||||| |||||||||
AAAATAAAATAAAATGTAA

GAM3556 FLJ10989 3' TATTTTATTTTATTTATTTATT 80586 TA_
TT TATTTTATTTTATTT TATTTT
||||| ||||||||| |||
ATAAAATAAAATAAA ATAAAA
TAA

GAM3556 FLJ10989 3' CATTTTATTTTATTTTAT 80587
TATTTTATTTTATTTTAT
||||| |||||||||

GTAAAATAAAATAAAATA

GAM3556 KALI 3' TATTTTCATTTTATTTTAT 80588
TATTTTATTTTATTTTAT
|||||||
ATAAAGTAAAATAAAATA

GAM3556 VEGFC 3' CATTTTATTTTAAACATATTTT 80589 TTT
TATTTTATTTTA TATATTTT
||||||| |||||
GTAAAATAAAAT GTATAAAA
TT_

GAM3556 ZIM3 3' TATTTTATTTTATCTTAT 80590
TATTTTATTTTATTTTAT
|||||||
ATAAATAAAATAGAATA

GAM3556 LOC134266 3' ATTTTATTTTATTTTATA 80591
ATTTTATTTTATTTTATA
|||||||
TAAAATAAAATAAAATAT

GAM3557 CCND2 3' GGATGTAAGAGTTGGCCAG 80594 T AGA
GGATGTAAGA TT TCGG
||||||| || |||
CCTACATTCT AA GGTC
C CC_

GAM3557 KNSL1 3' AGGGTTAAGATTTGAATCGA 80595 ATG AG
AGG TAAGATTT ATCGG
||| ||||| |||||
TCC ATTCTAAA TAGCT
CA_ CT

GAM3557 CLDN15 3' AGGATGTAAGCTCCCGGA 80596 ATTTAGA
AGGATGTAAG TCGGA
||||||| |||||
TCCTACATTC GGCCT
GAG_

GAM3557 KIAA1819 3' AGGTGTAAGATTTAAACAA 80597 A T
AGG TGTAAGATTTAGA CGG
||| ||||| ||||| |||
TCC ACATTCTAAATTT GTT
_ T

GAM3557 PSMD10 3' GGATATAAGGTACATGGGA 80598 ATT G C
GGATGTAAG TA AT GGA
||||||| || |||
CCTATATTC AT TA CCT
C_ G C

GAM3557 TCL6 5' GGATGCAAGATGCACGTGGAAG 80599 TTAGATC
GGATGTAAGAT GGAAG
||||||| |||||

			CCTACGTTCTA	CCTTC	
			CGTGCA_		
GAM3557	TCL6	5'	GGATGCAAGATGCACGTGGAAG	80599	TTAGATC
			GGATGTAAGAT	GGAAG	
			CCTACGTTCTA	CCTTC	
			CGTGCA_		
GAM3557	TCL6	5'	GGATGCAAGATGCACGTGGAAG	80599	TTAGATC
			GGATGTAAGAT	GGAAG	
			CCTACGTTCTA	CCTTC	
			CGTGCA_		
GAM3557	TCL6	5'	GGATGCAAGATGCACGTGGAAG	80599	TTAGATC
			GGATGTAAGAT	GGAAG	
			CCTACGTTCTA	CCTTC	
			CGTGCA_		
GAM3557	ZIM2	3'	AAGATGTAAGATTTACAG	80600	GAT
			AGGATGTAAGATTTA	CGG	
			TTCTACATTCTAAAT	GTC	
GAM3557	LOC145231	3'	AGGAGGTAAGATTAATGGAAG	80601	T TA C
			AGGA GTAAGATT GAT GGAAG		
			TCCT CATTCTAA TTA CCTTC		
			C		
GAM3557	LOC255098	5'	GGCATGTGAGATTTACATCAGA	80602	_ A G
	AG		GG ATGT AGATTTA ATCGGAAG		
			CC TACA TCTAAAT TAGTCTTC		
			G C G		
GAM3558	CLOCK	5'	AGGTATCTAGTGAGACTTGC	80605	CAGA AATA
			AGGT AGT AGACTTGC		
			TCCA TCA TCTGAACG		
			TAGA C_		
GAM3558	C9orf14	5'	TAGATCAGGAGGACTT	80606	A TAATAA
			TAGGTCAG AG GACTT		
			ATCTAGTC TC CTGAA		
			C		
GAM3558	MAGE-E1	3'	CAGGTCAGGAGCTCGACTTG	80607	A AATAA
			TAGGTCAG AGT GACTTG		
			GTCCAGTC TCG CTGAAC		
			C AG_		
GAM3558	OSMR	3'	TAAGTCAGAAAGTTACTTG	80608	AATAAG
			TAGGTCAGAAAGT ACTTG		

ATTCAGTCTTCA TGAAC
 A____
 GAM3558 UXS1 5' GGTCAGAAGTAATCCCTTGC 80609 AAGA
 GGTCAGAAGTAAT CTTGC
 ||||| ||||
 CCAGTCTTCATTA GAACG
 GG__
 GAM3558 LOC134111 3' GTCCAATAAGACTTG 80610 AGAAG
 GTC TAATAAGACTTG
 || |||||
 CAG GTTATTCTGAAC

 GAM3558 LOC144363 3' AGGTCAGAAGTAATGAC 80611 AA
 AGGTCAGAAGTAAT GAC
 ||||| ||
 TCCAGTCTTCATTA CTG

 GAM3558 LOC148195 5' TAGGTCAGAAGTGATTAAACAG 80612 A A TT
 C TAGGTCAGAAGT AT AGAC GC
 ||||| || |||| ||
 ATCCAGTCTTCA TA TTTG CG
 C A T_
 GAM3558 LOC91548 3' TAGGTCAGGGGTCGATCTG 80613 AA AATAA C
 TAGGTCAG GT GA TTG
 ||||| || ||||
 ATCCAGTC CA CT GAC
 CC G__ A
 GAM3559 ADCY8 5' GGCCGGCGGGCGCCCCGGCCT 80616 _ A
 TC GGCCGGCGGGCGCCTC GG CTTC
 ||||| || ||||
 CCGGCCGCCCGCGGGG CC GAAG
 G G
 GAM3559 DMPK 3' AGGCGGTGGGCGCGGCTT 80617 C C CTC A
 AGGC GG GGGCGC GG CTT
 ||| || |||| || ||
 TCCG CC CCCGCG CC GAA
 _ A _ _
 GAM3559 IL11 3' AGGCCGGTCTCAAACCTTTGGA 80618 _ GC C
 CTTC AGGCCGG CGGGC CT GGACTTC
 ||||| |||| || |||||
 TCCGGCC GTTTG GA CCTGAAG
 AGA A_ A
 GAM3559 MEN1 5' GGCGGTGGGCGGCGGCGGCTTC 80619 C C _CT A
 GGC GG GGGCG C CGG CTTC
 ||| || |||| | || ||||
 CCG CC CCCGC G GCC GAAG
 _ A C CC _
 GAM3559 MUCDHL 3' AGGTCGGCGGGCACCACG 80620 C T
 AGG CGGCGGGCGCC CG
 ||| ||||| ||

TCC GCCGCCCGTGG GC
 A T
 GAM3559 MUCDHL 3' AGGTCGGCGGGCACCACG 80620 C T
 AGG CGGCGGGCGCC CG
 ||| ||||| ||
 TCC GCCGCCCGTGG GC
 A T
 GAM3559 NEUROD2 5' AGGCGGCGGGCGCCGGCGTCTT 80621 C T_ GA
 C AGGC GGCGGGCGCC CG CTTC
 ||| ||||| || |||
 TCCG CCGCCCGCGG GC GAAG
 _ CC A_
 GAM3559 SIAT8E 5' AGGCAGGCGGGGGACT 80622 C CGCCTC
 AGGC GGCGGG GGACT
 ||| |||| ||||
 TCCG CCGCCC CCTGA
 T _
 GAM3559 ST7 5' GGCCGCGGGCGCGCCGGCTT 80623 G C A
 GGCCG CGGGCGC TCGG CTT
 |||| |||| ||| |||
 CCGGC GCCCGCG GGCC GAA
 _ C _
 GAM3559 ST7 5' GGCCGCGGGCGCGCCGGCTT 80623 G C A
 GGCCG CGGGCGC TCGG CTT
 |||| |||| ||| |||
 CCGGC GCCCGCG GGCC GAA
 _ C _
 GAM3559 TNFRSF11A 5' AGGCTGGCGGGCGCCGCGG 80624 C T
 AGGC GGCGGGCGCC CGG
 ||| ||||| ||| |||
 TCCG CCGCCCGCGG GCC
 A C
 GAM3559 FLJ10157 3' GGCTTGGACACCCCTCGGGCTT 80625 _ _ A
 C GGC GGGCGCC TCGG CTTC
 || ||||| ||| |||
 CCG CCTGTGG AGCC GAAG
 AA GG C
 GAM3559 GP3ST 3' GGCCGCGGGGCTGGG 80626 GC C
 GGCCGGCGGGC CT GG
 ||||| || ||
 CCGGCCGCCG GA CC
 _ C
 GAM3559 HSA404617 5' AGGCCGGCTGGGTGTGGCTTC 80627 _ CGCCTC A
 AGGCCGGC GGG GG CTTC
 ||||| || || |||
 TCCGGCCG CCC CC GAAG
 A ACA _ _
 GAM3559 LOC118812 5' AGGGTTCCAGCGCCTCGGACTT 80628 CCGGCG
 AGG GGCGCCTCGGACTT
 || ||||| |||||

		TCC TCGCGGAGCCTGAA		
		CAAGG_		
GAM3559	LOC133923 5'	AGGCCAGACTCACTTTGGGCTT 80629	CGGG	CTC A
	C	AGGCCGG CGC GG CTTC		
		TCCGGTC GTG CC GAAG		
		TGA_ AAA C		
GAM3559	LOC159199 5'	AGGCCGGCGGGTCCCTGCTGGA 80630	CG	C_
	CTT	AGGCCGGCGGG CCT GGACTT		
		TCCGGCCGCC GGA CCTGAA		
		AG CGA		
GAM3559	LOC219513 3'	AGGTCGGCGAGCGCCTCG 80631	C	
		AGG CGGCGGGCGCCTCG		
		TCC GCCGCTCGCGGAGC		
		A		
GAM3560	ABCC1 3'	GCGTGGGAGTGCAGAGGCTGC 80634	C	CAG T_ C
		GCG GGGG GCAG GC GC		
		CGC CCCT CGTC CG CG		
		A CA_ TC A		
GAM3560	ABCC1 3'	GCGTGGGAGTGCAGAGGCTGC 80634	C	CAG T_ C
		GCG GGGG GCAG GC GC		
		CGC CCCT CGTC CG CG		
		A CA_ TC A		
GAM3560	ABCC1 3'	GCGTGGGAGTGCAGAGGCTGC 80634	C	CAG T_ C
		GCG GGGG GCAG GC GC		
		CGC CCCT CGTC CG CG		
		A CA_ TC A		
GAM3560	ADARB1 3'	GCCTGGGGCAGACCACCTGC 80635	GC	AGT _
		GC GGGGCAGGC GCC GC		
		CG CCCCGTCTG TGG CG		
		GA G_ A		
GAM3560	ADRA1A 5'	GCGCGGAGGCGGGAGCGC 80636	_	A C
		GCGCGG GGC GG AGTGC		
		CGCGCC CCG CC TCGCG		
		T C _		
GAM3560	ADRA1A 5'	GCGCGGAGGCGGGAGCGC 80636	_	A C
		GCGCGG GGC GG AGTGC		
		CGCGCC CCG CC TCGCG		
		T C _		
GAM3560	ADRA1A 5'	GCGCGGAGGCGGGAGCGC 80636	_	A C
		GCGCGG GGC GG AGTGC		

			CGCGCC CCG CC TCGCG		
			T C _		
GAM3560	ADRA1A	5'	GCGCGGAGGCGGGAGCGC	80636	_ A C
			GCGCGG GGC GG AGTGC		
			CGCGCC CCG CC TCGCG		
			T C _		
GAM3560	APRT	5'	GCGCGGGGACGGGCGGGACCGC	80637	_ A AGT
			GCGCGGGG C GGC GCCGC		
			CGCGCCCC G CCG TGGCG		
			T C CCC		
GAM3560	AQP5	5'	GCGCGGGGGGGGCAGGGGGC	80638	CA T__
			GCGCGGGG GGCAG GC		
			CGCGCCCC CCGTC CG		
			C_ CCC		
GAM3560	ARF1	5'	GCGCGGGGACGCGC	80639	GGCAG
			GCGCGGGGCA TGCCG		
			CGCGCCCCGT GCGGC		
GAM3560	ARHGEF7	3'	GCATGGGGCAGGTCCAC	80640	C CAGTG
			GCG GGGGCAGG CCGC		
			CGT CCCC GTCC GTTG		
			A A__		
GAM3560	ATP1B2	5'	GCGCGGGGCGAGTCCG	80641	AGGC G
			GCGCGGGG AGT CCG		
			CGCGCCCCG TCA GGC		
			C__ _		
GAM3560	B4GALT7	5'	GCATGGGGCAGGCGCTCGC	80642	C A GC
			GCG GGGGCAGGC GT CGC		
			CGT CCCC GTCCG CG GCG		
			A _ A_		
GAM3560	BACE2	5'	GCGCGGAGGCGCAGAGCCGC	80643	_ AG T
			GCGCGG GGC GCAG GCCGC		
			CGCGCC CCG CGTC CGGCG		
			T _ T		
GAM3560	BACE2	5'	GCGCGGAGGCGCAGAGCCGC	80643	_ AG T
			GCGCGG GGC GCAG GCCGC		
			CGCGCC CCG CGTC CGGCG		
			T _ T		
GAM3560	BACE2	5'	GCGCGGAGGCGCAGAGCCGC	80643	_ AG T
			GCGCGG GGC GCAG GCCGC		

			CGCGCC CCG CGTC CGGCG	
			T _ T	
GAM3560	BAI2	5'	GCGCAGGGTAGGTAGCTGC 80644	C C _
			GCGCGGGG AGG AG TGC	
			CGCGTCCC TCC TC ACG	
			A A G	
GAM3560	BCAT1	5'	GCAGGGCAGAGGTGCCA 80645	CA
			GCGGGGCAGG GTGCCG	
			CGTCCCGTCT CACGGT	
			C _	
GAM3560	BCR	5'	GCGCGGGGCGGGGCGC 80646	A CA
			GCGCGGGGC GG GTGC	
			CGCGCCCCG CC CGCG	
			C _	
GAM3560	BCR	5'	GCGCGGGGCGGGGCGC 80646	A CA
			GCGCGGGGC GG GTGC	
			CGCGCCCCG CC CGCG	
			C _	
GAM3560	CACNA1B	5'	GCGCGGGGCGCGCCA 80647	AGGCA
			GCGCGGGGC GTGCCG	
			CGCGCCCCG CGCGGT	

GAM3560	CAPG	3'	GCATGGGGCAGGAAGACGC 80648	C C _
			GCG GGGGCAGG AG TGC	
			CGT CCCCCTCC TC GCG	
			A T T	
GAM3560	CDH11	5'	GCGCAGGGCAAGCGCTGC 80649	AG
			GCGCGGGGCAGGC TGC	
			CGCGTCCCGTTTCG ACG	
			CG	
GAM3560	CEBPA	5'	GCGCGGGGCGTCCGCGCCGC 80650	AGGCA
			GCGCGGGGC GTGCCG	
			CGCGCCCCG CGCGGCG	
			CAG_	
GAM3560	CHGA	5'	GCGCGGGGCTGGGGGCGC 80651	A CA
			GCGCGGGGC GG GTGC	
			CGCGCCCCG CC CGCG	
			A CC	
GAM3560	CKMT1	3'	GCGGGGGCAGGTCCAGAGC 80652	C _ T
			GCG GGGGCAGG CAG GC	

			CGC CCCC GTCC GTC CG		
			— AG T		
GAM3560	CNTN2	5'	GCTGGGGCAGGTGGATGCTGC	80653	GC CA_ C
			GC GGGGCAGG GTGC GC		
			CG CCCC GTCC TACG CG		
			A_ ACC A		
GAM3560	DIA1	3'	GCGCGGGGCGGTGGCCG	80654	CAG A _
			GCGCGGGG GC GTG CCG		
			CGCGCCCC CG CAC GGC		
			— C C		
GAM3560	DNMT3A	5'	GCGCGGGGCTGGGGGGCTGC	80655	A CAGT C
			GCGCGGGGC GG GC GC		
			CGCGCCCCG CC CG CG		
			A CCC_ A		
GAM3560	DSC2	5'	CGCGGGGCGAGGGCCGC	80656	_ CAGT
			CGCGGGGC AGG GCCGC		
			GCGCCCCG TCC CGGCG		
			C —		
GAM3560	DSC2	5'	CGCGGGGCGAGGGCCGC	80656	_ CAGT
			CGCGGGGC AGG GCCGC		
			GCGCCCCG TCC CGGCG		
			C —		
GAM3560	EFNA3	3'	GCAGCAGGCAGTGCTGC	80657	GG C
			GC GGCAGGCAGTGC GC		
			CG TCGTCCGTCACG CG		
			— A		
GAM3560	EGLN2	5'	GCGTGGGGCAGGGTGAGGC	80658	C CA CC
			GCG GGGGCAGG GTG GC		
			CGC CCCC GTCC CAC CG		
			A _ TC		
GAM3560	EGLN2	5'	GCGTGGGGCAGGGTGAGGC	80658	C CA CC
			GCG GGGGCAGG GTG GC		
			CGC CCCC GTCC CAC CG		
			A _ TC		
GAM3560	EN1	5'	GCACGGGGCGGGTGC	80659	A CA
			GCGCGGGGC GG GTGC		
			CGTGCCCCG CC CACG		
			— —		
GAM3560	ENG	3'	GCCGGGGCAGCCACCGC	80660	G G G
			GC CGGGGCAG CA TGC		

			CG GCCCGTC GT GCG		
			— G G		
GAM3560	ERBB2	5'	GCGCGGGGCGCGGGGTGCTGC 80661	A_ CA C	
			GCGCGGGGC GG GTGC GC		
			CGCGCCCCG CC CACG CG		
			CG C_ A		
GAM3560	F2RL1	5'	GCGCGGGGAATCCGCCGC 80662	C GCAG	
			GCGCGGGG AG TGCCGC		
			CGCGCCCC TT GCGGCG		
			_ AG_		
GAM3560	F2RL3	3'	GCGCGGAGCCACTGCCGC 80663	AGG G	
			GCGCGGGGC CA TGCCGC		
			CGCGCCTCG GT ACGGCG		
			_ G		
GAM3560	FGF18	5'	GCTGCGGGGCGGCAGCCGC 80664	_ A GT	
			GC GCGGGGC GGCA GCCGC		
			CG CGCCCCG CCGT CGGCG		
			A _ _		
GAM3560	FGF18	5'	GCTGCGGGGCGGCAGCCGC 80664	_ A GT	
			GC GCGGGGC GGCA GCCGC		
			CG CGCCCCG CCGT CGGCG		
			A _ _		
GAM3560	FHIT	5'	GCGCGGGGCCCGAGCGCCGC 80665	A C	
			GCGCGGGGC GG AGTGCCGC		
			CGCGCCCCG CC TCGCGGCG		
			G _		
GAM3560	FLNA	5'	GCCGGGGGGGCGGTGCTGC 80666	G CA A C	
			GC CGGGG GGC GTGC GC		
			CG GCCCC CCG CACG CG		
			_ C_ C A		
GAM3560	FOX E3	3'	GCGCTGGGGTGGGGGGCGCCGC 80667	_ CA CA	
			GCGC GGGG GG GTGCCGC		
			CGCG CCCC CC CGCGGCG		
			A AC CC		
GAM3560	FOXO1A	5'	GCCGGGGCAGAGCCTGC 80668	G _ AG	
			GC CGGGGCAG GC TGC		
			CG GCCCGTC CG ACG		
			_ T G_		
GAM3560	FUS1	3'	GCCGGGGCAGGGGGTGC 50015	G CA	
			GC CGGGGCAGG GTGC		

			CG GCCCCGTCC CACG		
			— CC		
GAM3560	GALGT	5'	GCGCGGGGAGGGCTCTGGCCGC 80669	CA	AGT_
			GCGCGGGG GGC GCCGC		
			CGCGCCCC CCG CGGCG		
			TC AGAC		
GAM3560	GALNT2	3'	GCGGGGCAGGACTCGCTGC 80670	CAG	C
			GCGGGGCAGG TGC GC		
			CGCCCCGTCC GCG CG		
			TGA A		
GAM3560	GARP	3'	GCCGGGGCAGGACTCACCGC 80671	G	CAG
			GC CGGGGCAGG TGCCGC		
			CG GCCCCGTCC GTGGCG		
			— TGA		
GAM3560	GFRA1	5'	GCGCGGGGCTGGTCCCCGC 80672	A	CAGTG
			GCGCGGGGC GG CCGC		
			CGCGCCCCG CC GGCG		
			A AGG_		
GAM3560	GLI4	3'	GCTGGGCAGTGCCACCG 80673	G	_ AG
			GC GGGCAG GC TGCCG		
			CG CCCGTC CG GTGGC		
			A A G_		
GAM3560	GTF2IRD1	5'	GCGCGGGGAGGGGGCGC 80674	C	CA
			GCGCGGGG AGG GTGC		
			CGCGCCCC TCC CGCG		
			— CC		
GAM3560	GUCY1A2	5'	CGCGGGGCGCTGCGGTCGC 80675	AG	A C_
			CGCGGGGC GC GTG CGC		
			GCGCCCCG CG CGC GCG		
			— A CA		
GAM3560	HADHSC	5'	GCGCGAGGCGGGCAGCCGC 80676	A	GT
			GCGCGGGGC GGCA GCCGC		
			CGCGCTCCG CCGT CGGCG		
			C _		
GAM3560	HHIP	5'	GCGCGGGGAGGTGCG 80677	C	CAG C
			GCGCGGGG AGG TGC G		
			CGCGCCCC TCC ACG C		
			— _ A		
GAM3560	HIC1	5'	GCGCGGGGGCAGCTCG 80678	CAG	GC
			GCGCGGGG GCAGT CG		

			CGCGCCCC CGTCG GC		
			_____ A_		
GAM3560	HLX1	5'	GCGCGGGGAGGGGCGC 80679	C	CA
			GCGCGGGG AGG GTGC		
			CGCGCCCC TCC CGCG		
			_____ C_		
GAM3560	IGFBP2	3'	GCGGGGGGCAGGGGCGC 80680	C	CA
			GCG GGGGCAGG GTGC		
			CGC CCCC GTCC CGCG		
			C C_		
GAM3560	INPP5A	3'	GCGCAGAGTCAGTGCCGC 80681		CAGG
			GCGCGGGG CAGTGCCGC		
			CGCGTCTC GTCACGGCG		
			A_____		
GAM3560	INPPL1	3'	GCGAGGGGCAGGATGC 80682	C	CA
			GCG GGGGCAGG GTGC		
			CGC CCCC GTCC TACG		
			T _____		
GAM3560	JAM2	5'	GCGCGGGGCTGCCAGC 80683		AGGCAG _
			GCGCGGGG TGCC GC		
			CGCGCCCCG ACGG CG		
			_____ T		
GAM3560	JUN	3'	GCGCGGGGACAGCCCG 80684	CAG	G
			GCGCGGGG GCAGT CCG		
			CGCGCCCC TGTCG GGC		
			_____ _		
GAM3560	KCNA5	5'	GCGCGGGAGCAGAGGGCATGCT 80685		_ _ _ G C
	GC		GCGCGGG GCA GGCA TGC GC		
			CGCGCCC CGT CCGT ACG CG		
			T CTC _ A		
GAM3560	KDR	5'	GCGCGGAGGTGGAAC TCGC 80686	CA	CAGT _
			GCGCGGGG GG GC CGC		
			CGCGCCTC CC TG GCG		
			CA T_ _ A		
GAM3560	LARGE	5'	GCGCGGCGGCGCCGCGC 80687		_ AG AG
			GCGCGG GGC GC TGCCGC		
			CGCGCC CCG CG GCGGCG		
			G _ _		
GAM3560	LARGE	5'	GCGCGGCGGCGCCGCGC 80687		_ AG AG
			GCGCGG GGC GC TGCCGC		

		CGCGCC CCG CG GCGGCG	
		G _ _	
GAM3560 LETM1	5'	GCGGGGCGGCCAGGCCGC 80688	A _ T
		GCGGGGC GGC AG GCCGC	
		CGCCCCG CCG TC CGGCG	
		_ G _	
GAM3560 LMO2	5'	GCGCGGGGCTGGCCGGCTGC 80689	A AGT C
		GCGCGGGGC GGC GC GC	
		CGCGCCCCG CCG CG CG	
		A GC_ A	
GAM3560 MAD1L1	3'	GCGGGGCAGGGGACCTGC 80690	CAGT _
		GCGGGGCAGG GCC GC	
		CGCCCCGTCC TGG CG	
		CC_ A	
GAM3560 MAP3K9	5'	GCGCGGGGTCACGTAGTTGC 80691	_ GGC _
		GCGCGGGG CA AGT GC	
		CGCGCCCC GT TCA CG	
		A GCA A	
GAM3560 MAP4K2	5'	GCGGGGCGGGCGCCCG 80692	A A G
		GCGGGGC GGC GT CCG	
		CGCCCCG CCG CG GGC	
		C _ _	
GAM3560 MYO6	5'	GCGCGGCGGCGGGGCTACC 80693	_ A_ AG
		GCGCGG GGC GGC TGCC	
		CGCGCC CCG CCG ATGG	
		G CC _	
GAM3560 NFATC2	5'	GCGCAGGGCGGGAAGGCTGC 80694	A C T C
		GCGCGGGGC GG AG GC GC	
		CGCGTCCCG CC TC CG CG	
		C T _ A	
GAM3560 NR2F6	5'	GCGCGGGGGGCACGGGCTGC 80695	CA GT_ C
		GCGCGGGG GGCA GC GC	
		CGCGCCCC CCGT CG CG	
		_ GCC A	
GAM3560 NRXN1	5'	GCGCGGAGCGGGTGGCTGC 80696	A CA_
		GCGCGGGGC GG G TGC	
		CGCGCCTCG CC C ACG	
		C AC G	
GAM3560 PABPC4	5'	GCGCGGGGCAGGCCGGAAGCG 80697	_____
		GCGCGGGGCAGGC AGTG	

			CGCGCCCCGTCCG	TCGC		
			GCCT			
GAM3560	PACE	3'	GCCGGGGCAAGCTGC	80698	G	AG
			GC CGGGGCAGGC	TGC		
			CG GCCCGTTTCG	ACG		
			— —			
GAM3560	PKD1	5'	GCGCGGGGCTGGATGGGGCTGC	80699		A CAGT_ C
			GCGCGGGGC	GC GC		
			CGCGCCCCG	CG CG		
			A TACCC	A		
GAM3560	PIIF	3'	GCACGGGGAAGTTAGTGTTC	80700		C GC CC
			GCGCGGGG	AG AGTG GC		
			CGTGCCCC	TC TCAC CG		
			T AA	AA		
GAM3560	PTGS2	5'	GCGCGGGGGTAGGCTTTGC	80701		C_ AG
			GCGCGGGG	AGGC TGC		
			CGCGCCCC	TCCG ACG		
			CA	AA		
GAM3560	RAB3B	5'	GCCGGGGCGGGGCGCTGC	80702	G	A CA C
			GC CGGGGC	GG GTGC GC		
			CG GCCCG	CG CGCG CG		
			— C —	A		
GAM3560	RNH	5'	GCGGGCCAGGCAGGCTGC	80703	G	T C
			GCGGG	CAGGCAG GC GC		
			CGCCC	GTCCGTC CG CG		
			G —	A		
GAM3560	RNH	5'	GCGGGCCAGGCAGGCTGC	80703	G	T C
			GCGGG	CAGGCAG GC GC		
			CGCCC	GTCCGTC CG CG		
			G —	A		
GAM3560	RPS6KA2	5'	GCGCGGGGCGTGGGGCGC	80704		A_ CA
			GCGCGGGGC	GG GTGC		
			CGCGCCCCG	CG CGCG		
			CA	C_		
GAM3560	RPS6KA2	5'	GCGTGGGGCGCGAGCTGC	80705	C	AG _ _
			GCG	GGGGC GC AG TGC		
			CGC	CCCCG CG TC ACG		
			A —	C G		
GAM3560	SLC22A5	5'	GCGCGGGGCACCCGCCGC	80706		AG AG
			GCGCGGGGC	GC TGCCGC		

CGCGCCCCG TG GCGGCG
 — G—
 GAM3560 SLC30A4 5' CGAGGGCAGTGCCGC 80707 CAG
 CGGGG GCAGTGCCGC
 |||| |||||
 GCTCC CGTCACGGCG

—
 GAM3560 SLC9A3R2 3' GCTCGGGGCAGGCTGAGGC 80708 G — T
 GC CGGGGCAGGC AG GC
 || ||||| ||
 CG GCCCGTCCG TC CG
 A AC —

GAM3560 SMT3H1 5' GCGCGGGGAGGCGGCGC 80709 C A
 GCGCGGGG AGGC GTGC
 ||||| ||| |||
 CGCGCCCC TCCG CGCG
 — C

GAM3560 SOX12 3' GCGTGGGGCAGAGACCTGC 80710 C CAGT —
 GCG GGGGCAGG GCC GC
 || ||||| ||| ||
 CGC CCCCCTCT TGG CG
 A C— A

GAM3560 SREBF2 5' ACGCGGGGGCGGTGCCG 80711 CAG A
 GCGCGGGG GC GTGCCG
 ||||| || |||||
 TCGCCCC CG CACGGC
 — C

GAM3560 ST14 5' GCGCGGGGCGCGGGGCGC 80712 A_ CA
 GCGCGGGGC GG GTGC
 ||||| || |||
 CGCGCCCCG CC CGCG
 CG C—

GAM3560 SURF4 3' GCTGGGAAAGGGCGGTGCTGC 80713 GC CA_ A C
 GC GGGG GGC GTGC GC
 || ||| || ||| ||
 CG CCT CCG CACG CG
 A_ TTC C A

GAM3560 TNFRSF11A 5' GCGCGGGACAGGCTGGC 80714 AGT
 GCGCGGGGCAGGC GC
 ||||| ||
 CGCGCCCTGTCCG CG
 AC—

GAM3560 TRC8 5' GCGCGGGGCAGGGCCCGGGGCC 80715 _ AGT_
 GC GCGCGGGGCAGG C GCCGC
 ||||| || |||
 CGCGCCCCGTCC G CGGCG
 C GGCCC

GAM3560 TRPV4 3' GCTGGGGCAGGGGTACGTTCGC 80716 GC CAG —
 GC GGGGCAGG TGC CGC
 || ||||| ||| |||

		CG CCCCCTCC GTG GCG	
		A_ CCA CA	
GAM3560 VHL	5'	ACGCGGGGCGGAGCTGC 80717	A C _
		GCGCGGGGC GG AG TGC	
		TGCGCCCCG CC TC ACG	
		_ _ G	
GAM3560 WNT4	5'	GCCCGGGGCAGCGGCTGC 80718	G _ AG
		GC CGGGGCA GGC TGC	
		CG GCCCGT CCG ACG	
		G CG _	
GAM3560 WNT7A	5'	GCGGGGGCGCTGCTGC 80719	C AG AG C
		GCG GGGC GC TGC GC	
		CGC CCCC CG ACG CG	
		_ _ _ A	
GAM3560 XRCC2	3'	CACTGATGGGCAGTGCTGC 80720	GG CA C
		CGC GG GGCAGTGC GC	
		GTG CT CCGTCACG CG	
		A_ AC A	
GAM3560 YWHAG	5'	GCGCGAGGCGGCTGC 80721	A AG
		GCGCGGGGC GGC TGC	
		CGCGCTCCG CCG ACG	
		_ _	
GAM3560 ALTE	5'	GCGCGGGGGGGCGGCTGC 80722	CA A _
		GCGCGGGG GGC G TGC	
		CGCGCCCC CCG C ACG	
		C_ C G	
GAM3560 APELIN	5'	CGCGGGGCAGCGCCGC 80723	GGCA
		CGCGGGGCA GTGCCGC	
		GCGCCCCGT CGCGGCG	
		_ _	
GAM3560 ASE-1	5'	GCGCGGGGGTAGGCATTGC 80724	C_ G
		GCGCGGGG AGGCA TGC	
		CGCGCCCC TCCGT ACG	
		CA A	
GAM3560 ATP6V1B2	3'	GCACGGGGTAGGGAAGTTGC 80725	C C_ _
		GCGCGGGG AGG AGT GC	
		CGTGCCCC TCC TCA CG	
		A CT A	
GAM3560 BTBD2	3'	ACGCGGGGTGGGTGGGGGC 80726	CA CA CC_
		GCGCGGGG GG GTG GC	

			TGCGCCCC CC CAC CG		
			A_ _ CCC		
GAM3560	CAMKK1	3'	GCGCGGGATGAGTGTGCTGC 80727	CA CA C	
			GCGCGGGG GG GTGC GC		
			CGCGCCCT TC CACG CG		
			AC A_ A		
GAM3560	CDCA4	5'	GCGCGGGGCGGGGCGAGC 80728	A_ _	
			GCGCGGGG GGC AGT		
			CGCGCCCCG CCG TCG		
			CC C		
GAM3560	CENTG2	5'	GCGCGGGGCTGGCCCG 80729	A AGTG	
			GCGCGGGG GGC CCG		
			CGCGCCCCG CCG GGC		
			A _		
GAM3560	CEP3	5'	GCGCGGGGCGGGGCCG 80730	A CAGT	
			GCGCGGGG GG GCCG		
			CGCGCCCCG CC CGGC		
			C _		
GAM3560	CEP3	5'	GCGCGGGGCGGCCGGACGC 80731	A AGTGC	
			GCGCGGGG GGC CGC		
			CGCGCCCCG CCG GCG		
			_ GCCT_		
GAM3560	CHRA1	3'	GCTAAAAGCGGGCAGTGC 80732	GC A	
			GC GGGG GGCAGTGC		
			CG TTTCG CCGTCACG		
			AT C		
GAM3560	COL12A1	3'	CGTGGGGCAGGGCGCGCCGC 80733	C CA	
			CG GGGG CAGG GTGCCG		
			GC CCGGTCC CGCGGCG		
			A CG		
GAM3560	COL12A1	3'	CGTGGGGCAGGGCGCGCCGC 80733	C CA	
			CG GGGG CAGG GTGCCG		
			GC CCGGTCC CGCGGCG		
			A CG		
GAM3560	DDX17	5'	GCTCAAACCGGGCAGTGCCGC 80734	G_ A_	
			GC GGGC GGCAGTGCCG		
			CG TTG CCGTCACGGCG		
			AG GC		
GAM3560	dJ383J4.3	5'	ACGCGGGGCGGGCCCTGC 80735	A AG	
			GCGCGGGG GGC TGC		

		TGCGCCCCG CCG ACG		
		C GG		
GAM3560	DKFZp434F054 5'	GCGCGGGGGAGCGGACGCTGC	80736	CA AG_ C
		GCGCGGGG GGC TGC GC		
		CGCGCCCC TCG GCG CG		
		C_ CCT A		
GAM3560	DKFZP434J154 5'	GCGCGAGGGCGGGTCAGGCTGC	80737	_ A _ T C
		GCGCG GGGC GG CAG GC GC		
		CGCGC CCCG CC GTC CG CG		
		T C A _ A		
GAM3560	DKFZp434K2435 5'	GCGCGGGGCGCGGGGCGACTGC	80738	A_ CA _ C
		GCGCGGGGC GG GTG C GC		
		CGCGCCCCG CC CGC G CG		
		CG C_ T A		
GAM3560	DKFZP434N014 5'	GCGCGGGGTGTGGGCGGTGCCG	80739	CA__ A
	C	GCGCGGGG GGC GTGCCGC		
		CGCGCCCC CCG CACGGCG		
		ACAC C		
GAM3560	DKFZP564I1171 5'	GCGCGGGGCGGCGGCGC	80740	A A
		GCGCGGGGC GGC GTGC		
		CGCGCCCCG CCG CGCG		
		_ C		
GAM3560	DKFZp762K222 5'	GCGCGGCGGCAGCGCTGC	80741	G A C
		GCG GGC GGCAGTGC GC		
		CGC CCG CCGTCGCG CG		
		G _ A		
GAM3560	DLL1 3'	ACGGAAGGCAGTGCCG	80742	GC
		GCGGG AGGCAGTGCCG		
		TGCCT TCGTCACGGC		
		—		
GAM3560	DMWD 5'	GCGCAGGGGTGGCTGACG	80743	CA AG C
		GCGCGGGG GGC TG CG		
		CGCGTCCC CCG AC GC		
		CA _ T		
GAM3560	E2IG3 5'	GCGCGGAGCAGGGATCGC	80744	CAG
		GCGCGGGGCAGG TGC		
		CGCGCCTCGTCC GCG		
		CTA		
GAM3560	EIF3S9 3'	GCGCAGGAGAAGGTGCCGC	80745	C CA
		GCGCGGGG AGG GTGCCGC		

CGCGTCCT TTC CACGGCG
 C _
 GAM3560 EPB41L1 5' CGCGGGGCGGGGCGGCGC 80746 A_ A
 CGCGGGGC GGC GTGC
 ||||| ||| |||
 GCGCCCCG CCG CGCG
 CC C
 GAM3560 FLJ10769 3' GCGTGGGACAGGAGGC 80747 C C T
 GCG GGGGCAGG AG GC
 || ||||| || ||
 CGC CCCTGTCC TC CG
 A _ _
 GAM3560 FLJ12242 5' ACGCGGGGCAGGCCGGGAGC 80748 AGT_
 GCGCGGGGCAGGC GC
 ||||| ||
 TGCGCCCCGTCCG CG
 GCCCT
 GAM3560 FLJ12443 3' GCGCTGGGAGGCAGTGCTGC 80749 G C C
 GCGC GGG AGGCAGTGC GC
 ||| || ||||| ||
 CGCG CCC TCCGTACG CG
 A _ A
 GAM3560 FLJ12526 5' CGGGGCAGCGCGCTGC 80750 G A C
 CGGGGCAG C GTGC GC
 ||||| | ||| ||
 GCCCCGTC G CGCG CG
 _ _ A
 GAM3560 FLJ12697 3' GCGCGGGGGCTGCTGGGGCGGT 80751 _A_____ A |||
 GCCGCG GGGG C GGC GTGCCG C G
 ||| | || ||||| |
 CCCC G CCG CACGGCG C
 C ACGACC C |||
 GAM3560 FLJ13189 5' GCGCGGGGAGGAGTTGC 80752 C C _
 GCGCGGGG AGG AGT GC
 ||||| ||| ||| ||
 CGCGCCCC TCC TCA CG
 _ _ A
 GAM3560 FLJ14154 3' GCTGGGGCAGGGTGGCGCCGC 80753 GC CA_
 GC GGGGCAGG GTGCCG
 || ||||| |||||
 CG CCCCCTCC CGCGGCG
 A_ CAC
 GAM3560 FLJ14668 3' GCTGGGGCAGGAACACTGC 80754 GC _ G
 GC GGGGCAGG CA TGC
 || ||||| || |||
 CG CCCCCTCC GT ACG
 A_ TT G
 GAM3560 FLJ14708 5' GCGTGGGGCTGCCCGGGCCGC 80755 C AG AGT_
 GCG GGGGC GC GCCGC
 || |||| || ||||

			CGC CCCCCG CG CGGCG		
			A A_ GGCC		
GAM3560	FLJ20309	3'	GCTGGGGGCAGAGAACTGC	80756	GC C _
			GC GGGGCAGG AG TGC		
			CG CCCCCGTCT TT ACG		
			A_ C G		
GAM3560	FLJ20464	3'	GCAGGACAGGTGCTGC	80757	CAG C
			GCGGGGCAGG TGC GC		
			CGTCCTGTCC ACG CG		
			_____ A		
GAM3560	FLJ20539	3'	GCGGGGGCAGGCGAGAGGC	80758	C _ T_
			GCG GGGGCAGGC AG GC		
			CGC CCCCCGTCCG TC CG		
			_ C TC		
GAM3560	FLJ20898	3'	GCGCAGGGCAGCCTCGC	80759	G AG
			GCGCGGGGCAG C TGC		
			CGCGTCCCGTC G GCG		
			_ GA		
GAM3560	FLJ21195	3'	GCGCGGGGCTGAGCTGC	80760	A_ AG
			GCGCGGGGC GGC TGC		
			CGCGCCCCG TCG ACG		
			AC _		
GAM3560	FLJ21562	5'	GCGCTGGGTAAACGCCGC	80761	G C AGT
			GCGC GGG AGGC GCCGC		
			CGCG CCC TTTG CGGCG		
			A A _		
GAM3560	FLJ21865	3'	GCGCGGGGGGCAGGTGCTGC	80762	CA _ C
			GCGCGGGG GGCAG TGC GC		
			CGCGCCCC CCGTC ACG CG		
			_ C A		
GAM3560	FLJ22362	5'	GCGCGGGGCCGAGCTGC	80763	A_ AG
			GCGCGGGGC GGC TGC		
			CGCGCCCCG TCG ACG		
			GC _		
GAM3560	FLJ22814	3'	GCGTGGGGCAAGAGTTTTC	80764	C C GCC
			GCG GGGGCAGG AGT GC		
			CGC CCCCCGTTT TCA CG		
			A _ AAA		
GAM3560	FLJ23519	5'	GCGGGCCAGGCAGGCTGC	80703	G T C
			GCGGG CAGGCAG GC GC		

CGCCC GTCCGTC CG CG
G _ A
GAM3560 FLJ31762 3' GCGCAGGGGTGGAGGCC 80765 CA C T
GCGCGGGG GG AG GCC
||||||| || || ||
CGCGTCCC CC TC CGG
CA _ _
GAM3560 HRD1 3' GCGGGGCAGGGTCCCTCAGTGC 80766 _____ C III
TGCG GGGGCAGG CAGTGC GC G
||||||| ||||| || |
CCCCGTCC GTCACG CG C
CAGGGA A III
GAM3560 HRH3 5' ACGCGGGGCAGGGCGC 80767 CA
GCGCGGGGCAGG GTGC
||||||| ||||
TGCGCCCCGTCC CGCG

GAM3560 HSPB7 3' GCACGGGGTGGGCAGGC 80768 CA T
GCGCGGGG GGCAG GC
||||||| ||||| ||
CGTGCCCC CCGTC CG
AC _
GAM3560 HSPC121 5' GCGCGGGGAGGCTAGGCTCGC 80769 C _ T _
GCGCGGGG AGGC AG GC CGC
||||||| |||| || || ||
CGCGCCCC TCCG TC CG GCG
_ A _ A
GAM3560 IL-17RC 3' ACGCGGGGCGCGAGGCTGC 80770 ____ AG
GCGCGGGGC AGGC TGC
||||||| |||| ||
TGCGCCCCG TCCG ACG
CGC ____
GAM3560 IL10RB 3' GCTGGAGTGCA GTGCCGC 80771 GC CAG
GC GGGG GCAGTGCCGC
|| |||| ||||| ||||
CG CCTC CGTCACGGCG
A_ A_
GAM3560 JDD1 5' GCCGGGGCAGGCACGC 80772 G G
GC CGGGGCAGGCA TGC
|| ||||| |||| ||
CG GCCCGTCCGT GCG

GAM3560 KIAA0125 3' GCCTGGGGCAGGTCTCAGGC 80773 GC ____ T
GC GGGGCAGG CAG GC
|| ||||| |||| ||
CG CCCC GTCC GTC CG
GA AGA _
GAM3560 KIAA0171 5' GCGCGGGACGGTCCGCCGC 80774 A CAG
GCGCGGGGC GG TGCCGC
||||||| || |||||

CGCGCCCTG CC GCGGCG
 _ AG_
 GAM3560 KIAA0346 3' GCGCGGGCAGGCAGGC 80775 G T
 GCGCGGG CAGGCAG GC
 ||||| ||||| ||
 CGCGCCC GTCCGTC CG

— —
 GAM3560 KIAA0476 5' ACGCGGGGACTGTGCTGC 80776 CAG A C
 GCGCGGGG GC GTGC GC
 ||||| || ||||| ||
 TGCGCCCC TG CACG CG

— A A
 GAM3560 KIAA0513 5' GCGTGGTGGCAGGTGCC 80777 C _ CAG
 GCG GG GGCAGG TGCC
 ||| || ||||| |||||
 CGC CC CCGTCC ACGG
 A A —

GAM3560 KIAA0552 5' GCCGGGGCAGGGGACGC 80778 G CA
 GC CGGGGCAGG GTGC
 || ||||| |||||
 CG GCCCGTCC TGCG
 — CC

GAM3560 KIAA0649 5' GCGCGGGGAGGGGGCGC 80674 C CA
 GCGCGGGG AGG GTGC
 ||||| ||| |||||
 CGCGCCCC TCC CGCG
 — CC

GAM3560 KIAA0720 3' GCGCTGGGCTGCCTGCTGC 80779 G AG AG C
 GCGC GGGC GC TGC GC
 |||| |||| || |||||
 CGCG CCCG CG ACG CG
 A A_ G_ A

GAM3560 KIAA0783 5' GCGCGAGGGCGGCTGC 80780 _ A AG
 GCGCG GGGC GGC TGC
 |||| |||| ||| |||||
 CGCGC CCCG CCG ACG
 T _ —

GAM3560 KIAA1026 3' GCGCAGGGGCAGGCAGGACTCG 80781 _ TG_
 GCGC GGGGCAGGCAG C CG
 |||| ||||| ||||| |||||
 CGCG CCCCGTCCGTC G GC
 T CTA

GAM3560 KIAA1032 3' GCGCAGGCGCAGTGCCGC 80782 G AG
 GCGCGGG C GCAGTGCCGC
 ||||| | ||||| |||||
 CGCGTCC G CGTCACGGCG

— —
 GAM3560 KIAA1036 3' GCGGGGGCAGACTGC 80783 C AG
 GCG GGGGCAGGC TGC
 ||| ||||| ||||| |||||

CGC CCCCCGTCTG ACG

GAM3560 KIAA1157 5' GCGCGGGGCATGCAGGCTGC 80784 G T C
GCGCGGGGCA GCAG GC GC
||||||| ||| ||
CGCGCCCCGT CGTC CG CG

A _ A
GAM3560 KIAA1533 5' GCGCGGGGCTGGGCTGC 80785 A_ AG
GCGCGGGGC GGC TGC
||||||| ||| ||
CGCGCCCCG CCG ACG

AC _
GAM3560 KIAA1576 5' GCGCGGGGCGCACGGGCTGC 80786 AG GT_ C
GCGCGGGGC GCA GC GC
||||||| ||| ||
CGCGCCCCG CGT CG CG

_ GCC A
GAM3560 KIAA1643 5' GCGCGGGGCAGGTGC 80787 CAG
GCGCGGGGCAGG TGC
||||||| |||
CGCGCCCCGTCC ACG

GAM3560 KIAA1706 3' GCGTGGGGCAAGGCCTCAAGTG 80788 C _ _
C GCG GGGGCA GGC AGTGC
||| ||||| ||| |||||
CGC CCCCCGT CCG TCACG
A T GAGT

GAM3560 KIAA1796 5' GCGCGGGGCTGGAGAGCCGC 80789 A C T
GCGCGGGGC GG AG GCCGC
||||||| ||| ||| |||||
CGCGCCCCG CC TC CGGCG

A _ T
GAM3560 KIAA1813 5' GCTGGGGCAGGAGCTGC 80790 GC C _
GC GGGGCAGG AG TGC
|| ||||| ||| |||
CG CCCCCGTCC TC ACG

A_ _ G
GAM3560 KIAA1872 5' GCGCGGGGCTGCGGCTGC 80791 A__ AG
GCGCGGGGC GGC TGC
||||||| ||| |||
CGCGCCCCG CCG ACG

ACG _
GAM3560 LIG-1 5' GCCGAGGGCAGTGCTGC 80792 G CA C
GC GGG GGCAGTGC GC
|| ||| ||||| ||
CG CTC CCGTCACG CG

G _ A
GAM3560 LIM 5' GCGCGGGGCTGCCTCCGC 80793 AG AGTG
GCGCGGGGC GC CCGC
||||||| || |||

CGCGCCCCG CG GGCG
A_ GA_
GAM3560 LRP16 5' GCGCGGGACGGCTCTCCGC 80794 A AGTG
GCGCGGGGC GGC CCGC
||||||| ||| |||
CGCGCCCTG CCG GGCG
_ AGA_
GAM3560 LW-1 5' ACGGGGTGTGGGTGGGCGGTGC 80795 CA_____ A |||
CGCG GGGG GGC GTGCCGC G
|||| ||| ||||| |
CCCC CCG CACGGCG C
ACACCCAC C |||
GAM3560 MGC:5244 3' GCGCGGGGTGAGGTCCGGGGGC 80796 C_ CAGT____
CGC GCGCGGGG AGG GCCGC
||||||| ||| |||||
CGCGCCCC TCC CGGCG
AC AGGCCCC
GAM3560 MGC10772 5' GCGCGGGGCGCGCGC 80797 AG A
GCGCGGGGC GC GTGC
||||||| || |||
CGCGCCCCG CG CGCG
— —
GAM3560 MGC10911 3' GCGCGGGGCGGCTGC 80798 A AG
GCGCGGGGC GGC TGC
||||||| ||| |||
CGCGCCCCG CCG ACG
— —
GAM3560 MGC13170 5' GCCGGGTGGGCAGTGCCG 80799 G GCA
GC CGGG GGCAGTGCCG
|| ||| |||||
CG GCCC CCGTCACGGC
_ AC_
GAM3560 MGC16202 5' GCGCGGGGCGCGTGGTGC 80800 AG A____
GCGCGGGGC GC GTGC
||||||| || |||
CGCGCCCCG CG CACG
_ CAC
GAM3560 MGC1842 3' GCGGGGGCACAGCTGC 80801 C AG _
GCG GGGGC GCAG TGC
||| |||| ||| |||
CGC CCCCCG TGTC ACG
— — G
GAM3560 MGC2555 5' GCGCGGGGCGGGCTCGGGGCTG 80802 A AGT__ C
C GCGCGGGGC GGC GC GC
||||||| ||| || |||
CGCGCCCCG CCG CG CG
C AGCCC A
GAM3560 MOT8 5' GCGCGGGGCGAGGGCGCCG 80803 _ CA
GCGCGGGGC AGG GTGCCG
||||||| ||| |||||

			CGCGCCCCG TCC CGCGGC		
			C _		
GAM3560 MSC	3'	GCGCGGGGAAGAACCTGC	80804	C _	AG
		GCGCGGGG AGG C TGC			
		CGCGCCCC TCT G ACG			
		T T G _			
GAM3560 NEIL1	5'	GCGGGGGCAGGTCTGAGGC	80805	C	C _ T
		GCG GGGGCAGG AG GC			
		CGC CCCC GTCC TC CG			
		_ AGAC _			
GAM3560 NEIL2	5'	GCGTGGGCAGCACCTCCGC	80806	_	G GTG
		GCG GGGCAG CA CCGC			
		CGC CCGTC GT GGCG			
		A _ GGA			
GAM3560 PELI2	5'	GCGCGGGGCGGCCAGTCCCGC	80807	A _	G
		GCGCGGGGC GGC AGT CCGC			
		CGCGCCCCG CCG TCA GGCG			
		_ G G			
GAM3560 PPP1R1B	5'	GCGCGGGGTGGGCGGTGGGGC	80808	CA A	CC
		GCGCGGGG GGC GTG GC			
		CGCGCCCC CCG CAC CG			
		AC C CC			
GAM3560 PTPRU	5'	GCGCGGAGCGGGACTGGCGC	80809	A _	A _
		GCGCGGGGC GG C GTGC			
		CGCGCCTCG CC G CGCG			
		C T AC			
GAM3560 PTPRU	5'	GCGCGGAGCGGGACTGGCGC	80809	A _	A _
		GCGCGGGGC GG C GTGC			
		CGCGCCTCG CC G CGCG			
		C T AC			
GAM3560 PTPRU	5'	GCGCGGAGCGGGACTGGCGC	80809	A _	A _
		GCGCGGGGC GG C GTGC			
		CGCGCCTCG CC G CGCG			
		C T AC			
GAM3560 QKI	5'	GCGCGGGGCGCGGGCTGC	80810	A _	AG
		GCGCGGGGC GGC TGC			
		CGCGCCCCG CCG ACG			
		CGC _			
GAM3560 Rab11-FIP3	5'	GCGCGGGGCGCCCGGGCTGC	80811	A _	AG
		GCGCGGGGC GGC TGC			

		CGCGCCCCG CCG ACG	
		CGGGC _	
GAM3560 RAB40C	3'	GCGCGGGTAGTGTGATGCCG 80812	GC GCA_
		GCGCGGG AG GTGCCG	
		CGCGCCC TC TACGGC	
		A_ ACAAC	
GAM3560 RBPMS	5'	GCGCGGGGCTGGGCGAGGGC 80813	A_ _ T
		GCGCGGGGC GGC AG GC	
		CGCGCCCCG CCG TC CG	
		AC C C	
GAM3560 RELB	5'	GCGCGGGGCGCGGGCCG 80814	A CAGT
		GCGCGGGGC GG GCCG	
		CGCGCCCCG CC CGGC	
		G _	
GAM3560 REPRIMO	3'	GCGTGGGAGCGGTTGCCGC 80815	C _ A CAG
		GCG GGG GC GG TGCCGC	
		CGC CCC CG CC ACGGCG	
		A T _ A_	
GAM3560 RIN3	5'	GGCGGGGCGGGGACCTGCTGC 80816	C A_ AG C
		G GCGGGGC GGC TGC GC	
		C CGCCCCG CTG ACG CG	
		_ CCC G_ A	
GAM3560 RIP5	5'	GCGCGGGGCGGGCTGC 80798	A AG
		GCGCGGGGC GGC TGC	
		CGCGCCCCG CCG ACG	
		_ _	
GAM3560 SDCCAG8	3'	GCGGGGACAGCGCCCCG 80817	CAG _
		GCGGGG GCAGTGCC GC	
		CGCCCC TGTCGCGG CG	
		_ G	
GAM3560 SEC61A1	5'	GCGCGGGGCGGGGCCG 80730	A CAGT
		GCGCGGGGC GG GCCG	
		CGCGCCCCG CC CGGC	
		C _	
GAM3560 SEPT1	3'	GCGCGAGGGCGGCACCCGC 80818	_ A GTG
		GCGCG GGGC GGCA CCGC	
		CGCGC CCCG CCGT GGCG	
		T _ G_	
GAM3560 SMARCF1	5'	CGCGGGGCTCCGCTGCTGC 80819	AG_ AG C
		CGCGGGGC GC TGC GC	

			GCGCCCCG CG ACG CG		
			AGG _ A		
GAM3560	SMARCF1	5'	CGCGGGGCTCCGCTGCTGC	80819	AG_ AG C
			CGCGGGGC GC TGC GC		
			GCGCCCCG CG ACG CG		
			AGG _ A		
GAM3560	SMARCF1	5'	CGCGGGGCTCCGCTGCTGC	80819	AG_ AG C
			CGCGGGGC GC TGC GC		
			GCGCCCCG CG ACG CG		
			AGG _ A		
GAM3560	SMARCF1	3'	GCGCGCGGGCAGCCCGCCGC	80820	_ G AG
			GCGCG GGGCAG C TGCCGC		
			CGCGC CCCGTC G GCGGCG		
			G _ G_		
GAM3560	SPRY1	5'	GCGCAGGGGCGGCCACATTGC	80821	_ A AG__
			GCGC GGGGC GGC TGC		
			CGCG CCCC CG CCG ACG		
			T _ GTGTA		
GAM3560	SPRY4	5'	GCCGGGGCAGGTTAGCCGC	80822	G CAGT
			GC CGGGGCAGG GCCGC		
			CG GCCCGTCC CGGCG		
			_ AAT_		
GAM3560	SSI-3	5'	GCGCGGCGGCGGCTGC	80823	_ A AG
			GCGCGG GGC GGC TGC		
			CGCGCC CCG CCG ACG		
			G _ _		
GAM3560	STRAIT11499	5'	GCCGGGGCAGGCCAGGGC	80824	G _ T
			GC CGGGGCAGGC AG GC		
			CG GCCCGTCCG TC CG		
			_ G C		
GAM3560	TOB2	5'	GCGCGGGGCGGAGGTCGC	80825	A C TGC
			GCGCGGGGC GG AG CGC		
			CGCGCCCCG CC TC GCG		
			_ _ CA_		
GAM3560	XT2	5'	GCGCGGGGCTGAGCCG	80826	A CAGT
			GCGCGGGGC GG GCCG		
			CGCGCCCCG CT CGGC		
			A _ _		
GAM3560	ZNF213	3'	GCGGGTCATTAGTGCCGC	80827	G GGC
			GCGGG CA AGTGCCGC		

		CGCCC GT TCACGGCG		
		A AA_		
GAM3560	ZNF313	3' GCGCGAGGTAGCACTTGC	80828	CA G_
		GCGCGGGG GGCA TGC		
		CGCGCTCC TCGT ACG		
		A_ GA		
GAM3560	LOC112703	5' GCCCGGGGCAGCGGCTGC	80718	G _ AG
		GC CGGGGCA GGC TGC		
		CG GCCCGT CCG ACG		
		G CG _		
GAM3560	LOC116349	3' GCACGGGGCAGGGCTCC	80829	CA G
		GCGCGGGGCAGG GT CC		
		CGTGCCCCGTCC CG GG		
		_ A		
GAM3560	LOC122401	3' GCGGGGCAGGCATCCG	80830	GTG
		GCGGGGCAGGCA CCG		
		CGCCCCGTCCGT GGC		
		A_		
GAM3560	LOC124045	3' GCGGGGGCAGGCCTGGTGC	80831	C A_
		GCG GGGGCAGGC GTGC		
		CGC CCCCCTCCG CACG		
		_ GAC		
GAM3560	LOC124045	3' GCGGGGGCAGGCCTGGTGC	80831	C A_
		GCG GGGGCAGGC GTGC		
		CGC CCCCCTCCG CACG		
		_ GAC		
GAM3560	LOC126299	5' GCGCGGGGGGCGCCG	80832	CA AGT
		GCGCGGGG GGC GCCG		
		CGCGCCCC CCG CGGC		
		_ _		
GAM3560	LOC130497	3' GCGGGGCTCTGAAGTGCCGC	80833	AGGC_
		GCGGGGC AGTGCCGC		
		CGCCCCG TCACGGCG		
		AGACT		
GAM3560	LOC130985	3' GCAGAGGGCAGTGCG	80834	CA C
		GCGGGG GGCAGTGC G		
		CGTCTC CCGTCACG C		
		_ A		
GAM3560	LOC145173	5' GCGCGGGGAAGGGAGACGC	80835	C C _
		GCGCGGGG AGG AG TGC		

CGCGCCCC TCC TC GCG
T C T

GAM3560 LOC145173 5' GCGCGGGGAGCGGAGCTGC 80836 CA_ C _
GCGCGGGG GG AG TGC
||||||| || |||||
CGCGCCCC CC TC ACG
TCG _ G

GAM3560 LOC145497 5' GCTTGGCAGAGCAGTGCTGC 80837 GG _ C
GC GGCAG GCAGTGC GC
|| ||||| ||||| ||
CG CCGTC CGTCACG CG
AA T A

GAM3560 LOC145501 3' GCTGGGCGGCCAGTGTGCTGC 80838 G A A__ C
GC GGGC GGC GTGC GC
|| ||||| || ||||| ||
CG CCCG CCG CACG CG
A _ GTCA A

GAM3560 LOC145773 5' GCGGGGGGTGGGCGCGCCGC 80839 C CA A
GCG GGGG GGC GTGCCGC
||| ||||| ||| |||||
CGC CCCC CCG CGCGGCG
C AC _

GAM3560 LOC146108 5' GCGCGGGAGCTTGCGTGCTGC 80840 _ AG A C
GCGCGGG GC GC GTGC GC
||||||| || || ||||| ||
CGCGCCC CG CG CACG CG
T AA _ A

GAM3560 LOC146226 5' ACGTGGGCTACAGGTGCTGC 80841 _ AG _ C
GCG GGGC GCAG TGC GC
||| ||||| ||||| ||||| ||
TGC CCCG TGTC ACG CG
A A_ C A

GAM3560 LOC146325 3' GCGGGGCAGGTCCCAGGC 80842 __ T
GCGGGGCAGG CAG GC
||||||| ||||| ||||| ||||| ||
CGCCCCGTCC GTC CG
AGG _

GAM3560 LOC148534 5' GCGCTGGCCAGTGCCG 80843 GG AGG
GCGC GGC CAGTGCCG
||||| ||| |||||
CGCG CCG GTCACGGC
A_ _

GAM3560 LOC149422 3' GCGCGGAGGCGGGAGCGC 80636 _ A C
GCGCGG GGC GG AGTGC
||||||| ||||| ||||| ||||| ||
CGCGCC CCG CC TCGCG
T C _

GAM3560 LOC150095 5' GCGCTGGGCAGCAGGTTGC 80844 G G _
GCGC GGGCAG CAG TGC
||||| ||||| ||||| ||||| ||

CGCG CCCGTC GTC ACG
A _ CA
GAM3560 LOC150207 3' GCGCGGGGTGAGGTCCGGGGGC 80796 C_ CAGT____
CGC CGCGGGG AGG GCCGC
||||||| ||| |||||
CGCGCCCC TCC CGGCG
AC AGGCCCC

GAM3560 LOC150577 3' GCGCGGGGAAGCTGC 80845 C AG
GCGCGGGG AGGC TGC
||||||| ||| |||
CGCGCCCC TTCG ACG

GAM3560 LOC151516 5' GCAGAGGCAGGCAGTGC 80846 C
GCG GGGGCAGGCAGTGC
||| |||||||||
CGT CTCCGTCCGTCACG

GAM3560 LOC152189 5' GCGCGGGGGAGGGGAGCGC 80847 C C_
GCGCGGGG AGG AGTGC
||||||| ||| |||||
CGCGCCCC TCC TCGCG
C CC

GAM3560 LOC152189 5' GCGCGGGGCAGGAGGTGC 80848 CA
GCGCGGGGCAGG GTGC
||||||| |||
CGCGCCCCGTCC CACG
TC

GAM3560 LOC153474 5' GCGCGGGGCGGCGGCGC 80740 A A
GCGCGGGGC GGC GTGC
||||||| ||| |||||
CGCGCCCCG CCG CGCG

GAM3560 LOC157729 5' GCCTGGGGCAGGTCAGGC 80849 GC _ T
GC GGGGCAGG CAG GC
|| ||||||| ||| ||
CG CCCCGTCC GTC CG
GA A _

GAM3560 LOC158293 3' AAAAAAGCAGGCAGTGC 80850 CG
GCG GGGCAGGCAGTGC
||| |||||||||
TGT TTCGTCCGTCACG
TT

GAM3560 LOC163682 5' GCGCGGGGAAAGGGCCG 80851 C_ CAGT
GCGCGGGG AGG GCCG
||||||| ||| |||||
CGCGCCCC TCC CGGC
TT ____

GAM3560 LOC165254 3' CGCGGGGCAGAACTCCGC 80852 CAGTG
CGCGGGGCAGG CCGC
||||||| |||

		GCGCCCCGTCT	GGCG		
		TGA__			
GAM3560	LOC196694 5'	GCGCGGAGTGGCGCCG	80853	CA	AGT
		GCGCGGGG GGC GCCG			
		CGCGCCTC CCG CGGC			
		A_ _			
GAM3560	LOC196761 3'	GCTGGAAGCAGCGGTGCTGC	80854	GC	G A C
		GC GGGGCAG C GTGC GC			
		CG CTTCGTC G CACG CG			
		AC _ C A			
GAM3560	LOC196985 5'	GCGCGGGGCTGGGCAGTGC	80855	A_	
		GCGCGGGGC GGCAGTGC			
		CGCGCCCCG CCGTCACG			
		AC			
GAM3560	LOC197320 5'	GCGCGAGGCAGGCGGGC	80856	AGT	
		GCGCGGGGCAGGC GC			
		CGCGCTCCGTCCG CG			
		CC_			
GAM3560	LOC201116 3'	GCGGGGCAGGAAGGCGCTGC	80857	CA_	C
		GCGGGGCAGG GTGC GC			
		CGCCCCGTCC CGCG CG			
		TTC A			
GAM3560	LOC201702 5'	GCGCGGGGCCGAGCGCCGC	80665	A	C
		GCGCGGGGC GG AGTGCCGC			
		CGCGCCCCG CC TCGCGGCG			
		G _			
GAM3560	LOC205888 5'	GCCGGGGCAGGCTCGC	80858	G	AG
		GC CGGGGCAGGC TGC			
		CG GCCCGTCCG GCG			
		_ A_			
GAM3560	LOC219333 5'	GCGCAGGGCGCAGCCG	80859	AG	GT
		GCGCGGGGC GCA GCCG			
		CGCGTCCCG CGT CGGC			
		_ _			
GAM3560	LOC219731 5'	GCCGGGGCAGGAGGATCG	80860	G	C TGC
		GC CGGGGCAGG AG CG			
		CG GCCCGTCC TC GC			
		_ _ CTA			
GAM3560	LOC221184 5'	GCGCGGGACAGGCTCAGGGC	80861	_	T
		GCGCGGGGCAGGC AG GC			

	CGCGCCCTGTCCG TC CG	
	AG C	
GAM3560 LOC222225 5'	GCGCGGGGACTCGGCCGC 80862	CAG AGT
	GCGCGGGG GC GCCGC	
	CGCGCCCC TG CGGCG	
	___ AGC	
GAM3560 LOC253148 3'	GCGCGGAGTCGGTGCTGC 80863	CA CAG C
	GCGCGGGG GG TGC GC	
	CGCGCCTC CC ACG CG	
	AG ___ A	
GAM3560 LOC253358 5'	GCGCGGGCAGGCAGGTGC 80864	G _
	GCGCGGG CAGGCAG TGC	
	CGCGCCC GTCCGTC ACG	
	_ C	
GAM3560 LOC253868 5'	GCTGGGGCAGGTTTCAGATCG 80865	GC _ TGC
	GC GGGGCAGG CAG CG	
	CG CCCCCTCC GTC GC	
	A_ AA TA_	
GAM3560 LOC253960 5'	GCGCGGGGCAGGCAACGC 80866	
	GCGCGGGGCAGGCAGTGC	
	CGCGCCCCGTCCGTTGCG	
GAM3560 LOC254102 3'	GCGCGGGGCGGTAGTGCC 80867	A C
	GCGCGGGGC GG AGTGCC	
	CGCGCCCCG CC TCACGG	
	_ A	
GAM3560 LOC255057 5'	GCGCGGGGGAGGCCGGCGC 80868	C A_
	GCGCGGGG AGGC GTGC	
	CGCGCCCC TCCG CGCG	
	C GC	
GAM3560 LOC256286 3'	GCGCGGGGTGAGGTCCGGGGGC 80796	C_ CAGT__
	CGC GCGCGGGG AGG GCCGC	
	CGCGCCCC TCC CGGCG	
	AC AGGCCCC	
GAM3560 LOC257479 5'	GCGCGGGGCAGAGCTGAGC 80869	_ AGT
	GCGCGGGGCAG GC GC	
	CGCGCCCCGTC CG CG	
	T ACT	
GAM3560 LOC51107 5'	GCGTGGGGTGGCAACGC 80870	C CA
	GCG GGGG GGCAGTGC	

		CGC CCCC CCGTTGCG		
		A A_		
GAM3560	LOC51246	5' GCGCCGGGCGCAGTGCCGC	80871	G AG
		GCGC GGGC GCAAGTGCCGC		
		CGCG CCG CGTCACGGCG		
		G _		
GAM3560	LOC56926	5' GCGCGGGGCAGCCCG	80872	G AGTG
		GCGCGGGGCAG C CCG		
		CGCGCCCCGTC G GGC		
		- - - - -		
GAM3560	LOC58512	3' GCACGGGGCGGCCCG	80873	A AGTG
		GCGCGGGGC GGC CCG		
		CGTGCCCCG CCG GGC		
		- - - - -		
GAM3560	LOC89932	5' GCACGGGGTAGGCTGC	80874	C AG
		GCGCGGGG AGGC TGC		
		CGTGCCCC TCCG ACG		
		A _		
GAM3560	LOC90313	3' GCGCGGGGAGGAGCCG	80875	C CAGT
		GCGCGGGG AGG GCCG		
		CGCGCCCC TCC CGGC		
		- T - - -		
GAM3560	LOC91137	5' GCGGGGGCAGGATGACGC	80876	C CA C
		GCG GGGGCAGG GTG CGC		
		CGC CCCC GTCC TAC GCG		
		- - - T - - -		
GAM3560	LOC91252	3' GCTTGGGACCAAGTGCTGC	80877	GC AGG C
		GC GGGGC CAGTGC GC		
		CG CCCTG GTCACG CG		
		AA _ A		
GAM3560	LOC91373	3' GCATGGGGCAGGCTGC	80878	C AG
		GCG GGGGCAGGC TGC		
		CGT CCCC GTCCG ACG		
		A _		
GAM3560	LOC91632	3' GCGCGGGGTGAGGTCCGGGGGC	80796	C_ CAGT_
	CGC	GCGCGGGG AGG GCCGC		
		CGCGCCCC TCC CGGCG		
		AC AGGCCCC		
GAM3560	LOC91978	3' GCGTGGGGCAGGGGCTCCCGC	80879	C CA G_
		GCG GGGGCAGG GT CCGC		

		CGC CCCC GTCC CG GGCG		
		A C_ AG		
GAM3560	LOC92715	5' GCGCGGGGCGGCGAGGC	80880	A _ T
		GCGCGGGGC GGC AG GC		
		CGCGCCCCG CCG TC CG		
		_ C _		
GAM3561	PCDHB9	3' GCAAATTAAATATTTTCACA	80883	T CT
		GCAA ATTA AATATTTTCACA		
		CGTT TAAT TTATAAAAGTGT		
		- -		
GAM3561	RB1CC1	3' ACATAACAATATTTTCACAC	80884	T T
		ATAT AC AATATTTTCACAC		
		TGTA TG TTATAAAAGTGTG		
		T _		
GAM3561	RET	3' ATTACACTTATTTTCACA	80885	TAA
		ATTAC TATTTTCACA		
		TAATG ATAAAAGTGT		
		TGA		
GAM3561	ZNF10	3' GCAATATTATTAATAATCAC	80886	C TTT
		GCAATATTA TAATA TCAC		
		CGTTATAAT ATTAT AGTG		
		A T__		
GAM3561	CAPS2	3' GCATATCCTTTAATATTTTCA	80887	A AC_
		GCA TATT TAATATTTTCA		
		CGT ATAG ATTATAAAAGT		
		_ GAA		
GAM3561	FLJ11896	3' GCAATATAACTAACACAATACA	80888	T TTTC
		GCAATAT ACTAATAT ACA		
		CGTTATA TGATTGTG TGT		
		T TTA_		
GAM3561	FLJ23033	3' GCATATGTGCATATATTTTCAC	80889	ATATTACTA
	AC	GCA ATATTTTCACAC		
		CGT TATAAAAGTGTG		
		ATACACGTA		
GAM3561	KIAA0010	3' GCAATATTACTAAAGTAGCCAC	80890	TATTT
	A	GCAATATTACTAA TCACA		
		CGTTATAATGATT GGTGT		
		TCATC		
GAM3561	KIAA1559	3' GCTGTATTACTAGTGACCTCAC	80891	AA ATAT
	A	GC TATTACTA TTTCACA		

		CG ATAATGAT GGAGTGT	
		AC CACT	
GAM3561 KIAA1701	3'	GCATATAACTCCATATTTTCAC 80892	A T A_
	AC	GCA TAT ACT ATATTTTCACAC	
		CGT ATA TGA TATAAAAGTGTG	
		_ T GG	
GAM3561 RAI1	3'	GCAATATACTAATAAGAACAC 80893	T TTTT
		GCAATAT ACTAATA CAC	
		CGTTATA TGATTAT GTG	
		_ TCTT	
GAM3561 LOC144519	3'	GCAATATTTCTCCTATTCAC 80894	A AA TT
		GCAATATT CT TAT TCAC	
		CGTTATAA GA ATA AGTG	
		A GG _	
GAM3561 LOC158219	3'	ACAATATTAATTTTCACA 80895	CTAAT
		GCAATATTA ATTTTCACA	
		TGTTATAAT TAAAAGTGT	

GAM3561 LOC256940	3'	GCATATTACAGCATTTCACAC 80896	A TAATAT
		GCA TATTAC TTTTCACAC	
		CGT ATAATG AAAGTGTG	
		_ TCGT_	
GAM3562 CG018	3'	GAATATAATGACTTTTGCT 80899	ACTAA
		GAATATAAT ACTTTGCT	
		CTTATATTA TGAAACGA	
		C_	
GAM3562 CTCFL	3'	AGAATATAATGCTCTTCCTGCT 80900	A AAAC
		AGAATATAAT CT TTTGCT	
		TCTTATATTA GA GGACGA	
		C GAA_	
GAM3562 KIAA0077	5'	AAGAACATGATCTTCTTTGCT 80901	A A AAA
		AAGAATAT AT CT CTTTGCT	
		TTCTTGTA TA GA GAAACGA	
		C _ A_	
GAM3562 POFUT1	3'	AGAACACAACCTGAATTTTGCT 80902	AT A C
		AGAATATA ACT AA TTTGCT	
		TCTTGTGT TGA TT AAACGA	
		_ C A	
GAM3562 LOC220115	5'	GAATATAAACTTTGC 80903	TACTAA
		GAATATAA ACTTTGC	

CTTATATT TGAAACG

GAM3563 B4GALT6 3' TATAGATTTTAGTATAAAA 80906 A
TATAGA TTTAGTATAGAA
||||| ||||||||
ATATCT AAATCATATTTT
A

GAM3563 CREB1 3' TAAGAATTTAGTACTAACT 80907 T AG
A AGAATTTAGTAT AACT
| |||||||| ||||
A TCTTAAATCATG TTGA
T A_

GAM3563 ETFA 3' TATAGATTTTAGTACAGAA 80908 A
TATAGA TTTAGTATAGAA
||||| ||||||||
ATATCT AAATCATGTCTT
A

GAM3563 FACL2 3' TATAGAATCTAAGGCAGA 80909 TA
TATAGAATTTAG TAGA
||||||||| ||||
ATATCTTAGATT GTCT
CC

GAM3563 LHCGR 3' ATAGAACAGATAGAACT 80910 TT T
ATAGAAT AG ATAGAACT
||||| || |||||||
TATCTTG TC TATCTTGA

GAM3563 NPC1 3' TAAAAATATGGTATAGAACT 80911 T TTA
A AGAAT GTATAGAACT
| |||| | |||||||
A TTTTA CATATCTTGA
T TAC

GAM3563 FLJ10110 3' TAGAATTTAAACAAAAC 80912 T
TAGAATTTAG ATAGAACT
||||||| |||||||
ATCTTAAATT TGTTTTGA

GAM3563 FLJ14054 5' TATAGAATTACTTAAGAACT 80913 TAGTAT
TATAGAATT AGAACT
||||||| |||||
ATATCTTAA TCTTGA
TGAAT_

GAM3563 KIAA1615 3' ATAGAATTTAGTTAGAA 80914 A
ATAGAATTTAGT TAGAA
||||||||| |||||
TATCTTAAATCA ATCTT

GAM3563 LOC131368 3' TATAAAATGGAGTATAGAA 80915 TT
TATAGAAT AGTATAGAA
||||||| |||||||

		ATATTTTA TCATATCTT		
		CC		
GAM3563	LOC144308 3'	TATGGAAATGTATAGAACT	80916	A TTTA
		TAT GAA GTATAGAACT		
		ATACTT CATATCTTGA		
		C TA__		
GAM3563	LOC150848 5'	TATAAAATTTAGCTTAAGA	80917	AT_
		TATAGAATTTAGT AGA		
		ATATTTTAAATCG TCT		
		AAT		
GAM3563	LOC222161 5'	TGAGAATTTAGTAATAGGAGAA	80918	T T_____
	CT	A AGAATTTAGTA AGAACT		
		A TCTTAAATCAT TCTTGA		
		C TATCC		
GAM3563	LOC253587 3'	TACAGAATTTACAAAGAACT	80919	AG T
		TATAGAATTT TA AGAACT		
		ATGTCTTAAA GT TCTTGA		
		GT T		
GAM3564	DYT1 3'	TACTTTTCTTTCAAAGACT	80922	G TAT
		TACTTT TCTTTCAA GACT		
		ATGAAA AGAAAGTTT CTGA		
		_ T__		
GAM3564	HPGD 3'	TACTTTGTCTTTAATACAT	80923	CAA
		TACTTTGTCTTT ATAT		
		ATGAAACAGAAA TGTA		
		TTA		
GAM3564	KCNS2 3'	TTTGTTTTCACATGACT	80924	C AA
		TTTGT TTTCA TATGACT		
		AAACA AAAGT GTACTGA		
		- -		
GAM3564	MLLT2 3'	CTTATGCTCAGATATGACTA	80925	_ CTT A
		CTT TGT TCA ATATGACTA		
		GAA ACG AGT TATACTGAT		
		T _ C		
GAM3564	MTM1 3'	TTTGTCTTTCAAAAAC	80926	TAT
		TTTGTCTTTCAA GACT		
		AAACAGAAAGTTT TTGA		
		-		
GAM3564	SEL1L 3'	TACTTTTTCTTTGCCATTGACT	80927	G CAA A
		TACTTT TCTTT AT TGACT		

		ATGAAA AGAA TA ACTGA	
		A CGG _	
GAM3564	TRHR	3' CTCTGTCTTCACATATGACTA 80928	T A
		CTTTGTCTT CA ATATGACTA	
		GAGACAGAA GT TATACTGAT	
		_ G	
GAM3564	BTN3A3	3' TACTTGCAAAATATGACT 80929	T CTTTC
		TACTT GT AAATATGACT	
		ATGAA CG TTTATACTGA	
		_ T____	
GAM3564	KHDRBS1	3' TACTTTGTCTTTTAAATAC 80930	C_
		TACTTTGTCTTT AAATAT	
		ATGAAACAGAAA TTTATG	
		AA	
GAM3564	KIAA0826	3' TACCTTGAAAATATGACT 80931	TCTTTC
		TACTTTG AAATATGACT	
		ATGGAAC TTTATACTGA	
		T____	
GAM3564	KIAA1254	3' CACTTTGTGCATGTATGACT 80932	TTTCAAA
		TACTTTGTC TATGACT	
		GTGAAACAG A TACTGA	
		TAC____	
GAM3564	PRO1635	3' TTTGTCTTTGGCAATATGA 80933	CA_
		TTTGTCTTT AATATGA	
		AAACAGAAA TTATACT	
		CCG	
GAM3564	SCDGF-B	3' TACATTGTCTTTTGTAGGACTA 80934	T CAAA T
		TAC TTGTCTTT TA GACTA	
		ATG AACAGAAA AT CTGAT	
		T AC_ C	
GAM3564	SCDGF-B	3' TACATTGTCTTTTGTAGGACTA 80934	T CAAA T
		TAC TTGTCTTT TA GACTA	
		ATG AACAGAAA AT CTGAT	
		T AC_ C	
GAM3564	LOC169611	3' ACTTTGTTCTAAATATGACT 80935	_ TTC
		ACTTTGT CT AAATATGACT	
		TGAAACA GA TTTATACTGA	
		A _	
GAM3564	LOC202460	5' TTTGTCTTTCAAGACT 80936	ATAT
		TTTGTCTTTCAA GACT	

AAACAGAAAGTT CTGA

GAM3564 LOC91133 3' TACTTGTCTTTCAACACTG 80937 T ATA
TACTT GTCTTTCAA TG
||||| ||||| ||
ATGAA CAGAAAGTT AC
_ GTG

GAM3565 FLJ11896 3' TATTTTCTATTACAAATT 80940 GC
TATTTTCTTAT TTACAATT
||||| |||||
ATAAAAAGATA AATGTTAA

GAM3565 KIAA0280 3' TATTTCTTCATTTGCAATTTCT 80941 GCTTA
TATTTTCTTAT CAATTTCT
||||| |||||
ATAAAGAAGTA GTTAAAGA
AAC_

GAM3566 DDX1 3' TAGCATTAAAGCTTACGTTAC 80944 A_ AAA
TAT TAGCATTAAATA ATGT ACTAT
||||| ||| ||||
ATCGTAATTAT TGCA TGATA
CGAA A_

GAM3566 PSEN2 3' GCACTAGAGTGTA AAACTAT 80945 ATAAA
GCATTA TGTA AAACTAT
||||| |||||
CGTGAT ACATTTTGATA
CTC_

GAM3566 PSEN2 3' GCACTAGAGTGTA AAACTAT 80945 ATAAA
GCATTA TGTA AAACTAT
||||| |||||
CGTGAT ACATTTTGATA
CTC_

GAM3566 KIAA0820 3' TAGCATGTGACAATA AAACTAT 80946 TAATAAAT
TAGCAT GTAA AACTAT
||||| |||||
ATCGTA TATTTTGATA
CACTGT_

GAM3567 LOC222224 3' CTGTTCCAATCTGCTGTGATC 80949 _ ACTAC
CTGTTCTGGTCTGCT GATC
||||| ||||| |||
GACAAG TTAGACGA CTAG
G CA_

GAM3568 ANKRA2 5' AGGGTCATTTCAGTTGACG 80952 A_ T_
AG TCATTTCAGTT CG
|| ||||| ||
TC AGTAAAGTCAA GC
CC CT

GAM3568 FCN2 3' TAAGATCATTGTCCTGGTCTTT 80953 TCA C_
TAAGATCATT GTTT GTCTTT
||||| ||| |||||

ATTCTAGTAA CAGG CAGAAA
 ____ AC
 GAM3568 DKFZP434K028 3' GACATTTTCAGCCACCTCTTT 80954 T TCG
 GA CATTTCAGTT TCTTT
 || ||||| ||||
 CT GTAAAGTCGG AGAAA
 _ TGG
 GAM3568 DKFZP564O0423 3' GATCACTTCTGGTTTTGT 80955 A_ C
 GATCATTTT GTTT GT
 ||||| ||| ||
 CTAGTGAAG CAAA CA
 AC A
 GAM3568 PRO2730 3' TAAGATCATTTGGTTTC 80956 CA
 TAAGATCATTT GTTTC
 ||||| ||||
 ATTCTAGTAAA CAAAG
 C_
 GAM3568 SS-56 3' TAAGGCCATTTTCAGTTTC 80957 AT
 TAAG CATTTCAGTTTC
 ||| |||||
 ATTC GTAAAGTCAAAG
 CG
 GAM3568 LOC149721 5' AAATCATTTTCAGGCCTT 80958 TTTC
 AGATCATTTTCAG GTCTT
 ||||| ||||
 TTTAGTAAAGTC CGGAA

 GAM3569 ATP5A1 3' TTCATGTGATTTCTGTACA 80961 C_
 TTCATGTGA TTTGTATA
 ||||| |||||
 AAGTACACT AGACATGT
 AA
 GAM3569 PCDHB16 5' TTCATGTGACTTTTCGTGTAT 80962 ____
 TTCATGTGACTT TGTAT
 ||||| ||||
 AAGTACACTGAA ACATA
 AGC
 GAM3569 FLJ10900 3' TATGAAAGTATAATTTAC 80963 CTTT
 TGTGA GTATAATTTAC
 |||| |||||
 ATACT CATATTAAATG
 TT_
 GAM3569 FLJ10900 3' TATGAAAGTATAATTTAC 80963 CTTT
 TGTGA GTATAATTTAC
 |||| |||||
 ATACT CATATTAAATG
 TT_
 GAM3569 INA 3' TTCGTGTGACTTTTAATTTA 80964 A GTA
 TTC TGTGACTTT TAATTTA
 || ||||| |||||

		AAG ACACTGAAA ATTAAAT		
		C —		
GAM3569	KIAA0608	3' TTCAGTGA	CTTAAATAATTTAC	80965 T TGT
		TTCA GTGACTT	ATAATTTAC	
		AAGT CACTGAA	TATTAAATG	
		— TT_		
GAM3569	MBLL39	3' TTCAGTGA	TTCCATAATTTAC	80966 T C G
		TTCA GTGA TTT	TATAATTTAC	
		AAGT CACT AAG	GTATTAAATG	
		— — G		
GAM3569	MIL1	3' TTCATGTG	ATTTTTCTCTGT	80967 —
		TTCATGTGA	CTTTGT	
		AAGTACACT	GAGACA	
		AAAAA		
GAM3569	LOC148114	3' TTCATGTG	GGA	CTTAAATGT 80968 — —
		TTCATGTG	ACTT TGT	
		AAGTACAC	TGAA ACA	
		C TTT		
GAM3570	HLA-A	3' AAGAGGGT	CATGGTGGACATGG	80971 — ATTTAAT
		AAGA GTCATGGT	TGG	
		TTCT CAGTACCA	ACC	
		CC CCTGT_		
GAM3570	C6orf5	3' TAAAGGTC	ATACAGCTAATTGG	80972 A GTAT
		TAAAG GTCATG	TTAATTGG	
		ATTTC CAGTAT	GATTAACC	
		— GTC_		
GAM3570	DKFZP547E2110	3' TAAAGGTC	CATGGTATTT	80973 A
		TAAAG GTCATGGT	ATTT	
		ATTTC CAGTACC	ATAAAA	
		—		
GAM3570	FLJ13102	3' AAGAGAGT	AGCATTTGGTTGG	80974 TCA AA
		AAGAG TGGTATTT	TTGG	
		TTCTC ATCGTAAA	AACC	
		TC_ CC		
GAM3570	JWA	3' TAAAGATC	ATGGCTGTAGGTTG	80975 G ATTTAA
	G	TAAAGA	TCATGGT TTGG	
		ATTTCT AGTACCG	AACC	
		— ACATCC		
GAM3570	TP53INP1	3' TAAACAGT	TGAAATTTAATTGG	80976 G CA T
		TAAA AGT	TGG ATTTAATTGG	

ATTT TCA ACT TAAATTAACC
 G _ T
 GAM3570 TP53INP1 3' TAAACAGTTGAAATTTAATTGG 80976 G CA T
 TAAA AGT TGG ATTTAATTGG
 |||| ||| ||| |||||
 ATTT TCA ACT TAAATTAACC
 G _ T
 GAM3570 LOC221833 3' GAGTTATATTTAATTGG 80977 CATG
 GAGT GTATTTAATTGG
 |||| |||||
 CTCA TATAAATTAACC
 A _
 GAM3570 LOC257490 3' AAGAGGGTCATGGTGGACATGG 80971 _ ATTTAAT
 AAGA GTCATGGT TGG
 |||| ||||| |||
 TTCT CAGTACCA ACC
 CC CCTGT_
 GAM3571 SOX4 3' TCTGCCATCGGCCAAA 80980 A ATGCT T
 TCT CCATC G GTCAAA
 ||| |||| | |||||
 AGA GG TAG C CGGTTT
 C _ _ _
 GAM3571 TAF4 3' TCTATGTCATGTGCCAAA 80981 CCA TGC
 TCTA TCA TGTGTCAAA
 |||| ||| |||||
 AGAT AGT ACACGGTTT
 AC_ _
 GAM3571 ATF3 3' CCTGCCATCATGCTGCCCA 80982 A G
 TCT CCATCATGCTGT TCA
 ||| ||||| ||||| |||
 GGA GG TAGTACGACG GGT
 C _
 GAM3571 DKFZP434K0427 3' TCTATGTCTATGTCAAAT 80983 _ _
 TC ATG CTGTGTCAAAT
 || ||| |||||
 AG TAC GATACAGTTTA
 A A
 GAM3571 FLJ23499 3' TACCAAGACTCTGTGTCAA 80984 TC G
 TACCA AT CTGTGTCAA
 |||| || |||||
 ATGGT TG GACACAGTT
 TC A
 GAM3571 LOC142941 3' TCTACCATTGCTGGGCACA 80985 CA T _
 TCTACCAT TGCTG GT CA
 ||||| |||| ||| ||
 AGATGGTA ACGAC CG GT
 _ C T
 GAM3571 LOC200299 3' ATCATCTTTGTCAAATT 80986 G G
 ATCAT CT TGTCAAATT
 |||| || |||||

				TAGTA GA ACAGTTTAA			
				_ A			
GAM3571	LOC200300	3'	ATCATCTTTGTCAAATT	80986		G G	
			ATCAT CT TGTCAAATT				
			TAGTA GA ACAGTTTAA				
			_ A				
GAM3571	LOC200304	3'	ATCATCTTTGTCAAATT	80986		G G	
			ATCAT CT TGTCAAATT				
			TAGTA GA ACAGTTTAA				
			_ A				
GAM3571	LOC200305	3'	ATCATCTTTGTCAAATT	80986		G G	
			ATCAT CT TGTCAAATT				
			TAGTA GA ACAGTTTAA				
			_ A				
GAM3571	LOC254182	3'	TCTGCAGTCATGCTGACCCA	80987		AC _	TG
			TCT CA TCATGCTG TCA				
			AGA GT AGTACGAC GGT				
			C_ C TG				
GAM3572	RFX5	3'	TTGAATTAGGTTTTCTGTGAT	80990		C TTTG	C
			TTGAA TAG TTCT GTGAT				
			AACTT ATC AAGA CACTA				
			A CAA_ _				
GAM3572	FLJ13224	3'	AGCGCTGTTTTCTGTGATC	80991		_ C	
			AGT TTGTT TCGTGATC				
			TCG GACAA AGCACTAG				
			C A				
GAM3573	SCA1	3'	TTTAATACAGTTGAACCA	80994		T TACATT	
			TTTAATAC AGTTG CCA				
			AAATTATG TCAAC GGT				
			_ TT___				
GAM3573	ZNF146 CAT	3'	CTTAATATTAGTTGTAGATGAC	80995		C CATT_	
			TTTAATA TAGTTGTA CCAT				
			GAATTAT ATCAACAT GGTA				
			A CTA CTACT				
GAM3573	ARPC5	3'	AATACTAGTTGTATACCTCAT	80996		C TC	
			AATACTAGTTGTA AT CAT				
			TTATGATCAACAT TG GTA				
			A GA				
GAM3573	KIAA1164 T	3'	TTTAATACAATTGAACATTTC	80997		T T C	
			TTTAATAC AGTTG ACATT CAT				

AAATTATG TTAAC TGTA A GTA
 _ T A
 GAM3573 LOC157867 5' TTTAACA CTGAATAATATTCCA 80998 _ T CA
 T TTTAATACT AGT GTA TTCCAT
 ||||| ||| ||| |||||
 AAATTGTGA TTA TAT AAGGTA
 C T _
 GAM3574 LOC154007 3' CAGTATATGATTCTTGG 81001 A CG
 TAGTATAT ATTTC GG
 ||||| ||||| ||
 GTCATATA TAAAG CC
 C AA
 GAM3574 LOC200609 5' TAGTATATGCATATGATGGATT 81002 A_ TTCCG
 ATT TAGTATAT AT GGATTATT
 ||||| || |||||
 ATCATATA TA CCTAATAA
 CG TACTA
 GAM3575 EDAR 3' TACGTTCCCTTCTGTCTTCTA 81005 G _
 TGCGT CC GTCTTCTA
 ||||| || |||||
 ATGCA GG CAGAAGAT
 A AAGA
 GAM3575 MXI1 3' TGCGTGCACAACTCTTCT 81006 _ _
 TGCGTGC CG TCTTCT
 ||||| || |||||
 ACGCACG GT AGAAGA
 T TG
 GAM3575 MXI1 3' TGCGTGCACAACTCTTCT 81006 _ _
 TGCGTGC CG TCTTCT
 ||||| || |||||
 ACGCACG GT AGAAGA
 T TG
 GAM3575 FLJ12747 3' ATACATAAGTTGTCTTCTA 81007 CC_
 GTGCGTG GTCTTCTA
 ||||| |||||
 TATGTAT CAGAAGAT
 TCAA
 GAM3575 KIAA0365 3' TAACATCACAAATGTCTTCTA 81008 _ TGCC
 TAACGT GCG GTCTTCTA
 ||||| ||| |||||
 ATTGTA TGT CAGAAGAT
 G TTA_
 GAM3575 KIAA1416 3' GTGCTATTTCTGTCTTCTA 81009 _ GC
 GTGC GT CGTCTTCTA
 ||||| || |||||
 CACG TA GCAGAAGAT
 A AA
 GAM3575 KIAA1710 3' TAACTGTGGGCATCTTCT 81010 _ CGT C
 TAAC GTG GC GTCTTCT
 ||||| ||| || |||||

ATTG CAC CG TAGAAGA
 A C__ _
 GAM3575 PRO0149 5' TAACGTGCTGCTCTTCT 81011 G CG
 TAACGTGC TGC TCTTCT
 ||||| || |||||
 ATTGCACG ACG AGAAGA

_ _
 GAM3575 RP4-622L5 5' CAACGCCGCTGTCTTCTA 81012 GCG C
 TAACGT TGC GTCTTCTA
 ||||| || |||||
 GTTGCG GCG CAGAAGAT

_ _ A
 GAM3575 LOC123036 3' TAATGGTAAAGTCTTCTA 81013 C C CC
 A GTG GTG GTCTTCTA
 | ||| || |||||
 A TAC CAT CAGAAGAT
 T _ TT

GAM3575 LOC199990 3' GTGGCAGAGCCGTCTTCT 81014 _ T_
 GTG CG GCCGTCTTCT
 ||| || |||||
 CAC GT CGGCAGAAGA
 C CT

GAM3575 LOC201617 5' CAACTGAGACGTTGTCTTCTA 81015 GT__ GCC
 TAAC GCGT GTCTTCTA
 ||| ||| |||||
 GTTG TGCA CAGAAGAT
 ACTC A__

GAM3575 LOC221540 3' ACGTGCAGCTCTTCT 81016 T CG
 ACGTGCG GC TCTTCT
 ||||| || |||||
 TGCACGT CG AGAAGA

_ _
 GAM3575 LOC257545 3' ACGTGCAGCTCTTCT 81016 T CG
 ACGTGCG GC TCTTCT
 ||||| || |||||
 TGCACGT CG AGAAGA

_ _
 GAM3575 LOC257598 3' ACGTGCAGCTCTTCT 81016 T CG
 ACGTGCG GC TCTTCT
 ||||| || |||||
 TGCACGT CG AGAAGA

_ _
 GAM3575 LOC90906 3' CAATACCTTTGCCGTCTTCT 81017 C G_
 A GTGC TGCCGTCTTCT
 | ||| |||||
 G TATG ACGGCAGAAGA
 T GAA

GAM3576 CDKN1B 5' GACCAGGCAAGCGGAGAGGGT 81020 A TCAA TCA
 GACCAG CAA AGA GGT
 ||||| || ||| |||

			CTGGTC GTT TCT CCA		
			C CGCC C__		
GAM3576 CREBBP	3'	AGACCAGATATTTAAATCAACT	81021	CAATCAA	___
	GGT	AGACCAGA AGATCA GGT			
		TCTGGTCT TTTAGT CCA			
		ATAAA__ TGA			
GAM3576 EIF2C1	3'	CAGAGAACAAATCAGGT	81022	C CAA	
		CAGA AAT AGATCAGGT			
		GTCT TTG TTTAGTCCA			
		C ___			
GAM3576 GAS7	3'	GATCAGATAATCAATCAGG	81023	C C AAG	
		GA CAGA AATCA ATCAGG			
		CT GTCT TTAGT TAGTCC			
		A A ___			
GAM3576 MOX2	3'	AGACCAGGGAATCACTTTCAGG	81024	AC AAGA	
		AGACCAG AATCA TCAGG			
		TCTGGTC TTAGT AGTCC			
		CC GAA_			
GAM3576 NEK6	3'	AGCTCAGACAATTGGAAGG	81025	AC CAAA TC	
		AG CAGACAAT GA AGG			
		TC GTCTGTTA CT TCC			
		GA AC__ _			
GAM3576 NOL3	3'	AGCCAGACAATTAACAG	81026	A CA T	
		AG CCAGACAAT AAGA CAG			
		TC GGTCTGTTA TTTT GTC			
		_ A_ _			
GAM3576 OLIG2	3'	AGCCAGACAGCGCTCGATCAGG	81027	A ATCAAA	
	T	AG CCAGACA GATCAGGT			
		TC GGTCTGT CTAGTCCA			
		_ CGCGAG			
GAM3576 TNFRSF4	3'	AGATCAGGAAATCAAGGACC	81028	C AC A	
		AGA CAG AATCAA GATC			
		TCT GTC TTAGTT CTGG			
		A CT C			
GAM3576 APOARGC	5'	AAACCAGATAGTCAAATTAAGT	81029	CAA GATC	
		AGACCAGA TCAAA AGGT			
		TTTGGTCT AGTTT TTCA			
		ATC AA__			
GAM3576 CAMKK1	3'	AGACCAGATGCTCAAGGAACA	81030	CAA A T	
		AGACCAGA TCAA GA CA			

		TCTGGTCT AGTT CT GT	
		ACG C T	
GAM3576 FLJ10103	3'	AGACCAGATAATCTGGCTCTGG 81031	C AAAGA A
	T	AGACCAGA AATC TC GGT	
		TCTGGTCT TTAG AG CCA	
		A ACCG_ A	
GAM3576 FLJ31168	3'	AGACCAGATGAATCAAGGAAAA 81032	C_ A TC
	G	AGACCAGA AATCAA GA AG	
		TCTGGTCT TTAGTT CT TC	
		AC C TT	
GAM3576 FLJ32940	5'	AGACGGGATGGTCAATCAGGT 81033	CA CAA AAG
		AGAC GA TCA ATCAGGT	
		TCTG CT AGT TAGTCCA	
		CC ACC _	
GAM3576 GABARAP	3'	AGACTGACAATCAAGA 81034	CA A
		AGAC GACAATCAA GA	
		TCTG CTGTTAGTT CT	
		A_ _	
GAM3576 KIAA1938	3'	GACCAGCCGAGAGCAGATCAGG 81035	ACAATCAA
	T	GACCAG AGATCAGGT	
		CTGGTC TCTAGTCCA	
		GGCTCTCG	
GAM3576 MGC10940	3'	AGATTAGAAGTCAAAGATCAAG 81036	CC CAA _
	GT	AGA AGA TCAAAGATCA GGT	
		TCT TCT AGTTTCTAGT CCA	
		AA TC_ T	
GAM3576 SERPINB7	3'	GATCAGGACAATCAACCAGGT 81037	C _ AAG
		GA CAG ACAATCA ATCAGGT	
		CT GTC TGTTAGT TGGTCCA	
		A C _	
GAM3576 SLC26A10	5'	AGACCAGGACAATTAGGTTTGG 81038	_ CAA ATCA
	T	AGACCAG ACAAT AG GGT	
		TCTGGTC TGTTA TC CCA	
		C A_ CAAA	
GAM3576 SS-56	3'	CAGGACAATCATATGAGGT 81039	_ AAG C
		CAG ACAATCA AT AGGT	
		GTC TGTTAGT TA TCCA	
		C A_ C	
GAM3576 TA-NFKBH	3'	GACTGGAAAATCAGTCCAGG 81040	CA C AA A
		GAC GA AATCA G TCAGG	

	CTG CT TTAGT C GGTCC		
	AC T _ A		
GAM3576 LOC149421 5'	AGACCAGGTAATCAATGCAGAT 81041	AC	AGAT
	AGACCAG AATCAA CAGGT		
	TCTGGTC TTAGTT GTCTA		
	CA AC_		
GAM3576 LOC149478 3'	GACTGACAATCAAAAACAGGT 81042	CA	T
	GAC GACAATCAAAGA CAGGT		
	CTG CTGTTAGTTTT GTCCA		
	A_ _		
GAM3576 LOC158972 3'	AGACCAGATATTCAGAGACC 81043	CAA	A
	AGACCAGA TCA AGATC		
	TCTGGTCT AGT TCTGG		
	ATA C		
GAM3576 LOC170132 5'	CCAGAACTTAAGATCAGGT 81044	CA	CA
	CCAGA AT AAGATCAGGT		
	GGTCT TG TTCTAGTCCA		
	_ AA		
GAM3576 LOC200515 5'	AGACCAGACAGCAGGACATGG 81045	ATCAA	AT _
	AGACCAGACA AG CA GG		
	TCTGGTCTGT TC GT CC		
	CG_ CT A		
GAM3576 LOC254571 3'	ACCAGACAGTCAAGCAGGT 81046	A	AGAT
	ACCAGACA TCAA CAGGT		
	TGGTCTGT AGTT GTCCA		
	C C_		
GAM3576 LOC254600 5'	AGACCAGGCTGGTCCTACCCAG 81047	ACAA_	AAAGA
GT	AGACCAG TC TCAGGT		
	TCTGGTC AG GGTCCA		
	CGACC GATG_		
GAM3576 LOC256515 5'	GACTGACGGACCAATCAGGT 81048	CA	A_ AAG
	GAC GAC ATCA ATCAGGT		
	CTG CTG TGGT TAGTCCA		
	A_ CC _		
GAM3577 CSF1R 3'	TGTGGAGTGAAGGCGGCGT 81051	A	GA
	TGTGGAGTGGA GCG GCGT		
	ACACCTCACTT CGC CGCA		
	C _		
GAM3577 HSF4 5'	TGTGGAGTGGAGTGGAG 81052	A	C
	TGTGGAGTGGA G GGAG		

		ACACCTCACCT C CCTC		
		_ A		
GAM3577	CDCA4	3' TGTGGGGTGAGGCGGGGC	81053	A AA A
		TGTGG GTGG GCGG GC		
		ACACC CACT CGCC CG		
		C C_ C		
GAM3577	KIAA0652	3' TGAGGGGTGGGAGCAGCTGAT	81054	T A A GG G
		TG GG GTGG AGC AGC TGAT		
		AC CC CACC TCG TCG ACTA		
		T C C _ _		
GAM3577	PRAX-1	3' TGTGCAGTGGAAGCGAGGT	81055	G G C
		TGTG AGTGGGAAGCG AG GT		
		ACAC TCACCTTCGC TC CA		
		G _ _		
GAM3577	LOC151632	5' TGTGGAGTGGGGGCTGTG	81056	AAGC A _
		TGTGGAGTGG GG GC GTG		
		ACACCTCACC CC CG CAC		
		_ _ A		
GAM3577	LOC152271	3' TGTGGAGTGGGGGCTGTG	81056	AAGC A _
		TGTGGAGTGG GG GC GTG		
		ACACCTCACC CC CG CAC		
		_ _ A		
GAM3577	LOC200904	5' TGTGGAGTGGGGGCTGTG	81056	AAGC A _
		TGTGGAGTGG GG GC GTG		
		ACACCTCACC CC CG CAC		
		_ _ A		
GAM3577	LOC203083	5' TGTGGAGTGGGGGCTGTG	81056	AAGC A _
		TGTGGAGTGG GG GC GTG		
		ACACCTCACC CC CG CAC		
		_ _ A		
GAM3577	LOC219919	5' TGTGGAGTGGGGGCTGTG	81056	AAGC A _
		TGTGGAGTGG GG GC GTG		
		ACACCTCACC CC CG CAC		
		_ _ A		
GAM3577	LOC254176	5' TGTGGAGTGGGGGCTGTG	81056	AAGC A _
		TGTGGAGTGG GG GC GTG		
		ACACCTCACC CC CG CAC		
		_ _ A		
GAM3577	LOC256594	5' TGTGGAGTGGGGGCTGTG	81056	AAGC A _
		TGTGGAGTGG GG GC GTG		

		ACACCTCACC CC CG CAC		
		_____ A		
GAM3577	LOC55885	3' TGGAGTGGAGGTGCACG 81057	AGC	A
		TGGAGTGGA GG GCGTG		
		ACCTCACCT CC CGTGC		
		_____ A		
GAM3578	RELN	3' TTATTTAAGCATGGGCTTT 81060	TGTGA	
		TTATTTGAGTGTG GCTTT		
		AATAAATTCGTAC CGAAA		
		C_____		
GAM3578	BICD2	3' TTTGGGTCTGTGTAAAGGTTT 81061	A G	CT
		TTTG GT TGTGTGAG TTC		
		AAAC CA ACACATTT AAG		
		C G CC		
GAM3578	DONSON	3' TCATTTGAGTTATCTGAGTTTT 81062	G G	C
		TTATTTGAGT TGT TGAG TTT		
		AGTAAACTCA ATA ACTC AAA		
		_____ G A		
GAM3578	FLJ20093	3' TTTGAGTGTGAGAGTTTT 81063	TGT	C
		TTTGAGTGTG GAG TTT		
		AAACTCACAC CTC AAA		
		T_____ A		
GAM3578	GPR105	3' TTGTCTGGGTGTCAGCTTT 81064	AG T	G
		TTG TG GTGT AGCTTT		
		AAC AC CACA TCGAAA		
		AG C G		
GAM3578	LOC144997	3' TATTTTGTATGTGTGGGCTTT 81065	GA	A
		TATTT GTGTGTGTG GCTTT		
		ATAAA CACACAC CGAAA		
		A_____ C		
GAM3578	LOC147929	3' TTCTTTGGGTGTGAGTTTT 81066	GAG T	C
		TTT TG GTGTGAG TTT		
		AAG AC CAACTC AAA		
		AA_____ C A		
GAM3578	LOC150333	5' TTCACCTGTGTGTGGGCTTTC 81067	AG	A
		TTTG TGTGTGTG GCTTTC		
		AAGT ACACACAC CGAAAG		
		GG C		
GAM3578	LOC221712	5' ATTTGATCTGTGAGCTTT 81068	GTG	G
		ATTTGA T TGTGAGCTTT		

TAAACT A ACACTCGAAA
— G
GAM3579 GYPA 3' TTAATTGCCATTGTAACAGTGT 81071 CC T T
TTAATTGCTA GT ACA TGT
||||||| || ||| |||
AATTAACGGT CA TGT ACA
AA T C
GAM3579 DKFZP434N093 3' TTAATTGCACACAGTTGTA 81072 T CGTT _
TTAATTGC AC ACA TTGTA
||||||| || ||| |||||
AATTAACG TG TGT AACAT
— — C
GAM3579 FLJ13231 3' ATTGCTACACATTGTA 81073 CGTT
ATTGCTAC ACATTGTA
||||||| |||||
TAACGATG TGTAACAT
—
GAM3579 U2AF65 3' TTAATTGCTGCCATTCCAGTTG 81074 A A _
C TTAATTGCT CCGTT CA TTGT
||||||| ||||| || |||
AATTAACGA GGTA GT AACG
C G C
GAM3579 LOC147072 3' TTAATAGCTTTGATACATTGT 81075 T ACCGT
TTAAT GCT TACATTGT
||||| ||| |||||
AATTA CGA ATGTAACA
T AACT_
GAM3580 ADORA2A 3' CACCTGGTGCAAGGCCTCAC 81078 TTTTA
CACCTGGTGCGA TCAC
||||||| |||
GTGGACCACGTT AGTG
CCGG_
GAM3580 ANKRD3 3' CCTGGGGGCTTCATCAC 81079 T GAT
CCTGG GC TTTATCAC
||||| || |||||
GGACC CG AAGTAGTG
C _
GAM3580 CCRL1 3' CTGTGTCATTTTATCAC 81080 G CG
CTG TG ATTTTATCAC
||| || |||||
GAC AC TAAAATAGTG
_ AG
GAM3580 CEBPA 3' CACCTGGTGACCCCATC 81081 GC
CACCTGGT GATTTTATC
||||||| |||||
GTGGACCA CTGGGGTAG
—
GAM3580 FMR2 3' CACCTGCTGTTTCTATCA 81082 G CGA
CACCTG TG TTTTATCA
||||| || |||||

			GTGGAC AC AAGATAGT		
			G A__		
GAM3580	MTMR8	3'	CACCTAGTGAATATTAC 81083	C T	
			CACCTGGTG GAT TTAT		
			GTGGATCAC TTA AATG		
			_ T		
GAM3580	NDRG2	3'	ACACTGGATGTTTTTATCAC 81084	_ _ CGA	
			AC CTGG TG TTTTATCAC		
			TG GACC AC AAAATAGTG		
			T T A__		
GAM3580	NDUFA5	3'	CACTTGTGCTATTTTATCAC 81085	CTG G	
			CAC GTGC ATTTTATCAC		
			GTG CACG TAAAATAGTG		
			AA_ A		
GAM3580	PCDHA9	3'	CTGATCATTTTATCAC 81086	G G	
			CTGGT C ATTTTATCAC		
			GACTA G TAAAATAGTG		
			--		
GAM3580	PSCD4	3'	CCGGGCTGCCCTTTATCAC 81087	T _ GA	
			CC GG TGC TTTTATCAC		
			GG CC ACG GAAATAGTG		
			C G G_		
GAM3580	SLC9A3R1	3'	CCTGGACCCATTTATCAC 81088	T GAT	
			CCTGG GC TTTATCAC		
			GGACC TG AAATAGTG		
			_ GGT		
GAM3580	STCH	3'	ACCTCAATTTTATCA 81089	GGTG	
			ACCT CGATTTTATCA		
			TGGA GTTAAAATAGT		

GAM3580	TRHDE	3'	TGGTAACTGGATTTTATCA 81090	C__	
			TGGTG GATTTTATCA		
			ACCAT CTAAAATAGT		
			TGAC		
GAM3580	VENTX2	3'	CACTTGTACTTTTATCAC 81091	CTG GA	
			CAC GTGC TTTTATCAC		
			GTG CATG AAAATAGTG		
			AA_ _		
GAM3580	C20orf154	3'	CATCTGGAGACTTTTATCAC 81092	C TGC	
			CA CTGG GATTTTATCAC		

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GT GACC CTGAAATAGTG
A T__
GAM3580 DEGS 3' CCCGGCTAATTTTATCA 81093 GC
CCTGGT GATTTTATCA
||||| |||||||
GGGCCG TTAAAATAGT
A_
GAM3580 DKFZp434F1819 5' CACTTTGTGCTTCATCTTATCA 81094 CTG G__
C CAC GTGC ATTTTATCAC
||| ||| |||||||
GTG CACG TAGAATAGTG
AAA AAG
GAM3580 DKFZP547L112 3' ACCTGGACATTTATCAC 81095 T AT
ACCTGG GCG TTTATCAC
||||| ||| |||||||
TGGACC TGT AAATAGTG
- -
GAM3580 DKFZP566D1346 3' TAATACAAGATTTTATCAC 81096 _
TGGTGC GATTTTATCAC
||||| |||||||
ATTATG CTAAAATAGTG
TT
GAM3580 EML4 3' ACCTGAACTTTATCA 81097 GTGC
ACCTG GATTTTATCA
||||| |||||||
TGGAC TTGAAATAGT
-
GAM3580 EPB41L4 3' CCTGATGCGGATTGGGTCAC 81098 _ TTA
CCTGGTGCG ATT TCAC
||||||| ||| |||
GGA CTACGC TAA AGTG
C CCC
GAM3580 FLJ00001 3' CACCTGCTCCTTATCA 81099 GGT GA
CACCT GC TTTTATCA
||||| || |||||||
GTGGA CG GGAATAGT
_ A_
GAM3580 FLJ20051 3' CCCTATGCAATTTTGTCA 81100 G A
CCT GTGCGATTTT TCA
||| ||||||| |||
GGG TACGTTAAAA AGT
A C
GAM3580 FLJ22477 3' CACCTGTGTGGACCACTCAC 81101 _ C TTA
CACCTG GTG GATT TCAC
||||| ||| ||| |||
GTGGAC CAC CTGG AGTG
A _ TG_
GAM3580 KIAA0155 3' CTGAAACATTTTATCAC 81102 T A
CTGG GCG TTTTATCAC
||||| ||| |||||||

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GACT TGT AAAATAGTG
 T A
 GAM3580 KIAA0420 3' CACCTGGTCAAGGTTAC 81103 G TT
 CACCTGGT CGA TTAT
 ||||| ||| |||
 GTGGACCA GTT AATG
 _ CC
 GAM3580 KIAA1223 3' CACATGCACATTTTTATCAC 81104 CTG TG A_
 CAC G CG TTTTATCAC
 ||| | || |||||
 GTG C GT AAAATAGTG
 TA_ GT AA
 GAM3580 KIAA1958 3' CTGGTGCGTGAATCTTTTATCA 81105 A____
 CTGGTGCG TTTTATCA
 ||||| |||||
 GACCACGC AAAATAGT
 ACTTAG
 GAM3580 KIAA1970 3' CACCTGGTTCTGTGGCATT TTT 81106 _____ G
 CACCTGGT GC ATTTT
 ||||| || |||
 GTGGACCA CG TAAAA
 AGACAC _
 GAM3580 LAT1-3TM 3' CACCTGGTCTGCAGCCGTCAC 81107 _ ATT TA
 CACCTGGT GCG T TCAC
 ||||| ||| | |||
 GTGGACCA CGT G AGTG
 GA C_ GC
 GAM3580 LUC7L 3' CCTGTGCAGCCCATCAC 81108 G AT
 CCTG TGCG TTTATCAC
 ||| ||| |||||
 GGAC ACGT GGGTAGTG
 _ C_
 GAM3580 RAB14 3' TGGTGACATACTTATCAC 81109 _ AT
 TGGTG CG TTTATCAC
 |||| || |||||
 ACCAC GT GAATAGTG
 T AT
 GAM3580 RNF2 3' CTAAGCAGTTTTATCAC 81110 T A
 CTGG GCG TTTTATCAC
 ||| || |||||
 GATT CGT AAAATAGTG
 _ C
 GAM3580 WSB1 3' ACCTCACCATT TTTATCA 81111 GG G
 ACCT TGC ATTTTATCA
 ||| || |||||
 TGGA GTG TAAAATAGT
 _ G
 GAM3580 LOC115129 3' CACCTGGCCTATTTTATCA 81112 GCG
 CACCTGGT ATTTTATCA
 ||||| |||||

		GTGGACCG TAAAATAGT		
		GA_		
GAM3580	LOC124045 3'	CACCTGCTGTCCATCA	81113	G CGAT
		CACCTG TG TTTATCA		
		GTGGAC AC AGGTAGT		
		G ____		
GAM3580	LOC145719 3'	CACCTGGTGGATTTCAT	81114	C
		CACCTGGTG GATTTTAT		
		GTGGACCAC CTAAAGTA		
		—		
GAM3580	LOC145720 3'	CACCTGGTGGATTTCAT	81114	C
		CACCTGGTG GATTTTAT		
		GTGGACCAC CTAAAGTA		
		—		
GAM3580	LOC146337 3'	CCTGGTGCGACCCACTCA	81115	TA
		CCTGGTGCGATTT TCA		
		GGACCACGCTGGG AGT		
		TG		
GAM3580	LOC147947 5'	CTTGACATTTTATCAC	81116	G G
		CT GTGC ATTTTATCAC		
		GA CATG TAAAATAGTG		
		A _		
GAM3580	LOC158337 5'	CACCTAGTCATTTTGTCA	81117	G G A
		CACCTGGT C ATTTT TCA		
		GTGGATCA G TAAAA AGT		
		— C		
GAM3580	LOC197114 3'	CACCTGGTGGATTTCAT	81114	C
		CACCTGGTG GATTTTAT		
		GTGGACCAC CTAAAGTA		
		—		
GAM3580	LOC197117 3'	CACCTGGTGGATTTTAT	81118	C
		CACCTGGTG GATTTTAT		
		GTGGACCAC CTAAAATA		
		—		
GAM3580	LOC197135 3'	CCATCTGCACTTTTATCAC	81119	TGG A
		CC TGCG TTTTATCAC		
		GG ACGT AAAATAGTG		
		TAG G		
GAM3580	LOC197423 5'	CACCTGGTTTGCAGCCGTCAC	81120	__ ATT TA
		CACCTGGT GCG T TCAC		

		GTGGACCA CGT G AGTG	
		AA C__GC	
GAM3580	LOC202865 3'	ACCTGGTGGCTTGTCA	81121 CGAT A
		ACCTGGTG TTT TCAC	
		TGGACCAC GAA AGTG	
		C__ C	
GAM3580	LOC203392 5'	CACCTAGCCTTTGTCA	81122 GCGA A
		CACCTGGT TTTT TCA	
		GTGGATCG GAAA AGT	
		_____ C	
GAM3580	LOC221312 3'	CCTTG TAGATTTTATCA	81123 G C
		CCT GTG GATTTTATCA	
		GGA CAT CTAAAATAGT	
		A _	
GAM3580	LOC253414 5'	CCTTGGTGGGAATTTATCAC	81124 _ C T
		CCT GGTG GA TTTATCAC	
		GGA CCAC CT AAATAGTG	
		A C T	
GAM3580	LOC253715 3'	CCTGGTGCTCATCAC	81125 GATT
		CCTGGTGC TTATCAC	
		GGACCACG AGTAGTG	

GAM3580	LOC254537 5'	CACTTGCTGCTTCATCAC	81126 C G GAT
		CAC TG TGC TTTATCAC	
		GTG AC ACG AAGTAGTG	
		A G _	
GAM3580	LOC255654 5'	ACCTGATGCCATATCA	81127 G TTT
		ACCTGGTGC A TATCA	
		TGGA CTACG T ATAGT	
		G _	
GAM3580	LOC257354 3'	CACCTGGTCAAGGTTAC	81103 G TT
		CACCTGGT CGA TTAT	
		GTGGACCA GTT AATG	
		_ CC	
GAM3580	LOC257355 3'	CACCTGGTGGCTCCTTTTAT	81128 _ GA_
		CACCTGGTG C TTTTAT	
		GTGGACCAC G AAAATA	
		C AGG	
GAM3580	LOC257469 5'	ACCTGGTACCTCCCCGTCAC	81129 GA TA
		ACCTGGTGC TTT TCAC	

		TGGACCATG GGG AGTG		
		GA GC		
GAM3580	LOC51172	3' CACCTGGTGGCTCCTTTTAT	81128	_ GA_
		CACCTGGTG C TTTTAT		
		GTGGACCAC G AAAATA		
		C AGG		
GAM3580	LOC91409	3' CACCTGGGCCCATCA	81130	T GATT
		CACCTGG GC TTATCA		
		GTGGACC CG GGTAGT		
		— —		
GAM3581	AXIN1	3' GCTGTGCTGTGGTGGACGTG	81133	_ T A_
		GC GTG CTG GTGGACGTG		
		CG CAC GAC CACCTGCAC		
		A _ AC		
GAM3581	FE65L2	5' GTTGCGTGTTTCCGTGTG	81134	_ A
		GTTGCGTG TCTG GTG		
		CAACGCAC AGGC CAC		
		AA A		
GAM3581	FE65L2	5' GTTGCGTGTTTCCGTGTG	81134	_ A
		GTTGCGTG TCTG GTG		
		CAACGCAC AGGC CAC		
		AA A		
GAM3581	FE65L2	5' GTTGCGTGTTTCCGTGTG	81134	_ A
		GTTGCGTG TCTG GTG		
		CAACGCAC AGGC CAC		
		AA A		
GAM3581	FE65L2	5' GTTGCGTGTTTCCGTGTG	81134	_ A
		GTTGCGTG TCTG GTG		
		CAACGCAC AGGC CAC		
		AA A		
GAM3581	GFAP	3' GTGCACTGGGGTGGACGTG	81135	_ A_
		GTGT CTG GTGGACGTG		
		CACG GAC CACCTGCAC		
		T CC		
GAM3581	ODC1	3' AGTAGCGTGTCTGAAGAGTG	81136	T GT C
		AGT GCGTGTCTGA GGA GTG		
		TCA CGCACAGACT TCT CAC		
		T — —		
GAM3581	SRGAP2	3' AAGTTGCTGTCTGAGACCCATG	81137	G TGGA
		AAGTTGC TGTCTGAG CGTG		

TTCAACG ACAGACTC GTAC
 _ TGG_
 GAM3581 FLJ21156 3' AGTTCACATTGAGTGGATGTG 81138 G TG C C
 AGTT CG T TGAGTGGA GTG
 |||| || | ||||| |||
 TCAA GT A ACTCACCT CAC
 _ GT _ A
 GAM3581 KIAA1718 3' GTTATTGCTGAGTGGGTGTG 81139 CG T AC
 GTTG TG CTGAGTGG GTG
 |||| || ||||| |||
 CAAT AC GACTCACC CAC
 A _ CA
 GAM3581 LOC155038 3' AAGTTGTGTGTCACAGGGGTGT 81140 C TG T AC
 G AAGTTG GTGTC AG GG GTG
 ||||| |||| || || |||
 TTCAAC CACAG TC CC CAC
 A TG _ CA
 GAM3582 CPSF2 3' AAACCAGATGCTTTAAATC 81143 _ A
 AAACCA AT CTTTAAATC
 ||||| || ||||| |||
 TTTGGT TA GAAATTTAG
 C C
 GAM3582 FENS-1 3' TATAGAGAAAAACACTTTAAAT 81144 _ CC
 TATA AGAAA AATACTTTAAAT
 |||| |||| ||||| |||||
 ATAT TCTTT TTGTGAAATTTA
 C _
 GAM3582 HSPC019 3' TAAGAAACCAGTTACCATAAAT 81145 A_ T
 C TAAGAAACCA TACT TAAATC
 ||||| |||| ||||| |||
 ATTCTTTGGT ATGG ATTTAG
 CA T
 GAM3582 LNX 3' TAAGAAATTTACCTTAAATC 81146 CCAA
 TAAGAAA TACTTTAAATC
 ||||| ||||| ||||| |||
 ATTCTTT ATGGAATTTAG
 AA_
 GAM3582 LOC115073 3' TAAGAAACCATTACACAAAAT 81147 A_ TTT
 TAAGAAACCA TAC AAAT
 ||||| |||| ||||| |||
 ATTCTTTGGT ATG TTTA
 AA TGT
 GAM3582 LOC255520 3' TACAAGAAACCAATTTTAAAT 81148 AC
 TATAAGAAACCAAT TTTAAAT
 ||||| |||| ||||| |||
 ATGTTCTTTGGTTA AAATTTA
 A_
 GAM3582 LOC63929 3' TAAGAAATCAACTTTAAAT 81149 C AT
 TAAGAAA CA ACTTTAAAT
 ||||| || ||||| |||

		ATTCTTT GT TGAAATTTA	
		A _	
GAM3583	ARHGEF12	3' TTTAAGCTTATTTAATAT 81152	G
		TTTAAGCTTATT TAATAT	
		AAATTCGAATAA ATTATA	
		-	
GAM3583	XRCC5	3' CCCTTGTAATATATATG 81153	A
		CTT TTGTAATATATATG	
		GGG AACATTATATATAC	
		-	
GAM3583	CMG2	3' TTCAAGCTAGAGGATATATATG 81154	TATTGTA
		TTTAAGCT ATATATATG	
		AAGTTCGA TATATATAC	
		TCTCC_	
GAM3583	PLSCR4	3' TTTAAGCTTACTTTGTATATG 81155	GTAATA
		TTTAAGCTTATT TATATG	
		AAATTCGAATGA ATATAC	
		AAC_	
GAM3583	TAF1B	3' TCTAAGCACACTTGATATATAT 81156	T GTA
	G	TTTAAGC TATT ATATATATG	
		AGATTTCG GTGA TATATATAC	
		T AC_	
GAM3583	LOC115123	3' TCTAAGTTTAATATATATATAT 81157	C T _
	ATG	TTTAAG TTA TGTA ATATATATG	
		AGATTTC AAT ATAT TATATATAC	
		A T A	
GAM3584	FLJ20825	3' TAATTTTTTTTACTTTTTGTAG 81160	G A
		TAATTTTTTTTA TTTT TAG	
		ATTAAAAAAAT AAAAA ATC	
		G C	
GAM3584	GCN2	3' TAATTTTTTTTAGTTTTTATAGA 81161	
		TAATTTTTTTTAGTTTTTATAGA	
		ATTAAAAAAATCAAAAATATCT	
GAM3584	KIAA1972	3' TTCTAATTTTTTATAGATT 81162	
		TTTTAGTTTTTATAGATT	
		AAGATTAAAAATATCTAA	
GAM3585	ARHH	3' TTGTGTGAAGTCTCTTGGG 81165	CA C GG
		TTGTG GA GT TTCTTGGG	

AACAC CT CA GAGAACCC
 A_ T _
 GAM3585 C12orf2 3' TTGTGCAGGAGTTTGG 81166 ACGT C
 TTGTGCAG GGT TTGG
 ||||| ||| |||
 AACACGTC TCAA AACC
 C___ _
 GAM3586 AF5Q31 3' TGATGTGACACAGTGTGT 81169 G TG
 TGATG TGACACA GTTGT
 |||| ||||| ||||
 ACTAC ACTGTGT CAACA
 _ CA
 GAM3586 ANXA9 5' TGAGGTGGGTGTCGTTGTTGT 81170 T ACACATG
 TGA GGTG GTTGTGT
 ||| ||| |||||
 ACT CCAC CAACAACA
 _ CCACAG_
 GAM3586 KIAA1458 3' TGGTGGTGACATGTGAGCT 81171 A CA _
 TG TGGTGACA TG GTT
 || ||||| |||
 AC ACCACTGT AC CGA
 C AC T
 GAM3586 KIAA1940 5' TGATGGTGGTGGTGCAGC 81172 ACACA T T
 TGATGGTG TGGT GT GT
 ||||| ||| |||
 ACTACCAC ACCA CG CG
 C___ _ T
 GAM3586 PEG10 3' ATGATGGTAAGGTGTTGT 81173 CACAT T
 ATGATGGTGA GGT GTTGT
 ||||| ||| |||
 TACTACCATT CCA CAACA
 _ _
 GAM3586 PSR 3' TGATGGTGTGATGGTGCTG 81174 CACA T
 TGATGGTGA TGGT GTTG
 ||||| ||| |||
 ACTACCACT ACCA CGAC
 _ _
 GAM3586 RI58 3' TGATGGTACATAATTGT 81175 GAC
 TGATGGT ACATGGTTGT
 ||||| |||||
 ACTACCA TGTATTAACA
 _
 GAM3586 RYBP 5' TGGTGGGGTGGCATACTGTTGT 81176 ACACA _
 TGGTG TGGT TGTGT
 |||| ||| |||||
 ACCAC ACCG ACAACA
 CCC_ TATG
 GAM3586 LOC146227 5' ATGATGGTGGTGGTGGT 81177 ACACA T
 ATGATGGTG TGGT GT
 ||||| ||| ||

		TACTACCAC ACCA CA		
		C_____ C		
GAM3586	LOC146237 3'	TGATGGTGACCGTGACTGT	81178	ACA GT
		TGATGGTGAC TG TGT		
		ACTACCACTG AC ACA		
		GC_ TG		
GAM3586	LOC150147 5'	TGGTGGCATAGCTGTTGT	81179	ACA
		TGGTG CATGGTTGTTGT		
		ACCAC GTATCGACAACA		
		C_		
GAM3586	LOC150311 5'	ATGATGGTGATAGTGGTTTTG	81180	CACAT G
	T	ATGATGGTGA GGTT TTGT		
		TACTACCACT CCAA AACA		
		ATCAT _		
GAM3586	LOC152137 3'	TGTGGTGACACATGCCTGT	81181	A G
		TG TGGTGACACATG TTGT		
		AC ACCACTGTGTAC GACA		
		_ G		
GAM3586	LOC161734 3'	ATGATGGTGACGTATAGATGAG	81182	AC T TT
	T	ATGATGGTGAC ATGG TG GT		
		TACTACCACTG TATC AC CA		
		CA T T_		
GAM3586	LOC257443 3'	TGGTGGTGACATGTGAGCT	81171	A CA _
		TG TGGTGACA TG GTT		
		AC ACCACTGT AC CGA		
		C AC T		
GAM3586	LOC51029 3'	TGATGGTGACTATAACTGT	81183	AC GG
		TGATGGTGAC AT TTGT		
		ACTACCACTG TA GACA		
		A_ TT		
GAM3587	ABCE1 3'	GTTTAGATAATGTGCTCT	81186	GT
		GTT GATAATGTGCTCT		
		CAA CTATTACACGAGA		
		AT		
GAM3587	BHMT 3'	TCGACAGTAAGATGTGATGTG	81187	____ TAA
		TCGATAGT TGTGA TGTG		
		AGCTGTCA ACACT ACAC		
		TTCT _		
GAM3587	KIAA1729 3'	TCGGGGTTGTGCCATCTGTGCT	81188	ATA ATAA_
	CT	TCG GTTGTG TGTGCTCT		

AGC CAACAC ACACGAGA
 CC_ GGTAG
 GAM3587 LOC220933 5' GATATTGTGATAAAACT 81189 G TGT
 GATA TTGTGATAA GCT
 |||| ||||| ||
 CTAT AACACTATT TGA
 _ TT_
 GAM3587 LOC221495 3' TCTGTAGTTGCAGGGTGTGTTC 81190 GA GATAA C
 T TC TAGTTGT TGTG TCT
 || ||||| |||||
 AG ATCAACG ACAC AGA
 AC TCCC_ A
 GAM3588 BRPF1 3' TGAAATAAATACAAACCAGTT 81193 A _
 TGAAA TAAATACAAA GGTT
 |||| ||||| ||||
 ACTTT ATTTATGTTT TCAA
 _ GG
 GAM3588 EGF 3' TGAAAATACATACAAATTC 81194 A AG
 TGAAAATA ATACAA GTTC
 ||||| ||||| ||||
 ACTTTTAT TATGTT TAAG
 G _
 GAM3588 FGF12 3' TGATGATAAATGGTTCCT 81195 AA ACAA
 TGA ATAAAT GGTTCCCT
 || ||||| |||||
 ACT TATTTA CCAAGGA
 AC _
 GAM3588 GARS 3' TGAAGATAAAATACGGTCCCTG 81196 A _ AAA
 TGAA ATAAA TAC GGTTCCCTG
 |||| ||||| |||||
 ACTT TATTT ATG CCAGGGAC
 C T _
 GAM3588 HDAC2 3' TGAAAATAAATACAGTCCATG 81197 AAG C
 TGAAAATAAATACA GTTC TG
 ||||| ||||| |||||
 ACTTTTATTTATGT CAGG AC
 _ T
 GAM3588 MS4A7 3' TGAAAATAATACAGAAACAGCC 81198 A A GG T_
 TG TGAAAATAA TACA A T CCTG
 ||||| ||||| |||||
 ACTTTTATT ATGT T G GGAC
 _ C TT TC
 GAM3588 PTP4A2 3' TGAAAATAGTGCAAGAGCCCCT 81199 AATA AG
 G TGAAAATA CAA GTTCCTG
 ||||| ||||| |||||
 ACTTTTAT GTT CGGGGAC
 CAC_ CT
 GAM3588 RENT1 3' TGGGAATAAATAAGAGTCCCTG 81200 AA CAAA
 TG AATAAATA GGTTCCCTG
 || ||||| |||||

AC TTATTTAT TCAGGGAC
 CC TC__
 GAM3588 SIRT1 3' TGAACGTAAATACAATAATCCT 81201 AA AG T
 G TGAA TAAATACAA GT CCTG
 |||| ||||| || ||||
 ACTT ATTTATGTT TA GGAC
 GC AT _
 GAM3588 SYN3 3' TGGGAACAAATATAGATAATCG 81202 CAAA_____ III
 GTTCCTGC TAAATA GGTCCTG C
 |||| | ||||| I
 GTTTAT CCAAGGAC G
 ATCTATTAG III
 GAM3588 SYN3 3' TGGGAACAAATATAGATAATCG 81202 CAAA_____ III
 GTTCCTGC TAAATA GGTCCTG C
 |||| | ||||| I
 GTTTAT CCAAGGAC G
 ATCTATTAG III
 GAM3588 SYN3 3' TGGGAACAAATATAGATAATCG 81202 CAAA_____ III
 GTTCCTGC TAAATA GGTCCTG C
 |||| | ||||| I
 GTTTAT CCAAGGAC G
 ATCTATTAG III
 GAM3588 ZNF207 3' AAAATAAATGTCCAATAGTTCC 81203 A__ A
 TG AAAATAAAT CAA GGTCCTG
 ||||| || |||||
 TTTTATTTA GTT TCAAGGAC
 CAG A
 GAM3588 AF053356_CDS3 3' GAAAATGAGTACAAATCCCTG 81204 AAA AG
 GAAAAT TACAA GTTCCTG
 |||| |||| |||||
 CTTTTA ATGTT TAGGGAC
 CTC _
 GAM3588 CGGBP1 3' TGAAATAAATACAAAAAT 81205 A
 TGAAA TAAATACAAAGGT
 |||| |||||
 ACTTT ATTTATGTTTTTA
 _
 GAM3588 DKFZp434N2030 5' GAAACCTACAGAGGTTCCCTG 81206 ATAAA A
 GAAA TACA AGGTTCCCTG
 ||| ||| |||||
 CTTT ATGT TCCAAGGAC
 GG__ C
 GAM3588 DKFZP564J0863 3' TGAAAATAGACACAGGCT 81207 A AA
 TGAAAATA ATACA GGTT
 ||||| |||| |||
 ACTTTTAT TGTGT CCGA
 C _
 GAM3588 FLJ11294 3' TGAAAACCTCATTGAGGGTTCC 81208 AAATACAAA
 TG TGAAAAT GGTCCTG
 ||||| |||||

		ACTTTTG	CCAAGGAC		
		GAGTAACTC			
GAM3588	FLJ14917	3'	GAAAATAGATACAAGGAACTG	81209	A A TTC
			GAAAATA ATACAA GG CTG		
			CTTTTAT TATGTT CC GAC		
			C _ TT_		
GAM3588	GTF3C3	3'	TAAAAATAAATACACTGTT	81210	AAG
			TGAAAATAAATACA GTT		
			ATTTTATTTATGT CAA		
			GA_		
GAM3588	KIAA1671	3'	TGGAAATAAATACAAGAGT	81211	A AG
			TG AAATAAATACAA GT		
			AC TTTATTTATGTT CA		
			C CT		
GAM3588	KIAA1952	5'	TGAAATAAGTGTAGCAGTTCCT	81212	A ATACAAA
		G	TGAAA TAA GGTTCCTG		
			ACTTT ATT TCAAGGAC		
			_ CACATCG		
GAM3588	MLCB	3'	TGAGAATAAATACAACAGG	81213	A _
			TGA AATAAATACAA AGG		
			ACT TTATTTATGTT TCC		
			C G		
GAM3588	NX-17	3'	TGAAAATATATACATATGCCTG	81214	A AAG T
			TGAAAATA ATACA GT CCTG		
			ACTTTTAT TATGT TA GGAC		
			A A_ C		
GAM3588	PRO2266	3'	TGAAAATAAATATATGAATAAC	81215	CAAAGGTT_
		CTG	TGAAAATAAATA CCTG		
			ACTTTTATTTAT GGAC		
			ATACTTATT		
GAM3588	USP24	3'	TGAAAATAAGGCAGGACCT	81216	ATACAA TT
			TGAAAATAA AGG CCT		
			ACTTTTATT TCC GGA		
			CCG_ T_		
GAM3588	LOC144193	3'	TGAAAATAAATCTATCCCT	81217	ACAAAG
			TGAAAATAAAT GTTCCT		
			ACTTTTATTTA TAGGGA		
			GA_		
GAM3588	LOC153727	5'	GAAAGAATATAAGATTCCTG	81218	ATA CA
			GAAA AATA AAGGTCCTG		

CTTT TTAT TTCTAAGGAC
 C_ A_
 GAM3588 LOC221773 3' TGAAAATCAATACAAAAAAA 81219 A TTC_
 CTG TGAAAAT AATACAAAGG CTG
 ||||| ||||| ||
 ACTTTTA TTATGTTTT GAC
 G TTTT
 GAM3588 LOC51004 3' TGAAAATATGTATGATGGGTCC 81220 AATACAAA T
 TG TGAAAATA GG TCCTG
 ||||| || |||||
 ACTTTTAT CC AGGAC
 ACATACTA C
 GAM3588 LOC91408 3' TGAAAAAATACAAGAGCT 81221 T AG
 TGAAAA AAATACAA GTT
 ||||| ||||| ||
 ACTTTT TTTATGTT CGA
 T CT
 GAM3589 MYO1E 3' CTA CTACTTAGTACATT CATACAT 81224 AA CC
 TTACTTGG ACA CATACAT
 ||||| || |||||
 GATGAATC TGT GTATGTA
 A_ AA
 GAM3589 C1orf19 3' TCACTTGGAACATCTTTGTGCA 81225 ACACCCATA_
 TAT TTACTTGGA CATAT
 ||||| |||||
 AGTGAACCTT GTATA
 GTAGAAACAC
 GAM3589 DKFZP434P0714 3' TTACTTGAAAATGCACATA 81226 CACCCA
 TTACTTGGA TACATA
 ||||| |||||
 AATGAACTTT GTGTAT
 AC____
 GAM3589 WDR7 3' CTTGGAAACTACATA 81227 ACCCA
 CTTGGAAAC TACATA
 ||||| |||||
 GAACCTTTG ATGTAT

 GAM3589 LOC135293 3' TTACTTGAAAATATTA ACTTCA 81228 C____ C_ |||
 TACATATA GGAAA AC CATACATAT A
 |||| || ||||| |
 CTTTT TG GTATGTATA T
 ATAAT AA |||
 GAM3589 LOC149175 3' TTACTTGAGAATACCAGTTCAT 81229 GA C CATA
 AT TTACTTG AA ACC CATAT
 ||||| || |||||
 AATGAAC TT TGG GTATA
 TC A TCAA
 GAM3589 LOC219347 3' TTACTTGGAACATCAACCAT 81230 A C____
 TTACTTGGAACA CCAT
 ||||| ||||| |||

		AATGAACC TTGT GGTA	
		C AGTT	
GAM3589	LOC90488 3'	TTACCTGGCACATTATACATAT 81231	AA CCC
		TTACTTGG ACA ATACATAT	
		AATGGACC TGT TATGTATA	
		G_ AA_	
GAM3589	LOC91250 5'	TTACTTGGACATGCAT 81232	AACACC A
		TTACTTGGGA CAT CAT	
		AATGAACCT GTA GTA	
		_____ C	
GAM3590	KLK3 3'	AGTCTTGGCCTGGTCATTTCC 81235	CA AAA
		AGTTT GTTT TCATTTCC	
		TCAGA CGGA AGTAAAGG	
		AC CC_	
GAM3590	SLC25A15 3'	TAAGTTTCCGTTCCCTCATTTCC 81236	A AAA
		TAAGTTTC GTTT TCATTTCC	
		ATTCAAAG CAAG AGTAAAGG	
		G G_	
GAM3590	TRRAP 3'	TAAGTTTCAGCTCTGCCATTTTC 81237	AAA
	C	TAAGTTTCAGTTT TCATTTCC	
		ATTCAAAGTCGAG GGTAAGG	
		AC_	
GAM3590	YWHAG 3'	AATTCCAGTAAATCATTTCC 81238	TT
		AGTTTCAGT AAATCATTTCC	
		TTAAGGTCA TTAGTAAAGG	

GAM3590	CGGBP1 3'	AGGTTCAAACAGAGATCATTTTC 81239	T TTAA_
	C	AG TTCAG ATCATTTCC	
		TC AAGTT TAGTAAAGG	
		C TGTCTC	
GAM3590	FLJ13150 3'	GCTTTAGTAGCTGTCATTTCC 81240	C TTAAA
		GTTT AGT TCATTTCC	
		CGAA TCA AGTAAAGG	
		A TCGAC	
GAM3590	FLJ20651 3'	AGGTTTCAGTTTTTCACATTTCC 81241	T AAAT
		AG TTCAGTTT CATTTCC	
		TC AAGTCAAA GTAAAGG	
		C AGT_	
GAM3590	GREB1 3'	AGTTTCAGTGCCATTT 81242	TTAAA
		AGTTTCAGT TCATTT	

		TCAAAGTCA	GGTAAA		
		C_____			
GAM3590	KIAA1715	3'	AGTTTCAGTTTCCTATTTCC	81243	AAATC
			AGTTTCAGTTT	ATTTCC	
			TCAAAGTCAAA	TAAAGG	
			GGA__		
GAM3590	LAP3	3'	TTTCAGTTTGCTCATGTTCC	81244	AAA _
			TTTCAGTTT	TCAT TTCC	
			AAAGTCAAA	AGTA AAGG	
			CG_ C		
GAM3590	My015	3'	AATTTTCAGTACTTCATTT	81245	TTAAA
			AGTTTCAGT	TCATTT	
			TTAAAGTCA	AGTAAA	
			TGA__		
GAM3590	ZNF221	5'	TAAATTCCAACTTTAAGTCATT	81246	_ A
	T		TAAGTTTCAG	TTTAA TCATTT	
			ATTTAAGGTT	AAATT AGTAAA	
			G C		
GAM3590	LOC145482	3'	CAAGTTTCAGTTTAAGAATC	81247	__
			TAAGTTTCAGTTTAA	ATC	
			GTTCAAAGTCAAATT	TAG	
			CT		
GAM3590	LOC147080	5'	AGCTTCAGTATTTGTCATTT	81248	TTAAA
			AGTTTCAGT	TCATTT	
			TCGAAGTCA	AGTAAA	
			TAAAC		
GAM3590	LOC152860	3'	GTTGTTTTTTTAAATCATTTCC	81249	TCAG
			GTT	TTTAAATCATTTCC	
			CAA	AAATTTAGTAAAGG	
			CAAA		
GAM3590	LOC200314	3'	AAGTTTCAGAAAGTGTCATTTTC	81250	TTTAAA
	C		AAGTTTCAG	TCATTTCC	
			TTCAAAGTC	AGTAAAGG	
			TTTCAC		
GAM3590	LOC219654	3'	AATTTTCAGGCTCATTTTC	81251	TTTAAA
			AGTTTCAG	TCATTTTC	
			TTAAAGTC	AGTAAAG	
			CG_____		
GAM3591	ZNF146	3'	TATAGTTCATGGTCTA	81254	T CTTAAG
			TAT GTTCATGG	TCTA	

			ATA CAAGTACC	AGAT	
			T		
GAM3592	AEGL1	3'	TTAAGGCAGGTGTTGGA	81257	TTGTT
			TTAAGGC GTGTTGGA		
			AATTCCG CACAACCT		
			TC__		
GAM3592	BAZ2A	5'	AAGGTTGGTGTGGA	81258	C TT
			AAGG TTG GTGTTGGA		
			TTCC AAC CACAACCT		
			- -		
GAM3592	BMPR1B	3'	TCAAGGCTTGTACTGTGGA	81259	TG T
			TTAAGGCTTGT TGT GGA		
			AGTTCCGAACA ACA CCT		
			TG _		
GAM3592	FACL2	3'	TTAAGGCTCATTTTGGA	81260	TG GTG
			TTAAGGCT TT TTGGA		
			AATTCCGA AA AACCT		
			GT __		
GAM3592	GJB3	5'	TCAAGGCCAGGCTGTTGG	81261	T_ TG
			TTAAGGCT GT TGTTGG		
			AGTTCCGG CG ACAACC		
			TC _		
GAM3592	IGF2R	3'	TTAAGGCTTCTTATAGG	81262	G TT
			TTAAGGCTT TTGTG GG		
			AATTCCGAA AATAT CC		
			G _		
GAM3592	KDR	3'	TTAAGGCTTGGGCTTGG	81263	TT G
			TTAAGGCTTG GT TTGG		
			AATTCCGAAC CG AACC		
			- -		
GAM3592	MTMR3	3'	TTAAGGCTGTTTTTGGA	81264	T GTG
			TTAAGGCT GTT TTGGA		
			AATTCCGA CAA AACCT		
			_ A_		
GAM3592	ODF2	3'	TTAAGGCCTGTCGAGGA	81265	TGTT
			TTAAGGCTTGTTG GGA		
			AATTCCGGACAGC CCT		
			T__		
GAM3592	OXTR	3'	TCAAGGCTTATTTGG	81266	GTGT
			TTAAGGCTTGTT TGG		

AGTTCCGAATAA ACC

GAM3592 PDE4D 3' TTAAGGCTGACGTGGG 81267 T T TT
TTAAGGCT G TGTG GG
||||||| | ||| ||
AATTCCGA C GCAC CC
_ T _

GAM3592 TRIM9 5' AGGCCTTGTGTTGTTGG 81268 _ _
AGGC TTGTTGT GTTGG
||| ||||| ||||
TCCG AACAACA CAACC
G A

GAM3592 DKFZP586A0522 3' TTAAGACTTGAGAACTGGA 81269 TTGTG
TTAAGGCTTG TTGA
||||||| ||||
AATTCTGAAC GACCT
TCTT_

GAM3592 FLJ20506 3' TCAAGGCTTGCCTGG 81270 TGTG
TTAAGGCTTGT TTGG
||||||| |||
AGTTCCGAACG GACC

GAM3592 FTSJ1 3' TCAGGGCTTGTGTTGTCCAGG 81271 A G _
TTA GGCTTGTT TGTT GG
||| ||||| ||| ||
AGT CCGAACAA ACAG CC
C _ GT

GAM3592 KIAA0254 3' TAAGGCTGATGTGTTGG 81272 T T
TAAGGCT G TGTGTTGG
||||||| | |||||
ATTCCGA C ACACAACC
_ T

GAM3592 KIAA0295 3' TCAAGGCCATGTTGG 81273 TGTT
TTAAGGCT GTGTTGG
||||||| |||||
AGTTCCGG TACAACC

GAM3592 KIAA1576 3' CTAAGGCTTGTGTTGGTGGA 81274 T T
TTAAGGCTTGTG GT GGA
||||||| || |||
GATTCCGAACAAC CA CCT

GAM3592 KIAA1906 3' TTAAGACTTCAGTTTGGA 81275 GTT G
TTAAGGCTT GT TTGGA
||||||| || ||||
AATTCTGAA CA AACCT
GT_ _

GAM3592 LHX6 3' TCAAGGCAGAGTGTGTTGG 81276 TTGT
TTAAGGC TGTGTTGG
||||||| |||||

		AGTTCCG ACACAACC		
		TCTC		
GAM3592	MGC1842	3' TCAAGGCTTGGGGTCTTGG	81277	TT G
		TTAAGGCTTG GT TTGG		
		AGTTCCGAAC CA AACC		
		CC G		
GAM3592	P4HA2	3' TTAAGGCTTCTGGTAGG	81278	G T T
		TTAAGGCTT TTG GT GG		
		AATTCCGAA GAC CA CC		
		_ _ T		
GAM3592	STRBP	5' AAGGCTTGTTCTCTGGA	81279	GTG
		AAGGCTTGTT TTGGA		
		TTCCGAACAA GACCT		
		GA_		
GAM3592	TRIM2	3' TTAGGGCTTGCTCCACTAG	81280	A G GT
		TTA GGCTTGTT T TGG		
		AAT CCGAACGA G ATC		
		C G TG		
GAM3592	LOC118851	5' TTAAGTGTTGGAGTTGGA	81281	GCT T_
		TTAAG TGTG GTTGGA		
		AATTC ACAAC CAACCT		
		_ CT		
GAM3592	LOC124152	3' TTAAAGCTTGTTTGCAATGA	81282	G TG_
		TTAAGGCTTGTT TGT GA		
		AATTTCGAACAA ACG CT		
		_ TTA		
GAM3592	LOC126536	3' TCAAGGCTTGTTGTCCTGA	81283	G
		TTAAGGCTTGTTGT TTGG		
		AGTTCCGAACAACA GACT		
		G		
GAM3592	LOC144453	3' AAAGCCATGTTGTGTTGGA	81284	_
		AAGGCT TGTTGTGTTGGA		
		TTTCGG ACAACACAACCT		
		T		
GAM3592	LOC149103	3' AGGTTATTTGGTGTGTTGGA	81285	C _
		AGG TTGTT GTGTTGGA		
		TCC AATAA CACAACCT		
		_ AC		
GAM3592	LOC150290	3' TTAAGGCTCTGGCTCTGG	81286	GTT G
		TTAAGGCTT GT TTGG		

AATTCCGAG CG GACC
 AC_ A
 GAM3592 LOC155435 3' AGGTCGGA CTGTGTTGGA 81287 C _
 AGG TTG TTGTGTTGGA
 ||| ||| |||||
 TCC AGC GACACAACCT
 _ CT
 GAM3592 LOC163782 5' TTAAGGCTGGTCGATGG 81288 T TGT
 TTAAGGCT GTTG TGG
 ||||| ||| |||
 AATTCCGA CAGC ACC
 C T_
 GAM3592 LOC196529 3' TTAAGACTTGAGAACTGGA 81269 TTGTG
 TTAAGGCTTG TTGA
 ||||| |||
 AATTCTGAAC GACCT
 TCTT_
 GAM3592 LOC254295 3' TCAAGGCTATGTTGG 81289 TGTT
 TTAAGGCT GTGTTGG
 ||||| |||||
 AGTTCCGA TACAACC

 GAM3592 LOC58489 3' TTAAGGCTTTTAAATGTGGA 81290 GTT_ T
 TTAAGGCTT GTGT GGA
 ||||| ||| |||
 AATTCCGAA TACA CCT
 AATT _
 GAM3592 LOC90630 5' TTAGGGCTTGTTCTGCAGG 81291 A _G T
 TTA GGCTTGT T TGT GG
 ||| ||||| | ||| ||
 AAT CCGAACA G ACG CC
 C A G T
 GAM3592 LOC91208 5' TTAGGGCTTGTTCTGCAGA 81292 A _G T
 TTA GGCTTGT T TGT GG
 ||| ||||| | ||| ||
 AAT CCGAACA G ACG CT
 C A G T
 GAM3593 NBEA 3' TAGCAGCTGGTGTTCAGTC 81295 AT
 TAGCGGCTGGTGTTCG GTC
 ||||| ||||| |||
 ATCGTCGACCACAAGT CAG

 GAM3593 SLC9A1 3' ACGTGGTTGTGCGATGTCAC 81296 GC GT
 GCG TGGT TCGATGTCAC
 ||| ||| |||||
 TGC ACCA AGCTACAGTG
 _ AC
 GAM3593 DKFZp434A1520 3' TAGCGGGTGGACGCTGATGTCA 81297 C _ C
 C TAGCGG TGG TGTT GATGTCAC
 ||||| ||| ||| |||||

ATCGCC ACC GCGA CTACAGTG
 C T _
 GAM3593 FLJ22056 3' CAGCGGCTGCTGGGTGTCAC 81298 G TTCGA
 TAGCGGCTG TG TGTCAC
 ||||| || |||||
 GTCGCCGAC AC ACAGTG
 G CC__
 GAM3593 FLJ32865 3' GGCTGGGTGACCTCAC 81299 T TC G
 GGCTGG GT GAT TCAC
 ||||| || || |||||
 CCGACC CA CTG AGTG
 _ _ G
 GAM3593 GFR 3' AGTGGCTTTTGGTGATGTCAC 81300 C GG TTC
 AG GGCT TG GATGTCAC
 || |||| || |||||
 TC CCGA AC CTACAGTG
 A AA CA_
 GAM3593 PAPOLG 3' GGTTGGTAACAATGTCA 81301 C TT
 GG TGGTG CGATGTCA
 || |||| |||||
 CC ACCAT GTTACAGT
 A T_
 GAM3593 LOC133634 3' AGTGGCTGATGATGTCA 81302 C GTTC
 AG GGCTGGT GATGTCA
 || ||||| |||||
 TC CCGACTA CTACAGT
 A _
 GAM3593 LOC158835 5' GCGGCTGGGGCAGATGTCA 81303 T TC
 GCGGCTGG GT GATGTCA
 ||||| || |||||
 CGCCGACC CG CTACAGT
 C T_
 GAM3593 LOC221931 3' TGGTTGCTCTGATGTCAC 81304 _ _
 TGGT GTTC GATGTCAC
 ||| |||| |||||
 ACCA CGAG CTACAGTG
 A A
 GAM3594 CHRN4 3' AGAAGTGTGTGAGGAAC 81307 C AGA A
 AG AAGT TG TGAGGAAC
 || |||| || |||||
 TC TTCA AC ACTCCTTG
 _ C_ _
 GAM3594 CKMT1 3' AGCAAGTAGAATGGGCCA 81308 TG A AA
 AGCAAGTAGA ATG GG CCA
 ||||| ||| || |||
 TCGTTCATCT TAC CC GGT
 _ _ _
 GAM3594 COL1A2 3' AGCAAGTAGATGTGCAG 81309 A A
 AGCAAGTAGATG TG GG
 ||||| ||| || ||

		TCGTTTCATCTAC AC TC	
		_ G	
GAM3594 DLEC1	3'	GCAGCTGGATGCTGGGACCAG 81310	A A_ A A A
		GCA GT GATG TG GGA CCAG	
		CGT CG CTAC AC CCT GGTC	
		_ AC G _ _	
GAM3594 FUS1	3'	GCAGGTAGGTCGGAAGAATCAG 81311	A ATGAT C
		GCA GTAG GAGGAA CAG	
		CGT CATC CTTCTT GTC	
		C CAGC_ A	
GAM3594 FUT1	3'	ACAGGTGGATGACAAGGTCAG 81312	A A TG AAC
		GCA GT GATGA AGG CAG	
		TGT CA CTACT TCC GTC	
		C C GT A__	
GAM3594 GGA3	3'	GCAAGGGGCAGGGAGGAACCAG 81313	TAGATGAT
		GCAAG GAGGAACCAG	
		CGTTC CTCCTTGGTC	
		CCCGTCC_	
GAM3594 GGA3	3'	GCAAGGGGCAGGGAGGAACCAG 81313	TAGATGAT
		GCAAG GAGGAACCAG	
		CGTTC CTCCTTGGTC	
		CCCGTCC_	
GAM3594 MAP1A G	3'	AGCAGGGGATGAGAAGGGATCA 81314	A TA T AAC
		AGCA G GATGA GAGG CAG	
		TCGT C CTACT TTCC GTC	
		_CC C CTA	
GAM3594 MNT	3'	AGCGGGTGGATGATGAGG 81315	AA A
		AGC GT GATGATGAGG	
		TCG CA CTACTACTCC	
		CC C	
GAM3594 PDE4A	3'	AAGTGGAAGCGGGAACCAG 81316	A TGA A
		AAGT GA TG GGAACCAG	
		TTCA CT GC CCTTGGTC	
		C TTC _	
GAM3594 SPG4	3'	AGCAAGCAGAAGGAAC 81317	TGATG
		AGCAAGTAGA AGGAAC	
		TCGTTTCGTCT TCCTTG	

GAM3594 BSMAP	3'	AGCGGGGACAAGGAGGAACCAG 81318	AAGTA TG T
		AGC GA A GAGGAACCAG	

TCG CT T CTCCTTGGTC
 CCC__ GT C
 GAM3594 BZW1 3' GTAGGAAGATGTAAGAACCAG 81319 AT_ _
 GTAG GATG AGGAACCAG
 ||| ||| |||||
 CATC CTAC TTCTTGGTC
 CTT A
 GAM3594 C20orf55 5' ACCGGAGAGATGAGGAGCCAG 81320 AAGT T A
 GC AGA GATGAGGA CCAG
 || ||| ||||| |||
 TG TCT CTA CTCCT GGTC
 GCC_ _ C
 GAM3594 C5orf4 3' AGACAGGATGAGGAGCCA 81321 _ A
 AGAT GATGAGGA CCA
 ||| ||||| |||
 TCTG CTA CTCCT GGT
 TC C
 GAM3594 DKFZp547I094 5' GCAGATGGGGAGGAACCA 81322 AT
 GTAGATG GAGGAACCA
 ||||| |||||
 CGTCTAC CTCCTTGGT
 CC
 GAM3594 DKFZp761K1423 3' GTAGGTGGTGATGAGGAAC 81323 A__
 GTAG TGATGAGGAAC
 ||| |||||
 CATC ACTACTCCTTG
 CACC
 GAM3594 FLJ12788 3' AGCAGGACTACAGAGGAACCAG 81324 _ GAT_
 AGTAG AT GAGGAACCAG
 |||| || |||||
 TCGTC TG CTCCTTGGTC
 C ATGT
 GAM3594 HRIHFB2122 3' GCTGGAGACAGAGGGGGACCAG 81325 AAGT GAT A__
 GC AGAT GAGG ACCAG
 || ||| ||| ||||
 CG TCTG CTCC TGGTC
 ACC_ T_ CCC
 GAM3594 KIAA0125 3' GCAGGTGCTGGGAACCA 81326 A A A
 GTAG TG TG GGAACCA
 |||| || || |||||
 CGTC AC AC CCTTGGT
 C G _
 GAM3594 KIAA0265 3' AGCAAGTATGGATGGAACCAG 81327 GAT GA
 AGCAAGTA GAT GGAACCAG
 ||||| || |||||
 TCGTTCAT CTA CCTTGGTC
 AC_ _
 GAM3594 KIAA1023 3' AGCAAGAGATGGGCAC 81328 T ATGA A
 AGCAAG AGATG GG AC
 ||||| |||| || ||

TCGTTC TCTAC CC TG
 _ _ _ G
 GAM3594 KIAA1032 3' GCAGCGTGGGGAACCAG 81329 A A A
 GTAG TG TG GGAACCAG
 |||| || || |||||
 CGTC GC AC CCTTGGTC
 _ _ C
 GAM3594 KIAA1508 3' AGCGGGTAGTGATGAAAA 81330 AA A
 AGC GTAG TGATGAGGA
 ||| |||| |||||
 TCG CATC ACTACTTTT
 CC _
 GAM3594 MGC32043 3' GCAAGTGATGAGACC 81331 AGAT GA
 GCAAGT GATGAG ACC
 ||||| ||||| |||
 CGTTCA CTACTC TGG
 _ _ _
 GAM3594 MKRN1 3' AGCAGTAGATGGACAAACCAG 81332 A AT G
 AGCA GTAGATG GA GAACCAG
 |||| ||||| || |||||
 TCGT CATCTAC CT TTTGGTC
 _ _ _ G
 GAM3594 NCOA5 3' AGTAAGTGGGAGGAGGCCA 81333 A AT A_
 AGTAG TG GAGGA CCA
 ||||| || ||||| |||
 TCATT AC CTCCT GGT
 C C_ CC
 GAM3594 NS1-BP 5' CAAGTAGAAGGACGAGGGGCCA 81334 T_ AA
 G CAAGTAGA GATGAGG CCAG
 ||||| ||||| |||||
 GTTCATCT CTGCTCC GGTC
 TC CC
 GAM3594 OSBPL7 3' GCAGGAGGAGTGAGGAACCAG 81335 AT_ _
 GTAG GA TGAGGAACCAG
 |||| || |||||
 CGTC CT ACTCCTTGGTC
 CTC C
 GAM3594 USP28 3' GCAGGCAGCCAGGAACCA 81336 A ATGATG
 GCA GTAG AGGAACCA
 ||| |||| |||||
 CGT CGTC TCCTTGGT
 C GG_
 GAM3594 LOC113828 3' AGTGCGTGGGGAACCAG 81337 AGA A A
 AGT TG TG GGAACCAG
 ||| || || |||||
 TCA GC AC CCTTGGTC
 CC_ _ C
 GAM3594 LOC136337 5' GCAGGTGAGGAACCAG 81338 ATGA
 GTAG TGAGGAACCAG
 |||| |||||

CGTC ACTCCTTGGTC
C____

GAM3594 LOC143903 5' GCGAGTCGCAGAGGGGAACCAG 81339 A AGAT TGA
GC AGT GA GGAACCAG
|| ||| || |||||
CG TCA CT CCTTGGTC
C GCGT CC_

GAM3594 LOC144133 3' AGCAAGTAGAGATTTGCCA 81340 T GAGGAA
AGCAAGTAGA GAT CCA
||||||| ||| |||
TCGTTTCATCT CTA GGT
_ AAC____

GAM3594 LOC146229 3' AGCAAGTAGGTGGTGTCTAG 81341 A A A_
AGCAAGTAG TG TG GG
||||||| || || ||
TCGTTTCATC AC AC TC
C C AG

GAM3594 LOC147669 5' AAGTACCTGACTGAGGAAC 81342 GA _
AAGTA TGA TGAGGAAC
|||| ||| |||||
TTCAT ACT ACTCCTTG
GG G

GAM3594 LOC148894 3' AGCAAGTAGGTGTGGACCAA 81343 A ATGA A
AGCAAGTAG TG GGA CCAG
||||||| || ||| |||
TCGTTTCATC AC CCT GGTT
C A____ _

GAM3594 LOC151579 3' GTAGGAAGATGTAAGAACCAG 81319 AT_ _
GTAG GATG AGGAACCAG
|||| ||| |||||
CATC CTAC TTCTTGGTC
CTT A

GAM3594 LOC152286 3' AGCAAGTAGATCGATGTTGAAC 81344 _ AG
AGCAAGTAGAT GATG GAAC
||||||| ||| |||
TCGTTTCATCTA CTAC CTTG
G AA

GAM3594 LOC152941 3' GCAATAGATATGAGGA 81345 G A
GCAA TAGATG TGAGGA
|||| ||||| |||||
CGTT ATCTAT ACTCCT
_ _

GAM3594 LOC155179 3' AGCAAGAGATGGGCAC 81328 T ATGA A
AGCAAG AGATG GG AC
|||| |||| || ||
TCGTTT TCTAC CC TG
_ _ _ G

GAM3594 LOC158191 3' CAGGTAGATGATGCCACC 81346 A AGGA
CA GTAGATGATG ACC
|| ||||| ||| |||

		GT CATCTACTAC TGG	
		C GG__	
GAM3594	LOC196759 3'	GCAAGTAGAAGGTGAGCAA 81347	TGA G
		GCAAGTAGA TGAG AA	
		CGTTCATCT ACTC TT	
		TCC G	
GAM3594	LOC199864 3'	GCAAGTAGAAGGTGAGCAA 81347	TGA G
		GCAAGTAGA TGAG AA	
		CGTTCATCT ACTC TT	
		TCC G	
GAM3594	LOC221981 3'	AGTGAATATTGAATGAGGAA 81348	CA GAT
		AG AGTA GATGAGGAA	
		TC TTAT TTA CTCCTT	
		AC AAC	
GAM3594	LOC255031 5'	GCGAAGAGCGGTGGGGAACCAG 81349	_ T A A A
		GC AAG AG TG TG GGAACCAG	
		CG TTC TC GC AC CCTTGGTC	
		C _ _ C C	
GAM3594	LOC255386 3'	AGCAAGTAGAATGGGCCA 81308	TG A AA
		AGCAAGTAGA ATG GG CCA	
		TCGTCATCT TAC CC GGT	
		— — —	
GAM3594	LOC256273 3'	AGCAAGCAGGTGGTGGTGATCA 81350	A A AG AC
	G	AGCAAGTAG TG TG GA CAG	
		TCGTCGTC AC AC CT GTC	
		C C CA A_	
GAM3594	LOC257169 3'	GCAAGTAGAGGTGAACAA 81351	TGA G
		GCAAGTAGA TGAG AA	
		CGTTCATCT ACTT TT	
		CC_ G	
GAM3594	LOC90485 3'	GCGGGTGGATAACGAAGTCAG 81352	AA A AAC
		GC GT GATGATGAGG CAG	
		CG CA CTATTGCTTC GTC	
		CC C A_	
GAM3594	LOC96597 5'	GCAGTTGGGGTCAGGAACCAG 81353	A ATG__
		GTAG TG AGGAACCAG	
		CGTC AC TCCTTGGTC	
		A CCCAG	
GAM3595	CSPG3 3'	GCGAGAACAGTTTGG 81356	TTT
		GCGGG AACAGTTTGG	

CGCTC TTGTCAAACC

GAM3595 ZFH1B 3' GCAAAAACAGTTTGG 81357 TTT
GCGGG AACAGTTTGG
||||| |||||||
CGTTT TTGTCAAACC

GAM3595 FLJ11726 3' TTCTTCTTTCCAAAGACAGTTT 81358 GCGGGTTTA
GG TTCTTC ACAGTTTGG
||||| |||||||
AAGAAG TGTCAAACC
AAAGGTTTC

GAM3595 KIAA0894 3' TTCTTTCGAAACACAGTTTGG 81359 CG TTTA
TTCTT CGGG ACAGTTTGG
||||| ||| |||||||
AAGAA GCTT TGTCAAACC
A_ TG_

GAM3595 LOC154792 5' TTCCTGACTTGTTTAACAGTTT 81360 C GG
GG TTCTT GC GTTTAACAGTTTGG
||||| || |||||||||||
AAGGA TG CAAATTGTCAAACC
C AA

GAM3596 PRO0097 3' GTAGATAAGGGAAGAGATAAG 81363 AATGT_
GTAGATAAG GATAAG
||||||| |||||
CATCTATTC CTATTC
CCTTCT

GAM3596 LOC149566 5' TATCGTAGATGAAGACATCGA 81364 _ ATG
TATCGTAGAT AAGA TGA
||||||| ||||| |||
ATAGCATCTA TTCT GCT
C GTA

GAM3597 RFXAP 3' TCCAGATTACTTATCATTTT 81367 A CT T
TC AGATTACTTA TC ATTTT
|| |||||||| || |||||
AG TCTAATGAAT AG TAAAA
G _ _

GAM3597 TAC1 3' AACCACTTATTTCTATTTTA 81368 C
GATTACTTA TTCTATTTTA
||||||| |||||||
TTGGTGAAT AAGATAAAAT
A

GAM3597 TAC1 3' AACCACTTATTTCTATTTTA 81368 C
GATTACTTA TTCTATTTTA
||||||| |||||||
TTGGTGAAT AAGATAAAAT
A

GAM3597 TAC1 3' AACCACTTATTTCTATTTTA 81368 C
GATTACTTA TTCTATTTTA
||||||| |||||||

		TTGGTGAAT AAGATAAAAT		
		A		
GAM3597	TAC1	3' AACCACTTATTTCTATTTTA 81368	C	
		GATTACTTA TTCTATTTTA		
		TTGGTGAAT AAGATAAAAT		
		A		
GAM3597	BHMT	3' TCAAGATTTACTTTGTACTTAT 81369	_	TC
	TTT	TCAAGATT ACT TACT TATTTT		
		AGTTCTAA TGA ATGA ATAAAA		
		A AAC _		
GAM3597	PGR1	3' TCAAGATCTTATCTTCTATTTT 81370	TA	_
	A	TCAAGAT CTTA CTTCTATTTTA		
		AGTTCTA GAAT GAAGATAAAAT		
		_ A		
GAM3598	DPP4	3' CAAAGCCTCCATAAAAAACAATT 81373	AA	A
		CAAA TTTCA TAAAAACAATT		
		GTTT GAGGT ATTTTGTGTTAA		
		CG _		
GAM3598	RANBP2L1	3' ACAAAAATTTCTCAACAAT 81374		AATAAA
		ACAAAAATTTTC AACAAAT		
		TGTTTTTAAAG TTGTTA		
		AG__		
GAM3598	FLJ11011	3' ACAAAAAGTTTCAATAAAA 81375	A	
		ACAAAA TTTCAATAAAA		
		TGTTTT AAAGTTATTTT		
		C		
GAM3598	FLJ20274	3' ACAAAAACCTTCACTAAACAATT 81376		ATAA
		ACAAAAATTTCA AAACAATT		
		TGTTTTTGAAGT TTTGTGTTAA		
		GA_		
GAM3598	KIAA0336	3' ACAAAAATTTCTCAACAAT 81374		AATAAA
		ACAAAAATTTTC AACAAAT		
		TGTTTTTAAAG TTGTTA		
		AG__		
GAM3598	KIAA0342	3' ACAAGCATTTCAAGGAAACAAT 81377	AA	TAA
	T	ACAA ATTTCAA AAACAATT		
		TGTT TAAAGTT TTTGTGTTAA		
		CG CC_		
GAM3598	MAIL	3' ACAAAAATTTCAACAGAACA 81378		AA
		ACAAAAATTTCAATA AACA		

			TGTTTTTAAAGTTGT TTGT		
			C_		
GAM3598	NMES1	3'	ACAAAAATTTCAATATGCAAT 81379	AAAA	
			ACAAAAATTTCAATA CAAT		
			TGTTTTTAAAGTTAT GTTA		
			AC_		
GAM3598	LOC220692	3'	ACAAAAATTTCTCAACAAT 81374	AATAAA	
			ACAAAAATTTTCAACAAT		
			TGTTTTTAAAG TTGTTA		
			AG_		
GAM3599	APOL1	3'	TCCCATTTTTCCCTTATTGCAG 81382	CAC A_	
	GC		TCCCA TTTTCC ATTGCAGGC		
			AGGGT AAAGGG TAACGTCCG		
			AA_ AA		
GAM3599	BAT1	5'	CCTTCACTTCCGGTTGCAGGC 81383	CA TT AA	
			CC CACT TCC TTGCAGGC		
			GG GTGA AGG AACGTCCG		
			AA _ CC		
GAM3599	BAT1	5'	CCTTCACTTCCGGTTGCAGGC 81383	CA TT AA	
			CC CACT TCC TTGCAGGC		
			GG GTGA AGG AACGTCCG		
			AA _ CC		
GAM3599	COL15A1	3'	CAACTTTTCCAGCAAG 81384	C ATT	
			CA ACTTTTCCA GCAGG		
			GT TGAAAAGGT CGTTC		
			-		
GAM3599	DAZ	3'	TCCTTTACTTTTCCTTAAGG 81385	CAC AA C	
			TCC ACTTTTCC TTG AGG		
			AGG TGAAAAGG AAT TCC		
			AAA _ -		
GAM3599	DAZL	3'	TCCCTTACTTTTCCTTAAGG 81386	AC AA C	
			TCCC ACTTTTCC TTG AGG		
			AGGG TGAAAAGG AAT TCC		
			AA _ -		
GAM3599	DTX1	5'	TCCCCCACTATTGCAG 81387	A TTTCCA	
			TCCC CACT ATTGCAG		
			AGGG GTGA TAACGTC		
			G _		
GAM3599	GNB3	3'	ACACTTTATTGCAGG 81388	TCCA	
			ACACTTT ATTGCAGG		

TGTGAAA TAACGTCC

GAM3599 MRPL49 3' TCCCCAGCCTTGATTGCAGG 81389 A _ TCCA
TCCC CA CTTT ATTGCAGG
|||| ||| |||||
AGGG GT GGAA TAACGTCC
_ C C_

GAM3599 NID 3' TCCCAACTTTTCTAGTCAGGC 81390 C AATTG
TCCCA ACTTTTCC CAGGC
|||| ||||| ||||
AGGGT TGAAAAGG GTCCG
_ ATCA_

GAM3599 RAB26 3' TCCCACATTTTATCACAAGGC 81391 C CCA TG _
TCCCACA TTTT AT CA GGC
||||| ||| || |||
AGGGTGT AAAA TA GT CCG
_ _ GT T

GAM3599 SEC13L1 5' CATCTTTTCCAGCACAAGC 81392 _ ATT
CA CTTTTTCCA GCAGGC
|| ||||| |||||
GT GAAAAGGT TGTTCG
A CG_

GAM3599 TRIM9 3' TCCCATGTTTTTCCAAACA 81393 CAC TT
TCCCA TTTTCCAA GCA
|||| ||||| |||
AGGGT AAAAGGTT TGT
ACA _

GAM3599 FLJ12595 5' TCCCATTTTGTTTTGCAGGC 81394 CAC CCAA
TCCCA TTTT TTGCAGGC
|||| ||| |||||
AGGGT AAAA AACGTCCG
_ CAA_

GAM3599 FLJ20170 5' ACATTTTCAATTGCAGGC 81395 C C
ACA TTTTC AATTGCAGGC
|| |||| |||||
TGT AAAAG TTAACGTCCG
_ _

GAM3599 FLJ20306 3' ACACTTTTTCATACAATAGGC 81396 C AT _
ACACTTTT CA TGCA GGC
||||| || ||| |||
TGTGAAAA GT ATGT CCG
A _ TAT

GAM3599 FLJ21459 3' CCAGCTTTTCCAGAAGCGG 81397 CA ATT A
CCA CTTTTC CA GC GG
|| ||||| || ||
GGT GAAAAGGT CG CC
C_ CTT _

GAM3599 FLJ23027 5' TCCCAC TTTTCTG GGC 81398 A AATT
TCCCAC CTTTTC GC
||||| ||||| ||

			AGGGTG GAAAAGG CG		
			A ACC_		
GAM3599	KCNB2	3'	TCCCATTTCCTTAGTTCACAGG	81399	CAC CCAA TG
		C	TCCCA TTTT T CAGGC		
			AGGGT AAAA A GTCCG		
			AA_ ATCA GT		
GAM3599	KIAA0275	3'	CACTTTTCCACATTGCAGGC	81400	_
			CACTTTTCCA ATTGCAGGC		
			GTGAAAAGGT TAACGTCCG		
			G		
GAM3599	KIAA0618	3'	TCCCTACAGGATTGCAGG	81401	_ CTTTCCA
			TCCC ACA ATTGCAGG		
			AGGG TGT TAACGTCC		
			A CC_____		
GAM3599	MGC15634	3'	TCCTGACTTCAGCTTTGCAGGC	81402	CAC TCCAA
			TCC ACTTT TTGCAGGC		
			AGG TGAAG AACGTCCG		
			AC_ TCGA_		
GAM3599	MGC17330	3'	TCCCACACTATATGCAGG	81403	TTTCCAAT
			TCCCACACT TGCAGG		
			AGGGTGTGA ACGTCC		
			TAT_____		
GAM3599	NYD-SP21	3'	CACGTCTTCTGATTGCAGG	81404	_ CA
			CAC TTTTC ATTGCAGG		
			GTG AGAAG TAACGTCC		
			C AC		
GAM3599	PTBP2	3'	TCCCCACTTTTCTGAACAG	81405	A CAATT
			TCCC CACTTTTC GCAG		
			AGGG GTGAAAAG TGTC		
			_ ACT_		
GAM3599	PTP4A1	3'	TCCCATTCTTTTCTCAGG	81406	CA CAATTG
			TCCCA CTTTTC CAGG		
			AGGGT GAAAAG GTCC		
			AA A_____		
GAM3599	SAE1	3'	CACACTTTTCTCTATAAGG	81407	CAAT C
			CACACTTTTC TG AGG		
			GTGTGAAAAG AT TCC		
			AGAT _		
GAM3599	STAG2	3'	TCCTACACTTTCTTCAGG	81408	C CCAATTG
			TCC ACACTTTT CAGG		

			AGG TGTGAAAG	GTCC	
			A	AA_____	
GAM3599	STAM2	5'	TCCCAACTTTTCTCCCGGGGC	81409	C CAA CA
			TCCCA ACTTTTC	TTG GGC	
			AGGGT TGAAAAG	GGC CCG	
			_	AG_ C_	
GAM3599	STARD7	3'	CCACATCCCAACAATTGCAGG	81410	CT TC
			CCACA TT	CAATTGCAGG	
			GGTGT GG	GTTAACGTCC	
			AG	TT	
GAM3599	STARD7	3'	CCACATCCCAACAATTGCAGG	81410	CT TC
			CCACA TT	CAATTGCAGG	
			GGTGT GG	GTTAACGTCC	
			AG	TT	
GAM3599	STK3	3'	CACACTTTTTTTGTGCAAG	81411	CCAAT
			CACACTTTT	TGCAGG	
			GTGTGAAAA	ACGTTC	
			AAC_		
GAM3599	TRAF2	3'	TCTCACACTTTTACCGCAGGC	81412	C T AAT
			TC CACACTTT	CC TGCAGGC	
			AG GTGTGAAA	GG GCGTCCG	
			A	T _	
GAM3599	WBSCR16	3'	ACTTTTCCAAGCCAGGC	81413	TTG
			ACTTTTCCAA	CAGGC	
			TGAAAAGGTT	GTCCG	
			CG_		
GAM3599	ZNF294	3'	CCACACTTTTATATTTTGGGC	81414	CCA GCA
			CCACACTTTT	ATT GGC	
			GGTGTGAAAA	TAA CCG	
			TA_	AAC	
GAM3599	LOC144766	3'	CCAGCACTTTTCCGGAAGG	81415	_ AATTGC
			CCA CACTTTTCC	AGG	
			GGT GTGAAAAGG	TCC	
			C	CCT_	
GAM3599	LOC146452	3'	CACCTTTCCATCCTCCAGG	81416	A_ G
			CACTTTTCCA	TT CAGG	
			GTGGAAAGGT	GA GTCC	
			AG	G	
GAM3599	LOC151996	5'	CCCACTTTTCTGCAGG	81417	A CAAT
			CC CACTTTTC	TGCAGG	

GG GTGAAAAG ACGTCC

GAM3599 LOC158428 3' CATATTTCCAATTGCAGGC 81418 CT
CA TTTCCAATTGCAGGC
|| |||||
GT AAAGGTTAACGTCCG
AT

GAM3599 LOC159176 3' CATACTGCCAGAATTGCAGGC 81419 C TTT _
CA ACT CCA ATTGCAGGC
|| ||| ||| |||||
GT TGA GGT TAACGTCCG
A C_ CT

GAM3599 LOC255927 3' CACACTTTATTAAGCAGG 81420 TCC TT
CACACTTT AA GCAGG
||||| || |||||
GTGTGAAA TT CGTCC
TAA TT

GAM3599 LOC51696 3' CACATATTTTCCAAAGG 81421 C_ TTGC
CACA TTTTCCAA AGG
||| ||||| |||
GTGT AAAAGGTT TCC
ATA _

GAM3599 LOC89944 3' TCCCACCTTTCCTGCAGG 81422 A AAT
TCCCAC CTTTTC TGCAGG
||||| ||||| |||||
AGGGTG GAAAGGG ACGTCC

GAM3599 LOC90826 5' TCCCATACTTTTCACAATTAGC 81423 C _ _
TCCCA ACTTTTC CAATT GC
||||| ||||| ||||| |||
AGGGT TGAAAAG GTTAA CG
A T T

GAM3599 LOC93589 3' TCCCACATTTCTCCATGGC 81424 C ATT
TCCCACA TTTTCCA GC
||||| ||||| |||
AGGGTGT AAGAGGT CG
A AC_

GAM3599 LOC93622 3' ACTCATCCCAATTGTAGG 81425 _ C
ACTT TTCCAATTG AGG
||| ||||| |||
TGAG AGGGTTAAC TCC
T A

GAM3600 GEM 3' TATCAAATGTAAAATGGTT 81428 C A
TATCAAATGTTA AAT GTT
||||||| ||| |||
ATAGTTTACAAT TTA CAA
T C

GAM3600 MAP3K13 3' TATCAATGTTACAGTAGCT 81429 A A
TATCAA TGTTACA TAGTT
||||| ||||| |||||

		ATAGTT ACAATGT ATCGA		
		— C		
GAM3600	BCAA	3' TATCAAATGTTCCAGCTTT 81430	ACAA	
		TATCAAATGTT TAGTTTT		
		ATAGTTTACAA GTCGAAA		
		G__		
GAM3600	KIAA1463	3' TACCAAATGTTAACATTTTTT 81431	CAATA	
		TATCAAATGTTA GTTTTTT		
		ATGGTTTACAAT TAAAAAA		
		TG__		
GAM3600	LOC121441	3' TATCAAATGTACAATAA 81432	T	
		TATCAAATGT ACAATAG		
		ATAGTTTACA TGTTATT		
		—		
GAM3600	LOC153516	3' CATCAAGTGTTACAATGATTTT 81433	A	A
	TT	TATCAA TGTTACAAT GTTTTTT		
		GTAGTT ACAATGTTA TAAAAAA		
		C C		
GAM3600	LOC158450	5' TCAAATGTAACAATACTT 81434	T	G
		TCAAATGT ACAATA TT		
		AGTTTACA TGTTAT AA		
		T G		
GAM3600	LOC158504	5' TCAAATGTAACAATACTT 81434	T	G
		TCAAATGT ACAATA TT		
		AGTTTACA TGTTAT AA		
		T G		
GAM3601	CAST	3' AAGGGCAAACCTGAAAATACAA 81437	A_	CA
		AAG CAAAC AAAATACAA		
		TTC GTTTG TTTTATGTT		
		CC AC		
GAM3601	KLHL1	3' TACAAAACAAATTACCAA 81438	—	
		TACAAGACAA ACCAA		
		ATGTTTTGTT TGGTT		
		TAA		
GAM3601	MTMR2	3' CACAAGACAGACTGAACCAA 81439	—	
		TACAAGACA AACCAA		
		GTGTTCTGT TTGGTTT		
		CTGAC		
GAM3601	NRAS	3' AAACAAACCAAACAGCAAT 81440	AATA	
		AGACAAACCAA CAAT		

TTTGTTTGGTTT GTTA
 GTC_
 GAM3601 ABCA5 5' CACAAGACAGACCAAAAA 81441 A
 TACAAGACA ACCAAAA
 ||||| |||||
 GTGTTCTGT TGGTTTT
 C
 GAM3601 BAG5 3' TACAGATCACAAAAATACAAT 81442 A _ AAC
 TACA GA CA CAAAAATACAAT
 ||| || |||||
 ATGT CT GT GTTTTTATGTTA
 _ A _
 GAM3601 C1QR1 3' TACAAGAACAGACCAAAACACA 81443 _ A A
 AT TACAAGA CA ACCAAAA TACAAT
 ||||| || ||||| |||||
 ATGTTCT GT TGGTTTT GTGTTA
 T C _
 GAM3601 FLJ22004 3' TACAAAACCCAAAAATA 81444 AAA
 TACAAGAC CAAAAATA
 ||||| |||||
 ATGTTTTG GGTTTTTAT
 _
 GAM3601 FLJ25006 3' ACAAACAGAAAAATACAA 81445 C_
 ACAAAC AAAAAATACAA
 ||||| |||||
 TGTTTG TTTTATGTT
 TC
 GAM3601 KIAA0826 3' TACAACACAAACCAACAGCTAC 81446 G AAA_
 AAT TACAA ACAAACCAA TACAAT
 ||||| ||||| |||||
 ATGTT TGTTTGGTT ATGTTA
 G GTCG
 GAM3601 KIAA1679 3' TACAAAACAAAATACA 81447 CCAAAA
 TACAAGACAAA ATACA
 ||||| |||||
 ATGTTTTGTTT TATGT
 _
 GAM3601 KIAA1735 3' CAAGACAAACTGTATTGGAAAT 81448 CAA_____ |||
 ACAATA ACAAAC AAATACAAT A
 ||||| ||||| |
 TGTTTG TTTATGTTA T
 ACATAACC |||
 GAM3601 MAIL 3' TACAAGACATACTGGGTCAAAC 81449 A CAAAAAT_
 AAT TACAAGACA AC ACAAT
 ||||| || |||||
 ATGTTCTGT TG TGTTA
 A ACCCAGTT
 GAM3601 NDST3 5' CAGGACTCACAGAAAATACA 81450 A AA CA
 CA GAC AC AAAATACA
 || ||| || |||||

		GT CTG TG TTTTATGT	
		C AG TC	
GAM3601	pcnp	3' TACAAAACAAACACCCTACAAT 81451	CAAAAA
		TACAAGACAAAC TACAAT	
		ATGTTTGTGTTG ATGTTA	
		TGGG__	
GAM3601	TRAF3	3' CACAAGACAGACTAGACACA 81452	A CAAAA
		TACAAGACA AC ATACA	
		GTGTTCTGT TG TGTGT	
		C ATC__	
GAM3601	LOC220936	3' CAAGACAAATTAGAAAAACAAT 81453	CCAA T
		CAAGACAAA AAA ACAAT	
		GTTCTGTTT TTT TGTTA	
		AATC T	
GAM3601	LOC221509	3' AGACAAACCAGTATTACAAT 81454	AAAA
		AGACAAACCA TACAAT	
		TCTGTTTGGT ATGTTA	
		CATA	
GAM3602	ABCB9	3' TCCGTGAAGGCGTTGGC 81457	C GCC
		TCCGTGGA GGCG GGC	
		AGGCACTT CCGC CCG	
		_ AA_	
GAM3602	ABCC12	3' TCCGTGGATGGGAGGGGC 81458	C C CC
		TCCGTGGA GG GG GGC	
		AGGCACCT CC CT CCG	
		A _ CC	
GAM3602	ADRA1A	3' CGTGGACGGGAAGCTGGC 81459	C_ C
		CGTGGACGG GGC GGC	
		GCACCTGCC TCG CCG	
		CT A	
GAM3602	AHR	5' CCACTGCGGCGGCCGGC 81460	_ GA
		CCG TG CGGCGGCCGGC	
		GGT AC GCCGCCGGCCG	
		G _	
GAM3602	ALDOA	5' TCCGTGGACGGAGTGTGG 81461	C CC_
		TCCGTGGACGG GG GG	
		AGGCACCTGCC TC CC	
		_ ACA	
GAM3602	BAZ1B	5' TCGGTCCCGGCGGCCGGC 81462	C GGA
		TC GT CGGCGGCCGGC	

			AG CA GCCGCCGGCCG		
			C GG_		
GAM3602	BCL7A	5'	TCCATGGGAGACAGCCGG	81463	AC
			TCCGTGG GGC GGCCGG		
			AGGTACC CTGTCGGCC		
			CT		
GAM3602	EDARADD	5'	TCCGAGCGGGGCTGGC	81464	T A C C
			TCCG GG CGG GGC GGC		
			AGGC TC GCC CCG CCG		
			- - - A		
GAM3602	FBXL3A	5'	TCCGGGGACGGCGGCGGC	81465	T C
			TCCG GGACGGCGGC GGC		
			AGGC CCTGCCGCCG CCG		
			C -		
GAM3602	GALNT1	3'	TCCATGGACAGGAAGGCTGG	81466	C_ C
			TCCGTGGACGG GGC GG		
			AGGTACCTGTC CCG CC		
			CTT A		
GAM3602	GJA5	3'	TCCGTAGATGAAGTACTGGC	81467	C CG_ C
			TCCGTGGA GG GC GGC		
			AGGCATCT CT TG CCG		
			A TCA A		
GAM3602	GPR30	5'	TCCGTGGAGGCGAGGGC	81468	C CC
			TCCGTGGA GGCGG GGC		
			AGGCACCT CCGCT CCG		
			- C_		
GAM3602	GPR48	5'	TCCATGGACGCGCAGAGGC	81469	- CC
			TCCGTGGACG GCGG GGC		
			AGGTACCTGC CGTC CCG		
			G T_		
GAM3602	LBX1	3'	CCGCTGGTGGCGGCCGGC	81470	- AC
			CCG TGG GGCGGCCGGC		
			GGC ACC CCGCCGGCCG		
			G A_		
GAM3602	MTCP1	5'	CCCGGACCGCGGCCGGC	81471	G G
			CC TGGAC GCGGCCGGC		
			GG GCCTG CGCCGGCCG		
			- G		
GAM3602	NFATC2	5'	TCCGGGGACGGCGCGCCTGGC	81472	T - -
			TCCG GGACGGCG GCC GGC		

			AGGC CCTGCCGC CGG CCG		
			C G A		
GAM3602	NRG1	3'	TCCGCGGACGCGTGGGC 81473	G GCC	
			TCCGTGGACG CG GGC		
			AGGCGCCTGC GC CCG		
			_ AC_		
GAM3602	PTS	5'	CCCGCCGCGCGGCCGG 81474	GGA _	
			TCCGT CG GCGGCCGG		
			GGGCG GC CGCCGGCC		
			_ G		
GAM3602	RALBP1	3'	TCTGTGGATGCACCAGGC 81475	C CG G _	
			TC GTGGA GCG CC GGC		
			AG CACCT CGT GG CCG		
			A A_ _ T		
GAM3602	SACM2L	3'	TCCATGGAGATGACCGGC 81476	C GC	
			TCCGTGGA G GGCCGGC		
			AGGTACCT C CTGGCCG		
			_ TA		
GAM3602	SACM2L	3'	TCCATGGAGATGACCGGC 81476	C GC	
			TCCGTGGA G GGCCGGC		
			AGGTACCT C CTGGCCG		
			_ TA		
GAM3602	SECTM1	3'	CCCTCAGGGCGGCCGGC 81477	GT AC	
			TCC GG GGCGGCCGGC		
			GGG TC CCGCCGGCCG		
			AG _		
GAM3602	SMURF1	3'	TCTATGGACAACAGTGGC 81478	CG CC	
			TC TGGACGGCGG GGC		
			AG ACCTGTTGTC CCG		
			AT A_		
GAM3602	ST14	5'	TCCCTGCCGGCGGCCGGC 81479	G GA	
			TCC TG CGGCGGCCGGC		
			AGG AC GCCGCCGGCCG		
			G G_		
GAM3602	TJP1	5'	TCCGCTGGCTCAGCCGGC 81480	_ ACGG	
			TCCG TGG CGGCCGGC		
			AGGC ACC GTCGGCCG		
			G GA_		
GAM3602	TRADD	3'	CCCGTGGATGGACAGGGG 81481	C _ CC	
			TCCGTGGA GG CGG GG		

		GGGCACCT CC GTC CC	
		A T C_	
GAM3602	TRAF5	5' TCCTGGCTGCGGCCGGC	81482 G ACG
		TCC TGG GCGGCCGGC	
		AGG ACC CGCCGGCCG	
		_ GA_	
GAM3602	WHN	3' CCCGATGTGGGCGGCCGGC	81483 _ GAC
		TCCG TG GCGGCCGGC	
		GGGC AC CCGCCGGCCG	
		T AC_	
GAM3602	ZNF236	3' CCGTGGATGCGCTCCCGGC	81484 CG G__
		CCGTGGA GCG CCGGC	
		GGCACCT CGC GGCCG	
		A_ GAG	
GAM3602	C22orf4	3' TCCATGGAGGAACCGG	81485 C C
		TCCGTGGA GG GGCCGG	
		AGGTACCT CC TTGGCC	
		- -	
GAM3602	CDC14B	5' TCCTGCCGCGGCCGGC	81486 G GA G
		TCC TG CG CGGCCGGC	
		AGG AC GC GCCGGCCG	
		_ G_ _	
GAM3602	CDC14B	5' TCCTGCCGCGGCCGGC	81486 G GA G
		TCC TG CG CGGCCGGC	
		AGG AC GC GCCGGCCG	
		_ G_ _	
GAM3602	CDC14B	5' TCCTGCCGCGGCCGGC	81486 G GA G
		TCC TG CG CGGCCGGC	
		AGG AC GC GCCGGCCG	
		_ G_ _	
GAM3602	CHAF1B	3' TCCATGGAAGCCCTGG	81487 C GG _
		TCCGTGGA GGC CC GG	
		AGGTACCT TCG GG CC	
		- _ _ A	
GAM3602	COTL1	5' TCCGGGGCGGCCGAGC	81488 T ACG _
		TCCG GG GCGGCCG GC	
		AGGC CC CGCCGGC CG	
		- _ _ T	
GAM3602	DGKD	3' TCCATGGACTTGGAGCTGGC	81489 _ C C
		TCCGTGGAC GG GGC GGC	

AGGTACCTG CC TCG CCG
 AA _ A
 GAM3602 DKFZP434C245 5' TCCATGGAGCCACTGGC 81490 CG G C
 TCCGTGGA GC GC GGC
 ||||| || || ||
 AGGTACCT CG TG CCG
 _ G A
 GAM3602 DKFZP564J102 5' TCCGTGGATGAGCCGG 81491 C GC
 TCCGTGGA G GGCCGG
 ||||| | |||||
 AGGCACCT C TCGGCC
 A _
 GAM3602 FLJ31564 5' TCCGGGCAGGCGGCCGGC 81492 T AC
 TCCG GG GGCGGCCGGC
 ||| || |||||
 AGGC CC CCGCCGGCCG
 _ GT
 GAM3602 FLJ32356 5' TCCTGGGCGGCCGGGCCGGC 81493 G A _
 TCC TGG CGGC GGCCGGC
 ||| ||| ||| |||||
 AGG ACC GCCG CCGGCCG
 _ C GC
 GAM3602 GEMIN7 5' TCAGTGGACAAACATTTGGC 81494 C _ GCC
 TC GTGGACGG CG GGC
 || ||||| || |||
 AG CACCTGTT GT CCG
 T T AAA
 GAM3602 HSP105B 5' CCCGGGGACAGCGCGGC 81495 T C
 TCCG GGACGGCGGC GGC
 ||| ||||| |||
 GGC CCTGTCGCCG CCG
 C _
 GAM3602 KIAA0153 3' CCCGTGGAGTGCCCGGC 81496 CG GG
 TCCGTGGA GC CCGGC
 ||||| || |||||
 GGGCACCT CG GGCCG
 CA _
 GAM3602 KIAA0435 3' TCCTTGTAGGGCGGCCGGC 81497 G GAC
 TCC TG GGCGGCCGGC
 ||| || |||||
 AGG AC CCGCCGGCCG
 A ATC
 GAM3602 KIAA1276 5' TCCTGGGGCAGCCGGC 81498 G AC
 TCC TGG GGCGGCCGGC
 ||| || |||||
 AGG ACC CCGTCGGCCG
 _ _
 GAM3602 KIAA1337 3' CCGTGAGCAGGCGGCCGGC 81499 GA _
 CCGTG C GGCGGCCGGC
 |||| | |||||

GGCAC G CCGCCGGCCG
TC T
GAM3602 KIAA1813 3' CCTGTGAACAGGGTTGGC 81500 _ C CC
CC GTGGACGG GG GGC
|| ||||| || |||
GG CACTTGTC CC CCG
A _ AA
GAM3602 LCHN 5' TCCGGGGCGGCCGGC 81501 T ACG
TCCG GG GCGGCCGGC
|||| || |||||
AGGC CC CGCCGGCCG
_ _
GAM3602 MGC15438 3' CCCGGGCGCGGCCGGC 81502 T A G
TCCG GG CG CGGCCGGC
|||| || |||||
GGGC CC GC GCCGGCCG
_ _ _
GAM3602 MGC16332 5' TCCTGGAACAGCAGGTCGGC 81503 G _ _ C
TCC TGA CGGC GG CGGC
|| ||| ||| || |||
AGG ACCT GTCG CC GCCG
_ T T A
GAM3602 NBL1 5' TCGGCGAGGCGGCCGGC 81504 C AC
TC GTGG GGCGGCCGGC
|| ||| |||||
AG CGCT CCGCCGGCCG
C _
GAM3602 NEUROG3 3' CCCGTGGAGGCCTGGGCCGGC 81505 C _
TCCGTGGA GGC GGCCGGC
||||| || |||||
GGGCACCT CCG CCGGCCG
_ GAC
GAM3602 NTSR2 5' CCCGCTCCCGCGGCCGGC 81506 GGA G
TCCGT CG CGGCCGGC
|||| || |||||
GGGCG GC GCCGGCCG
AGG _
GAM3602 PANX1 5' TCCGGGTACAGCCGGC 81507 T ACG
TCCG GG GCGGCCGGC
|||| || |||||
AGGC CC TGTCGGCCG
_ A_
GAM3602 PRKCZ 5' TCCGCGGAACTCCGGC 81508 CG GG
TCCGTGGA GC CCGGC
||||| || |||
AGGCGCCT TG GGCCG
_ A_
GAM3602 QKI 5' CCCCGGGGCGGCCGGC 81509 G AC
CC TGG GGCGGCCGGC
|| ||| |||||

GG GCC CCGCCGGCCG
G _
GAM3602 RAB10 5' TCCGAGGGCGGCGACCGCGGC 81510 T A _
TCCG GG CGGCGGCC GGC
||||| || ||||| |||
AGGC CC GCCGCTGG CCG
T C CG
GAM3602 RDH-E2 5' TCCGCGGAGAAGCCGGC 81511 C C
TCCGTGGA GG GGCCGGC
||||| || |||||
AGGCGCCT CT TCGGCCG
- -
GAM3602 SCAMP-4 3' CCTGTGGACGGCAGAGGC 81512 _ CC
CC GTGGACGGCGG GGC
|| ||||| |||
GG CACCTGCCGTC CCG
A T_
GAM3602 SLC37A1 5' TCCGTGGAGCGGCTGCCGGC 81513 _ G
TCCGTGGA CGGC GCCGGC
||||| ||| |||||
AGGCACCT GCCG CGGCCG
C A
GAM3602 SMARCF1 5' TCCGCGGAGAGACCCGGC 81514 C_ GG
TCCGTGGA GGC CCGGC
||||| ||| |||||
AGGCGCCT CTG GGCCG
CT _
GAM3602 SMARCF1 5' TCCGCGGAGAGACCCGGC 81514 C_ GG
TCCGTGGA GGC CCGGC
||||| ||| |||||
AGGCGCCT CTG GGCCG
CT _
GAM3602 SMARCF1 5' TCCGCGGAGAGACCCGGC 81514 C_ GG
TCCGTGGA GGC CCGGC
||||| ||| |||||
AGGCGCCT CTG GGCCG
CT _
GAM3602 SPS 5' CCGGGCGCGGCCGGC 81515 T A G
CCG GG CG CGGCCGGC
||| || |||||
GGC CC GC GCCGGCCG
- - -
GAM3602 SRCRB4D 5' TCCATGGAGCTGGCTGG 81516 CG _ C
TCCGTGGA GC GGC GG
||||| || ||| ||
AGGTACCT CG CCG CC
_ A A
GAM3602 LOC124895 5' CCTGGAGCTGGCGGCCGGC 81517 G C_
CC TGGA GGCGGCCGGC
|| ||| |||||

		GG ACCT CCGCCGGCCG		
		_ CGA		
GAM3602	LOC126295 5'	CCGTGGCCTCGCGGCCCGGC	81518	ACG_
		CCGTGG GCGGCCCGGC		
		GGCACC CGCCGGCCG		
		GGAG		
GAM3602	LOC126526 5'	TCCTGGAGGAATGCCGGC	81519	G C CG_
		TCC TGGA GG GCCGGC		
		AGG ACCT CC CGGCCG		
		_ _ TTA		
GAM3602	LOC129080 3'	TCCCTGGAGGCAGCTGGC	81520	G C C
		TCC TGGA GGCGGC GGC		
		AGG ACCT CCGTCG CCG		
		G _ A		
GAM3602	LOC145725 3'	CCCGTGGACGACACCTGG	81521	G _
		TCCGTGGACGGCG CC GG		
		GGGCACCTGCTGT GG CC		
		_ A		
GAM3602	LOC145732 3'	CCCGTGGACGACACCTGG	81521	G _
		TCCGTGGACGGCG CC GG		
		GGGCACCTGCTGT GG CC		
		_ A		
GAM3602	LOC146346 5'	TCCTGGACAACACGG	81522	G GC
		TCC TGGACGGCG CGG		
		AGG ACCTGTTGT GCC		
		_ _		
GAM3602	LOC147791 5'	TCCGCGGATGCCCCGGC	81523	CG GG
		TCCGTGGA GC CCGGC		
		AGGCGCCT CG GGCCG		
		A_ G_		
GAM3602	LOC151475 3'	TCCGTAGATGAACAGGGC	81524	C_ CC
		TCCGTGGA GGCGG GGC		
		AGGCATCT TTGTC CCG		
		AC _		
GAM3602	LOC196957 3'	CCCGTGGACGACACCTGG	81521	G _
		TCCGTGGACGGCG CC GG		
		GGGCACCTGCTGT GG CC		
		_ A		
GAM3602	LOC196961 3'	CCCGTGGACGACACCTGG	81521	G _
		TCCGTGGACGGCG CC GG		

	GGGCACCTGCTGT GG CC	
	— A	
GAM3602 LOC197138 3'	CCCGTGGACGACACCTGG 81521	G _
	TCCGTGGACGGCG CC GG	
	GGGCACCTGCTGT GG CC	
	— A	
GAM3602 LOC199992 5'	TCCGCGGGCGGCCAGC 81525	ACG
	TCCGTGG GCGGCCGGC	
	AGGCGCC CGCCGGTCG	
	—	
GAM3602 LOC203276 3'	TCCATGGAGCAGCTGGC 81526	CG C
	TCCGTGGA GCGGC GGC	
	AGGTACCT CGTCG CCG	
	— A	
GAM3602 LOC203305 3'	TCCATGGAGCAGCTGGC 81526	CG C
	TCCGTGGA GCGGC GGC	
	AGGTACCT CGTCG CCG	
	— A	
GAM3602 LOC204579 5'	TCCGTGGACGCGGATGC 81527	G CCG
	TCCGTGGACG CGG GC	
	AGGCACCTGC GCC CG	
	— TA_	
GAM3602 LOC219513 5'	TCCGCGGAGCCGCCCGGC 81528	CG G _
	TCCGTGGA GC GCC GGC	
	AGGCGCCT CG CGG CCG	
	— G GG	
GAM3602 LOC222486 5'	CCTATGGTGCGGCGGCCGGC 81529	_ A_
	CC GTGG CGGCGGCCGGC	
	GG TACC GCCGCCGGCCG	
	A AC	
GAM3602 LOC245727 3'	CCCGTGGACGACACCTGG 81521	G _
	TCCGTGGACGGCG CC GG	
	GGGCACCTGCTGT GG CC	
	— A	
GAM3602 LOC253367 3'	CCGTATTGCAGCGGCCGGC 81530	GA_
	CCGTG CGGCGGCCGGC	
	GGCAT GTCGCCGGCCG	
	AAC	
GAM3602 LOC254243 3'	TCCATGGAGCAGCTGGC 81526	CG C
	TCCGTGGA GCGGC GGC	

		AGGTACCT CGTCG CCG		
		— A		
GAM3602	LOC57862 5'	TCCGGGAAGCCGGCCGGC 81531	T C _	
		TCCG GGA GGC GGCCGGC		
		AGGC CCT TCG CCGGCCG		
		_ _ G		
GAM3602	LOC89941 3'	TCCCTGACAGCGGTGGCCGGC 81532	G G _	
		TCC TG ACGGC GGCCGGC		
		AGG AC TGTCG CCGGCCG		
		G _ CCA		
GAM3602	LOC90038 3'	TCCATGGAGCAGCTGGC 81526	CG C	
		TCCGTGGA GCGGC GGC		
		AGGTACCT CGTCG CCG		
		— A		
GAM3602	LOC91179 5'	CCCGTGGACGCCAGGGC 81533	G CC	
		TCCGTGGACG CGG GGC		
		GGGCACCTGC GTC CCG		
		G _		
GAM3602	LOC91828 5'	TCCGCGGAGATGGCGCCGGC 81534	C_ G	
		TCCGTGGA GGCG CCGGC		
		AGGCGCCT CCGC GGCCG		
		CTA _		
GAM3602	LOC91828 3'	TCCCTGCCAGCGGCCGGC 81535	G GA	
		TCC TG CGGCGGCCGGC		
		AGG AC GTCGCCGGCCG		
		G G_		
GAM3602	LOC91978 5'	TCCGTGAAACCGGCCGGC 81536	CGG	
		TCCGTGGA CGGCCGGC		
		AGGCACTT GCCGGCCG		
		TG_		
GAM3603	ZNF142 5'	TGTGCGACCGCCTCCGGCTC 81539	C GTC	
		TG GCGACCGCCTC GTTC		
		AC CGCTGGCGGAG CGAG		
		A GC_		
GAM3604	ATRX 3'	TGACAAATGTCAGGAAGAAATG 81542	A AAT C	
		TGACAAATG CA GA AAATG		
		ACTGTTTAC GT TT TTTAC		
		A CC_ C		
GAM3604	ATRX 3'	TGACAAATGTCAGGAAGAAATG 81542	A AAT C	
		TGACAAATG CA GA AAATG		

ACTGTTTAC GT TT TTTAC
 A CC_ C
 GAM3604 EGR3 3' TGACAAAGGAGCAAATGA 81543 T _
 TGACAAA GA CAAATGA
 ||||| || |||||
 ACTGTTT CT GTTTACT
 C C
 GAM3604 HLA-DQA1 3' TGACAAATGATCTGGTAAATGA 81544 CAAA AC
 TGACAAATGA TG AAATGA
 ||||| || |||||
 ACTGTTTACT AC TTTACT
 AG_ CA
 GAM3604 ISL1 3' CAAATGACATGAAAAGTG 81545 AA C A
 CAAATGACA TGA AA TG
 ||||| || || ||
 GTTTACTGT ACT TT AC
 _ T C
 GAM3604 KCNS3 3' TGAGTAAATGACAAACACAGAA 81546 C_ G _
 TGA TGA AAATGACAAAT ACA AATGA
 || ||||| || |||||
 ACT TTTACTGTTTG TGT TTACT
 CA _ C
 GAM3604 MMP20 3' TAACAAATGATGGCCAAATGA 81547 CAAA A_
 TGACAAATGA TG CAAATGA
 ||||| || |||||
 ATTGTTTACT AC GTTTACT
 _ CG
 GAM3604 YWHAZ 3' GACAGCATGGATGACAAATG 81548 A_ ACAA
 GACA ATG ATGACAAATG
 ||| || |||||
 CTGT TAC TACTGTTTAC
 CG C_
 GAM3604 DKFZp434C0328 5' TGAAAAC TACTAGTGACAAATG 81549 C G AAA
 A TGA AAAT AC TGACAAATGA
 || ||| || |||||
 ACT TTTG TG ACTGTTTACT
 _ A ATC
 GAM3604 DKFZP434P0721 3' ATGATAAATGACAGATAATGA 81550 C _
 ATGA AAATGACA AATGA
 ||| ||||| |||||
 TACT TTTACTGT TTACT
 A CTA
 GAM3604 FLJ14600 3' TGAAACAAATGACAAATG 81551 CAAAT
 TGA GACAAATGACAAATG
 || |||||
 ACT TTGTTTACTGTTTAC
 _
 GAM3604 HMP19 3' TGACAAATGAATTTACAGGTGA 81552 CAAATG AA
 TGACAAATGA ACA TGA
 ||||| || |||

ACTGTTTACT TGT ACT
 TAAA__ CC
 GAM3604 KIAA0557 3' TGACTAGGTGACAAATGCAATG 81553 AAA_ A A
 TGAC TGACAAATG CAA TG
 |||| ||||||| ||||
 ACTG ACTGTTTAC GTT AC
 ATCC _ _
 GAM3604 KIAA0731 3' ATGACAAACCCAGATGA 81554 GA A
 ATGACAAAT CA ATGA
 ||||||| || ||||
 TACTGTTTG GT TACT
 GG C
 GAM3604 KIAA1843 3' TGACAAATGGAAATGTATTCAT 81555 AC AC____
 AAATGA ACAAATG AAATG AAATGA
 ||||||| |||| ||||||
 TGTTTAC TTTAC TTTACT
 C_ ATAAGTA
 GAM3604 TRIP-Br2 3' TGACTGAATATTGACAAATGA 81556 AAA CAAA
 TGAC TGA TGACAAATGA
 |||| ||| ||||||||
 ACTG ACT ACTGTTTACT
 _ TATA
 GAM3604 YME1L1 3' GATAAATGTGACAAATG 81557 C ACAA
 GA AAATG TGACAAATG
 || ||||| ||||||||
 CT TTTAC ACTGTTTAC
 A _
 GAM3604 YME1L1 3' GATAAATGTGACAAATG 81557 C ACAA
 GA AAATG TGACAAATG
 || ||||| ||||||||
 CT TTTAC ACTGTTTAC
 A _
 GAM3604 YME1L1 3' GATAAATGTGACAAATG 81557 C ACAA
 GA AAATG TGACAAATG
 || ||||| ||||||||
 CT TTTAC ACTGTTTAC
 A _
 GAM3604 LOC120406 3' TGACAAATGCTACAATATGGAT 81558 _ _ ACAA
 GA TGACAAATG ACAA ATG ATGA
 ||||||| |||| ||| ||||
 ACTGTTTAC TGTT TAC TACT
 GA A C_
 GAM3604 LOC150311 5' TGACAAATGGTGAATCACAATG 81559 ACA G A
 TGACAAATG AAT ACAA TG
 ||||||| ||| |||| ||
 ACTGTTTAC TTA TGTT AC
 CAC G _
 GAM3604 LOC151473 3' TGACAATGGCATTACAAATGA 81560 A A AATG
 TGACAA TG CA ACAAATGA
 |||||| ||| || |||||||

ACTGTT AC GT TGT TACT
 _ C AAA_
 GAM3604 LOC163861 5' TGACAAATGACTGAATGCA 81561 A_ A
 TGACAAATGAC AATG CA
 ||||| |||
 ACTGTTTACTG TTAC GT
 AC _
 GAM3604 LOC170063 3' AATGACAAACAAATG 81562 AAT
 AATGACA GACAAATG
 ||||| |||||
 TTACTGT TTGTTTAC
 —
 GAM3604 LOC199907 3' TGACAAATGACAGAATTCAGGT 81563 _ GA AA
 GA TGACAAATGACA AAT CA TGA
 ||||| ||| ||
 ACTGTTTACTGT TTA GT ACT
 C A_ CC
 GAM3604 LOC220739 3' CACAGTCCAAGGTGACAAATGA 81564 AATGA A_
 CA CAA TGACAAATGA
 || ||| |||||
 GT GTT ACTGTTTACT
 GTCAG CC
 GAM3604 LOC256866 5' GACAAAGGCCAAATGACAGGTG 81565 TGA AA
 A GACAAA CAAATGACA TGA
 ||||| ||||| ||
 CTGTTT GTTTACTGT ACT
 CCG CC
 GAM3604 LOC51277 3' ACAAATGACAACACATGAATGA 81566 ATGACA
 ACAAATGACAA AATGA
 ||||| ||||
 TGT TACTGTT TTACT
 GTGTAC
 GAM3605 EN2 5' CTCGGGCTCCGGCGCGCCG 81569 CA
 CTCG CTCCGGCGCCGT
 ||| |||||
 GAGC GAGGCCGCGCGC
 CC
 GAM3605 NR2F2 5' CTCGGGCTCCGGCGCGCCG 81570 CA C GTT
 CTCG CTCCGGCGC GT CG
 ||| ||||| || ||
 GAGC GAGGCCGCG CG GC
 CC _ —
 GAM3605 RAP1GA1 5' CTCGGCACTCTGGTGCCCGC 81571 _ C C G
 CTCG CACTC GG GCC TGT
 ||| |||| || |||
 GAGC GTGAG CC CGG GCG
 C A A _
 GAM3605 SPINT2 5' CTCGCGTTCAGGTGCCGACGC 81572 AC C C TGTT
 CTCGC TC GG GCCG CGC
 |||| || || ||| |||

GAGCG AG CC CGGC GCG
 CA T A T____
 GAM3605 FLJ12876 5' CTCGCACTCTCGAGTTGTTCTG 81573 _ CGCCG
 CTCGCACTC CGG TGTTCTG
 ||||| || |||||
 GAGCGTGAG GCT ACAAGC
 A CA____
 GAM3605 FLJ20006 5' CTCACACTCTGGTGCCAGCGT 81574 C C _
 CTCGCACTC GG GCC GTGT
 ||||| || || |||||
 GAGTGTGAG CC CGG CGCA
 A A T
 GAM3605 HSMPP8 5' CTCGCGTTCCGCGCTCGGC 81575 AC G _ T
 CTCGC TCCG CGC CG GT
 |||| |||| || || ||
 GAGCG AGGC GCG GC CG
 CA _ A _
 GAM3605 HSP105B 5' CTCGCACACCGGCGCCGGC 81576 T T
 CTCGCAC CCGGCGCCG GT
 ||||| ||||| || ||
 GAGCGTG GGCCGCGGC CG
 T _
 GAM3605 HUMAGCGB 5' CTCGGGCTCCGGCGCTGGCGCG 81577 CA _____ TGTT
 AACACG CTCCGGCGC CG CG
 ||||| || ||
 GAGGCCGCG GC GC
 CC ACCG|||C TTGT
 GAM3605 KIAA1157 5' CTCGGCTCCGGCGTGCGC 81578 CA CC
 CTCG CTCCGGCG GTGT
 |||| ||||| |||||
 GAGC GAGGCCG CGCG
 C_ A_
 GAM3605 KIAA1323 5' CTCCACTTCGACAATGTTCTGC 81579 G C C C
 CTC CACT CGG GC GTGTTCTGC
 || |||| || || |||||
 GAG GTGA GCC TG TACAAGCG
 _ A _ T
 GAM3605 KIAA1932 5' CTCGTGCATCGGCGTCTCCATG 81580 CACTC ____
 C CTCG CGGCG CCGTGT
 |||| |||| |||||
 GAGC GCCGC GGTACG
 ACGTA AGA
 GAM3605 P311 3' CTCACACTCTGGTAGCATTCGC 81581 C CGCC
 CTCGCACTC GG GTGTTCTGC
 ||||| || |||||
 GAGTGTGAG CC CGTAAGCG
 A AT____
 GAM3605 RAB32 5' CTCGCGCTCTGCCGCCGC 81582 A CG _
 CTCGC CTC GC GCCGT
 |||| || || |||||

GAGCG GAG CG CGGCG
 C A_ G
 GAM3605 TGOLN2 5' CTCGCCTTCGGCTGCTTCG 81583 A C _ CGTG
 CTCGC CT CGGC GC TTCG
 ||||| || ||||| || |||||
 GAGCG GA GCCG CG AAGC
 _ A A _
 GAM3605 LOC127294 3' CTCCACTTTGGTGCATCCG 81584 G CC C CGT
 CTC CACT GG GC GTTCG
 ||| |||| || || |||||
 GAG GTGA CC CG TAGGC
 _ AA A _
 GAM3605 LOC146227 5' CTCGTA CTCTCGGTGTCA 81585 C _ CGCCG C
 CTCG ACTC CGG TGTT G
 |||| |||| || |||||
 GAGC TGAG GCC ACAG T
 A A _ _ C
 GAM3605 LOC255037 3' CTCCCACTCTGCGTGTTTCG 81586 G CGGC C
 CTC CACTC GC GTGTTCG
 ||| |||| || |||||
 GAG GTGAG CG CACAAGC
 G A _ _
 GAM3605 LOC255533 5' CTCTGCTCCGGCGTCCCGT 81587 GCA _
 CTC CTCCGGCG CCGT
 ||| ||||| |||||
 GAG GAGGCCGC GGCA
 AC_ AG
 GAM3605 LOC256310 5' CTCAGCATTCTGGCGCTCACTG 81588 _ C C _ _ TTC
 ATGC CTC GCA TC GGCGC CG TG GC
 ||| ||| || ||||| || || ||
 GAG CGT AG CCGCG GT AC CG
 T A A A G TA_
 GAM3605 LOC257478 5' CTCGCACTCCGCGCTGTTG 81589 G CG C
 CTCGCACTCCG CGC TGTT G
 ||||| ||||| || |||||
 GAGCGTGAGGC GCG ACAA C
 _ _ _
 GAM3606 DAPP1 3' ACCGAGATCGGATCGTGCTT 81592 C C ATA
 ACCGAGATC GG ATC CCTT
 ||||| || || |||||
 TGGCTCTAG CC TAG GGAA
 _ _ CAC
 GAM3606 TCF20 5' ACTGAGATCCAGCATTACA 81593 C _
 AC GAGATCCGGCAT CATA
 || ||||| |||||
 TG CTCTAGGTCGTA GTGT
 A A
 GAM3606 KIAA1715 3' CACCAGATGCTAGCATCATGCC 81594 G CC_ A
 TT CACC AGAT GGCATCAT CCTT
 |||| |||| ||||| |||||

			GTGG TCTA TCGTAGTA GGAA		
			— CGA C		
GAM3607	FACL4	3'	TAAGTATTTTCTTCATAAATAT 81597	CT	C
	TT		TAAG TTTTC TCATAAATATTT		
			ATTC AAAAG AGTATTTATAAA		
			AT A		
GAM3607	FACL4	3'	TAAGTATTTTCTTCATAAATAT 81597	CT	C
	TT		TAAG TTTTC TCATAAATATTT		
			ATTC AAAAG AGTATTTATAAA		
			AT A		
GAM3607	PCDHA11	5'	TTCTTCCCCCAAATATTT 81598	A	
			TTTTTCCTC TAAATATTT		
			AAGAAGGGG GTTTATAAA		
			—		
GAM3607	PCDHA11	5'	TTCTTCCCCCAAATATTT 81598	A	
			TTTTTCCTC TAAATATTT		
			AAGAAGGGG GTTTATAAA		
			—		
GAM3607	BCAA	3'	TAAGCTTTTTTCTTCAACATTT 81599	C	CATA
			TAAGCTTTTT CT AATATTT		
			ATTCGAAAA GA TTGTAA		
			A AG__		
GAM3607	QKI	3'	TAAGTTTTTCTCTCATGGCACA 81600	C	— AA_
	CTT		TAAG TTTTC CTCAT ATATTT		
			ATTC AAAAG GAGTA TGTGAA		
			— A CCG		
GAM3607	SEC24D	3'	TAAGCTTTTTTTTCTCAT 81601	C__	
			TAAGCTTTTT CTCAT		
			ATTCGAAAA GAGTA		
			AAA		
GAM3608	OAS2	3'	TGGTGGAGAGAACCAAGTATA 81604	C	TTA C
			TGGT GGAGAG TAAG ATA		
			ACCA CCTCTC GTTC TAT		
			— TTG A		
GAM3608	CL25084	3'	TGGTTGAGAGTCATTTTATACC 81605	CG	AAGC
			TGGT GAGAGTTAT ATACC		
			ACCA CTCTCAGTA TATGG		
			A_ AAA_		
GAM3608	DORFIN	3'	TGGCACTAGTGTTATAAGCATA 81606	CGG	A
			TGGT AG GTTATAAGCATA		

ACCG TC CAATATTCGTAT
 TGA A
 GAM3608 GLCCI1 5' TGGTTTGGGAGATGAAGCATAC 81607 C__ GTTAT
 TGGT GGAGA AAGCATAC
 ||| ||| |||||
 ACCA CCTCT TTCGTATG
 AAC AC__
 GAM3608 Spir-1 3' TGGTTAGTCATTTGTAAGCATA 81608 CG AGAG A
 CC TGGT G TT TAAGCATACC
 ||| | || |||||
 ACCA C AA ATTCGTATGG
 AT AGTA C
 GAM3608 ZNF333 3' TGGTGGGAGAGTTTAAACATACC 81609 C ATA
 TGGT GGAGAGTT AGCATACC
 ||| ||||| |||||
 ACCA CCTCTCAA TTGTATGG
 C A__
 GAM3609 HNRPF 3' TAGTACTTGAAACTAAAGT 81612 AGCAT
 TAGTAT AAACATAAGT
 |||| |||||
 ATCATG TTTGATTCA
 AAC__
 GAM3609 ITPR1 3' AGTATCTTTGAAACTAAAGT 81613 AGCAT
 AGTAT AAACATAAGT
 |||| |||||
 TCATA TTTGATTCA
 GAAAC
 GAM3609 UTY 3' CAGTATAGCATTTCAAAGTC 81614 AAAC
 TAGTATAGCAT TAAAGTC
 ||||| |||||
 GTCATATCGTA GTTTCAG
 AA__
 GAM3609 DDM36 3' TAGTACAGCATAAACTAAA 81615
 TAGTATAGCATAAACTAAA
 |||||
 ATCATGTCGTATTTGATT
 GAM3609 HRIHFB2072 3' ATATTCACACAGCTAAAGTC 81616 A_ AA
 GTAT GCATA CTAAAGTC
 ||| ||| |||||
 TATA TGTGT GATTTCAG
 AG C_
 GAM3609 KIAA1712 3' GTATAGTAACCAAAGTC 81617 CATA
 GTATAG AACTAAAGTC
 |||| |||||
 CATATC TTGGTTTCAG
 A__
 GAM3609 NAV3 3' GCTTAGAAATAAACTAAAGT 81618 A C_
 GT TAG ATAACTAAAGT
 || ||| |||||

		CG ATC TATTTGATTTCA	
		A TT	
GAM3609	PCDH20	3' TAGTATAGCAGAATACTACAG	81619 T _ A
		TAGTATAGCA AA ACTA AG	
		ATCATATCGT TT TGAT TC	
		C A G	
GAM3609	SGKL	3' CAGTATAGATATTAAAGTC	81620 C AAC
		TAGTATAG ATA TAAAGTC	
		GTCATATC TAT ATTCAG	
		_ A _	
GAM3609	LOC254043	3' ATATAGCACCTAGAGT	81621 AAA A
		GTATAGCAT CTA AGT	
		TATATCGTG GAT TCA	
		_ C	
GAM3609	LOC254820	3' TAGCATAGTAATTTTAAAGTC	81622 CATAAAC
		TAGTATAG TAAAGTC	
		ATCGTATC ATTCAG	
		ATTAAA_	
GAM3610	FUT9	3' TATTATATTTAACGTCTTATAT	81625 T TA
	TT	TATTATATTT A TTTTATATTT	
		ATAATATAAA T AGAATATAAA	
		T GC	
GAM3611	FLJ20730	3' TAATAAAATAAAATGCC	81628 A
		TAATAAGA TAAATGCT	
		ATTATTTT ATTTTACGG	
		_	
GAM3611	KIAA0342	3' TAATGAGAATAAAAAGCAATG	81629 A T T
		TAAT AGAATAAAA GC AATG	
		ATTA TCTTATTTT CG TTAC	
		C T _	
GAM3611	KIAA0472	3' TAATAAGAATGGATGCC	81630 AAA
		TAATAAGAAT ATGCT	
		ATTATTCTTA TACGG	
		CC_	
GAM3611	LOC147353	3' ATAAGAATAAAACTGTGTC	81631 GCTAA
		ATAAGAATAAAAT TGTC	
		TATTCTTATTTTG ACAG	
		AC_	
GAM3612	ADAM11	3' CCAGAGAGATAAGAC	81634 AAA
		TCAGAGAGATA AGAT	

GGTCTCTCTAT TCTG

GAM3612 ADAM11 3' CCAGAGAGATAAGAC 81634 AAA
TCAGAGAGATA AGAT
||||||| |||
GGTCTCTCTAT TCTG

GAM3612 AKT1 3' CCAGAGAGATGACAG 81635 AAAAA
TCAGAGAGAT GATAG
||||||| |||
GGTCTCTCTA CTGTC

GAM3612 ATP1A1 5' TCAGAGAGAAAAGCACAGA 81636 TAA _
TCAGAGAGA AAAG ATAGA
||||||| ||| |||
AGTCTCTCT TTTC TGTCT
_ G

GAM3612 BACH2 3' TCAGAAGATAAATAGCAG 81637 G A A
TCAGA AGATAAA AG TAG
||||| ||||| |||
AGTCT TCTATTT TC GTC

GAM3612 CA12 3' TCAGAGAGAGAGAAGTAGA 81638 TAAA A
TCAGAGAGA AAG TAGA
||||||| ||| |||
AGTCTCTCT TTC ATCT
CTC_ _
A _

GAM3612 CBFA2T3 3' CAGAGAGGAAAAGAGAG 81639 ATA T
CAGAGAG AAAAGA AG
||||||| ||||| ||
GTCTCTC TTTTCT TC
C_ C

GAM3612 DCTN1 5' CAGAGAGAAAAGGTAGA 81640 TAA A
CAGAGAGA AAAG TAGA
||||||| ||| |||
GTCTCTCT TTTC ATCT
_ C

GAM3612 DDX11 3' TCAGAAAGAAAAAGGTAG 81641 TA A
TCAGAGAGA AAAAG TAG
||||||| ||||| |||
AGTCTTTCT TTTTC ATC
_ C

GAM3612 DEC1 3' CCAGAGAGATAACACACATAG 81642 AAAG_
TCAGAGAGATAA ATAG
||||||| |||
GGTCTCTCTATT TATC
GTGTG

GAM3612 EIF2C1 3' AGAGGGATAAAAAGTTTAGA 81643 A A_
AGAG GATAAAAAG TAGA
||| ||||| |||

		TCTC CTATTTTTC ATCT		
		C AA		
GAM3612	FOXP2	5' AAAGAGATGAAAAATTAG 81644	A A	
		AGAGAGAT AAAAG TAG		
		TTTCTCTA TTTT ATC		
		C A		
GAM3612	GATA2	3' TCAGAGAGGGAAGCCAGA 81645	ATAAA A	
		TCAGAGAG AAG TAGA		
		AGTCTCTC TTC GTCT		
		CC__ G		
GAM3612	GPR85	5' AAGAACAAGGAAAAGATAGA 81646	ATA__	
		GAGAG AAAAGATAGA		
		TTCTT TTTTCTATCT		
		GTTCC		
GAM3612	HSPA5	3' AGAAAGATAAGGGGAAATAG 81647	AA__	
		AGAGAGATAA AGATAG		
		TCTTTCTATT TTTATC		
		CCCC		
GAM3612	IL7R	5' AGAGAGATAGAGAGAGA 81648	AAA T	
		AGAGAGATA AGA AGA		
		TCTCTCTAT TCT TCT		
		C__ C		
GAM3612	LSP1	3' TCAGAGAGTGGAAGGGCAGA 81649	ATAAA A_	
		TCAGAGAG AAG TAGA		
		AGTCTCTC TTC GTCT		
		ACC__ CC		
GAM3612	MS4A3	3' TCAGAGAGATTAGATA 81650	AAAA	
		TCAGAGAGAT AGATA		
		AGTCTCTCTA TCTAT		
		A__		
GAM3612	PIP5K1A	3' TCAGAGAGAAAGAACTAAGGTA 81651	TAAA__ A	
	G	TCAGAGAGA AAG TAG		
		AGTCTCTCT TTC ATC		
		TTCTTGA C		
GAM3612	PKD2	3' TCAAGAGAAAGTAAAGATAGA 81652	_ TAA	
		TCA GAGAGA AAAGATAGA		
		AGT CTCTTT TTTCTATCT		
		T CA_		
GAM3612	SLC16A2	3' TCAGAGAGGAGAAAAAGA 81653	AT_	
		TCAGAGAG AAAAAGA		

			AGTCTCTC TTTTCT		
			CTC		
GAM3612	USH2A	3'	CCAGAATTCTAAAAAGATGGA 81654	AGA	A
			TCAGAG TAAAAAGAT GA		
			GGTCTT ATTTTCTA CT		
			AAG C		
GAM3612	WNT5A	3'	CAGAGAGATAACCCCA 81655	AAAGA	
			CAGAGAGATAA TAGA		
			GTCTCTCTATT GTCT		
			GGG__		
GAM3612	APOL6	3'	CAGAGAGATAACTTTGAATAGA 81656	AAA__	
			CAGAGAGATAA GATAGA		
			GTCTCTCTATT TTATCT		
			GAAAC		
GAM3612	C20orf36	3'	CCAGAATTATAAAAGATAGA 81657	AG	A
			TCAGAG ATAAAA GATAGA		
			GGTCTT TATTTT CTATCT		
			AA _		
GAM3612	CIP29	3'	TCAAGAAAGAAGATAG 81658 _	TAAAA	
			TCA GAGAGA AGATAG		
			AGT CTTTCT TCTATC		
			T _		
GAM3612	CYB5-M	3'	TCACGGAGATAAAATACAGA 81659	GA	AG
			TCA GAGATAAAA ATAGA		
			AGT CTCTATTTT TGTCT		
			GC A_		
GAM3612	CYB5-M	3'	TCACGGAGATAAAATACAGA 81659	GA	AG
			TCA GAGATAAAA ATAGA		
			AGT CTCTATTTT TGTCT		
			GC A_		
GAM3612	DIO2	3'	CCAGGGAGACAAAGAT 81660	A	AA
			TCAG GAGATAA AGAT		
			GGTC CTCTGTT TCTA		
			C _		
GAM3612	DIO2	3'	CCAGGGAGACAAAGAT 81660	A	AA
			TCAG GAGATAA AGAT		
			GGTC CTCTGTT TCTA		
			C _		
GAM3612	FLJ11275	3'	AGACATGATGAAAAGATAGA 81661	GA_	A
			AGA GAT AAAAGATAGA		

		TCT CTA TTTTCTATCT		
		GTA C		
GAM3612	FLJ11730	3' TCAGAAAGATTTAAGATAG 81662	AAA	
		TCAGAGAGAT AAGATAG		
		AGTCTTTCTA TTCTATC		
		AA_		
GAM3612	FLJ13111	3' TCAGAGAAGGGTAAAGATGGA 81663	ATAA	A
		TCAGAGAG AAAGAT GA		
		AGTCTCTT TTTCTA CT		
		CCCA C		
GAM3612	FLJ13187	3' CCAGAAAGTAAGAAGGTAG 81664	A A A	
		TCAGAGAG TAA AAG TAG		
		GGTCTTTC ATT TTC ATC		
		_ C C		
GAM3612	FLJ14753	3' TCAGAGAAACAGGAAGGTAGA 81665	AA	A
		TCAGAGAGATA AAG TAGA		
		AGTCTCTTTGT TTC ATCT		
		CC C		
GAM3612	FLJ20436	3' TCAGAGGATAAAAAGCCAGA 81666	A	A
		TCAGAG GATAAAAAG TAGA		
		AGTCTC CTATTTTTC GTCT		
		_ G		
GAM3612	FLJ23604	3' TCAGAGAGAAAAGTGCAGA 81667	TAA	A_
		TCAGAGAGA AAAG TAGA		
		AGTCTCTCT TTTC GTCT		
		_ AC		
GAM3612	FLJ33069	3' TCAGAGAGTATCACATAGA 81668	_	AAAAAG
		TCAGAGAG AT ATAGA		
		AGTCTCTC TA TATCT		
		A GTG_		
GAM3612	H3FJ	3' AAGAAACCCAAGATAGA 81669	AAA	
		GAGAGAT AAGATAGA		
		TTCTTTG TTCTATCT		
		GG_		
GAM3612	HIC	3' AGAGAGATCAAAGTGAAGTAG 81670	_	AA _
		AGAGAGAT AAA GA TAG		
		TCTCTCTA TTT CT ATC		
		G GA C		
GAM3612	KCNMB2	3' AGATGAGAAAGATAGA 81671	_	TAAA
		AGA GAGA AAGATAGA		

		TCT CTCT TTCTATCT		
		A ____		
GAM3612 KIAA0446	3'	TCAAAGAGATCAAGAT 81672	AAA	
		TCAGAGAGAT AAGAT		
		AGTTTCTCTA TTCTA		
		G__		
GAM3612 KIAA0876	3'	GAGAGAAACAAAGATAGA 81673	TAA	
		GAGAGA AAAGATAGA		
		CTCTCT TTTCTATCT		
		TTG		
GAM3612 KIAA1052	3'	GAGAGGGTCAAAAAGAGAGA 81674	A__ T	
		GAGAG TAAAAAGA AGA		
		CTCTC GTTTTCT TCT		
		CCA C		
GAM3612 KIAA1443	3'	GAGGATTTTGGAAAGATAGA 81675	A AA__	
		GAG GAT AAAGATAGA		
		CTC CTA TTTCTATCT		
		_ AAACC		
GAM3612 KIAA1514	3'	CAGAGAGAGAAGATAG 81676	TAAA	
		CAGAGAGA AAGATAG		
		GTCTCTCT TTCTATC		
		C__		
GAM3612 KIAA1817	3'	AGAGAGACAAATCCACAG 81677	AAG	
		AGAGAGATAAA ATAG		
		TCTCTCTGTTT TGTC		
		AGG		
GAM3612 MGC2306	3'	TCAGAGAGGGAAGCCAGA 81645	ATAAA A	
		TCAGAGAG AAG TAGA		
		AGTCTCTC TTC GTCT		
		CC__ G		
GAM3612 MGC25056	5'	TCAGAGAAGGGCCCCAAAAGGT 81678	ATA__ A	
	AG	TCAGAGAG AAAAG TAG		
		AGTCTCTT TTTTC ATC		
		CCCGGGG C		
GAM3612 MUF1	3'	CAGAAAGAGAAAGATAGA 81679	TAA	
		CAGAGAGA AAAGATAGA		
		GTCTTTCT TTTCTATCT		
		C__		
GAM3612 NUDC	3'	TCAGGGAGGAAAAAACAG 81680	A ATA	
		TCAG GAG AAAAGATAG		

AGTC CTC TTTTGTGTC
 C C__
 GAM3612 PCDH10 3' GAGAGAGAAAGATAGA 81681 TAA
 GAGAGA AAAGATAGA
 ||||| |||||
 CTCTCT TTTCTATCT
 C__
 GAM3612 PRO1600 5' TCAGAGAAATCTCAAGAGATAG 81682 AA_ _
 TCAGAGAGAT AA AGATAG
 ||||| || |||||
 AGTCTCTTTA TT TCTATC
 GAG C
 GAM3612 RDH-E2 3' CCAGAGAGGATAGCAAGGGGGT 81683 _ AA A__
 AGA TCAGAGAG ATA AAG TAGA
 ||||| || || |||||
 GGTCTCTC TAT TTC ATCT
 C CG CCCC
 GAM3612 U5-100K 3' TCAGAGAATAGAAAACAGA 81684 ATAAA
 TCAGAGAG AAGATAGA
 ||||| |||||
 AGTCTCTT TTTGTCT
 ATC__
 GAM3612 UBXD2 3' TCAGAGACATAGGACCTCAATA 81685 G AAAA__
 GA TCAGAGA ATA GATAGA
 ||||| || |||||
 AGTCTCT TAT TTATCT
 G CCTGGAG
 GAM3612 ZNF294 3' TCAGAAAGAGACATAGAAAGAT 81686 _ A__
 AGA TCAGA GAGATA AAAGATAGA
 |||| |||| |||||
 AGTCT CTCTGT TTTCTATCT
 TT ATC
 GAM3612 LOC130026 3' AGGAGATGGGAAGATAGA 81687 A AAA
 AG GAGAT AAGATAGA
 || |||| |||||
 TC CTCTA TTCTATCT
 _ CCC
 GAM3612 LOC144289 5' AGAGAACTAAGAGATAG 81688 A A
 AGAGAGAT AA AGATAG
 ||||| || |||||
 TCTCTTTG TT TCTATC
 A C
 GAM3612 LOC145082 5' TCAGCAGAAGAAGATAGA 81689 AG TAAA
 TCAG AGA AAGATAGA
 ||| || |||||
 AGTC TCT TTCTATCT
 G_ TC__
 GAM3612 LOC146909 3' TCAAAAAAAAAAAGAT 81690 T
 TCAGAGAGA AAAAAGAT
 ||||| |||||

AGTTTTTTTT TTTTCTA

GAM3612 LOC148930 3' CAGAGGACAGCAGAAGATAGA 81691 A AA__
CAGAG GATA AAGATAGA
||||| ||| |||||
GTCTC CTGT TTCTATCT
_ CGTC

GAM3612 LOC149386 5' TCAGAGAATGGATATGAATAG 81692 ____ AAAA
TCAGAGA GATA GATAG
||||| ||| |||||
AGTCTCT CTAT TTATC
TAC AC__

GAM3612 LOC151438 3' CCAGAGAGGAAAAGGGAG 81693 ATA AT
TCAGAGAG AAAAG AG
||||| ||| ||
GGTCTCTC TTTTC TC
C__ CC

GAM3612 LOC152317 3' GAGAGATAAAGAGATGGA 81694 A A
GAGAGATAAA AGAT GA
||||||| ||| ||
CTCTCTATTT TCTA CT
C C

GAM3612 LOC152453 5' CCAGAGAGAAGATAG 81695 TAAAA
TCAGAGAGA AGATAG
||||||| |||||
GGTCTCTCT TCTATC

GAM3612 LOC200010 3' GAGAATAGAAAGATAGA 81696 A A
GAGAG TA AAAGATAGA
||||| || |||||
CTCTT AT TTTCTATCT
_ C

GAM3612 LOC221301 3' TCAGAGAGAAAGAAAAAGA 81697 T__
TCAGAGAGA AAAAAGA
||||||| |||||
AGTCTCTCT TTTTCT
TTC

GAM3612 LOC254439 3' CCAGAGAGCTGTGAAGAGGTAG 81698 ATAAA __
TCAGAGAG AAGA TAG
||||||| ||| |||
GGTCTCTC TTCT ATC
GACAC CC

GAM3612 LOC255835 3' AAGAAACCCAAGATAGA 81669 AAA
GAGAGAT AAGATAGA
||||| |||||
TTCTTTG TTCTATCT
GG_

GAM3612 LOC51326 3' TCAGGGAGACAAAATAGA 81699 A AAA
TCAG GAGATAA GATAGA
||| ||||| |||||

		AGTC CTCTGTT TTATCT		
		C _		
GAM3612	LOC90520	3' TCAGAGAGAGAAAAGAT 81700	TA	
		TCAGAGAGA AAAAGAT		
		AGTCTCTCT TTTTCTA		
		C_		
GAM3612	LOC92539	5' GAACAAGATAGAAAAGATAGA 81701	_ A	
		GA GAGATA AAAGATAGA		
		CT TTCTAT TTTCTATCT		
		TG C		
GAM3613	DPYD	3' GGGATTTTACTTAATAAA 81704	TAT	
		GGGGTTTTACTT GTGAA		
		CCCTAAAATGAA TATTT		
		T_		
GAM3613	GABPB1	3' AAGGGGTTTTGTTTTTGT 81705	AC A	
		AAGGGGTTTT TTT TGT		
		TTCCCCAAAA AAA ACA		
		C_ A		
GAM3613	PDGFB	3' AAGGAGTCTTTGTGTGAAT 81706	TTTA A	
		AAGGGGT CTTT TGTGAAT		
		TTCCTCA GAAA ACACTTA		
		_ C		
GAM3613	PTPRCAP	3' AAGGAGTTTTATTTCAAATG 81707	C T	
		AAGGGGTTTTA TTTA GTG		
		TTCCTCAAAAT AAGT TAC		
		A T		
GAM3613	TCF8	3' AAGGGGTTTTGTGTTGGAATC 81708	ACTTTA T	
		AAGGGGTTTT TG GAATT		
		TTCCCCAAAA AC CTTAG		
		CACA_ _		
GAM3613	FLJ31890	3' AAGGTGTACCTCTTGTGTGAAT 81709	TT A_	
	T	GGGGT TACTTT TGTGAATT		
		TTCCA ATGGAG ACACTTAA		
		C_ AAC		
GAM3613	FYCO1	3' GGGTTTTGCTCTTGGA 81710	A A T	
		GGGTTTT CTTT TG GA		
		CCCCAAA GAGA AC CT		
		C _ _		
GAM3613	KIAA0237	3' AAGGGGTTCCTTGCCTTCTGTGA 81711	A_ A	
		AAGGGGTTTT CTTT TGTGA		

	TTCCCCAAGA GGAA ACACT	
	AC G	
GAM3613 KIAA0453	3' AGGAGAGCACTTTTATGTG 81712	TTT _
	AGGGG TACTTT ATGTG	
	TCCTC GTGAAA TACAC	
	TC_ A	
GAM3613 KIAA0563	5' GGGTTTTATTTAAATTGAATT 81713	C TG_
	GGGTTTTA TTTA TGAATT	
	CCCAAAT AAAT ACTTAA	
	_ TTA	
GAM3613 NUP54	5' AAGGGATTTTCTTGTGTGAATT 81714	A TA
	AAGGGGTTTT CTT TGTGAATT	
	TTCCCTAAAA GAA ACACTTAA	
	_ C_	
GAM3613 STAF42	3' AGGGGCTTTATTTTGT 81715	C A
	AGGGGTTTTA TTT TGT	
	TCCCGAAAT AAA ACA	
	- -	
GAM3613 LOC147071	5' GGGTTTTATTTAAATTGAATT 81713	C TG_
	GGGTTTTA TTTA TGAATT	
	CCCAAAT AAAT ACTTAA	
	_ TTA	
GAM3613 LOC148388	3' AAAGGGTTTTCTCTGTGTGA 81716	A_ A
	AAGGGGTTTT CTTT TGTGA	
	TTTCCCAAAA GAGA ACACT	
	AG C	
GAM3613 LOC149194	3' GGGTTTTACTGGTGAATT 81717	TTAT
	GGGTTTTACT GTGAATT	
	CCCAAATGA CACTTAA	
	C_	
GAM3613 LOC149830	3' GGGTTTTACTTAGAAT 81718	TATGT
	GGGTTTTACTT GAAT	
	CCCAAATGAA CTTA	
	T_	
GAM3613 LOC166034	5' AAGGGATTTTACATGA 81719	TTTAT
	AAGGGGTTTTAC GTGA	
	TTCCCTAAAATG TACT	

GAM3613 LOC201173	5' GGGTTTTATTTAAATTGAATT 81713	C TG_
	GGGTTTTA TTTA TGAATT	

	CCCAAAAT AAAT ACTTAA	
	— TTA	
GAM3613 LOC201220 5'	GGGTTTTATTTAAATTGAATT 81713	C TG_
	GGGTTTTA TTTA TGAATT	
	CCCAAAAT AAAT ACTTAA	
	— TTA	
GAM3613 LOC221431 3'	AAGGGGTTTTTAACTGAAT 81720	ACTT TG
	AAGGGGTTTT TA TGAAT	
	TTCCCCAAAA AT ACTTA	
	_____ TG	
GAM3613 LOC57086 3'	AAGGGTTTTTGCTTTCTTGT 81721	A A_
	AGGGGTTTT CTTT TGT	
	TTCCCCAAAA GAAA ACA	
	C GA	
GAM3613 LOC90092 5'	AGGGTTTCAGCATGTG 81722	CTT
	GGGGTTTTA TATGTG	
	TCCCAAAGT GTACAC	
	C_	
GAM3613 LOC93166 3'	AAGGGCTTTTCTCCAGTGTG 81723	A _
	AGGGGTTTT CTTTA TGTG	
	TTCCCGAAA GAGGT ACAC	
	A C	
GAM3614 CD9 3'	CATTGCAGGATTTCTGCT 81726	T_
	TATTGC ATTTCTGCT	
	GTAACG TAAAGACGA	
	TCC	
GAM3614 DYRK1A 3'	ATATTGCTATACTCA 81727	TTCT
	ATATTGCTAT GCTCA	
	TATAACGATA TGAGT	

GAM3614 DYRK1A 3'	ATATTGCTATACTCA 81727	TTCT
	ATATTGCTAT GCTCA	
	TATAACGATA TGAGT	

GAM3614 DYRK1A 3'	ATATTGCTATACTCA 81727	TTCT
	ATATTGCTAT GCTCA	
	TATAACGATA TGAGT	

GAM3614 MS4A7 3'	TCTGTGTATCACCTTCTGCTCA 81728	GCA_ TG AT
	TC TAT CT TTCTGCTCA	

AG ATA GG AAGACGAGT
 ACAC GT ____
 GAM3614 AF038169 5' GCTCCCTATTTCTGCT 81729 ATA G
 GC TT CTATTTCTGCT
 || || |||||
 CG AG GATAAAGACGA
 ____ G
 GAM3614 BBX 3' CATTCTGTTTCTGCTCA 81730 G A
 TATT CT TTTCTGCTCA
 |||| || |||||
 GTAA GA AAAGACGAGT
 _ C
 GAM3614 C21orf42 3' GCATGTGTTCTGCTCA 81731 AT CTAT
 GCAT TG TTCTGCTCA
 |||| || |||||
 CGTA AC AAGACGAGT
 C_ ____
 GAM3614 CCNG2 3' GCATACTTCCAATCTGCT 81732 G TT
 GCATATT CTA TCTGCT
 ||||| ||| |||||
 CGTATGA GGT AGACGA
 A T_
 GAM3614 FLJ22037 5' GCATTGATTTCTGCT 81733 AT CT
 GCAT TG ATTTCTGCT
 |||| || |||||
 CGTA AC TAAAGACGA
 ____ _
 GAM3614 KIAA1024 3' TCTTATGTTGCTATTTCC 81734 GC A
 TC AT TTGCTATTTCT
 || || |||||
 AG TA AACGATAAAGG
 AA C
 GAM3614 KIAA1239 3' TCACATATTTCTGCT 81735 GCTATT
 TCGCATATT TCTGCT
 ||||| |||||
 AGTGTATAA AGACGA

 GAM3614 LCHN 3' TCGTATTGCTATAACTC 81736 CA TTCT
 TCG TATTGCTAT GCTC
 ||| ||||| |||
 AGC ATAACGATA TGAG
 _ T_
 GAM3614 MGC10067 3' GCATATTGCTATCATCTTCAA 81737 _ GC
 GCATATTGCTATT TCT TCAA
 ||||| ||| |||
 CGTATAACGATAG AGA AGTT
 T _
 GAM3614 LOC145609 5' GCATTTATTTCTGCTCA 81738 ATTGC
 GCAT TATTTCTGCTCA
 ||| |||||

		CGTA ATAAAGACGAGT		
		A_____		
GAM3614	LOC254719 5'	TCGTATTGCTATAACTC	81736	CA TTCT
		TCG TATTGCTAT GCTC		
		AGC ATAACGATA TGAG		
		____ T____		
GAM3615	PREB 3'	CATAGCCAAGCCTTTTCACTA	81741	TAA A C
		TATAGCCAA TT TTC ACTA		
		GTATCGGTT GA AAG TGAT		
		CG_ A _		
GAM3615	SACS 3'	TAAGCCGATAATTATAAACTA	81742	T A TCC
		A AGCC ATAATTAT ACTA		
		A TCGG TATTAATA TGAT		
		T C TT_		
GAM3615	TEM7R 3'	TATAGATGACATTCCACTA	81743	CCAATAAT
		TATAG TATTCCACTA		
		ATATC GTAAGGTGAT		
		TACT_____		
GAM3615	KIAA0332 3'	TAGCCAGGCATTCCACTAA	81744	ATAAT
		TAGCCA TATTCCACTAA		
		ATCGGT GTAAGGTGATT		
		CC_____		
GAM3615	KIAA0355 3'	AGCCAATAGTTATTTTACT	81745	A CC
		AGCCAATA TTATT ACT		
		TCGGTTAT AATAA TGA		
		C AA		
GAM3615	LOC254423 3'	TAGCCAATGATGTCCCT	81746	A TAT A
		TAGCCAAT AT TCC CT		
		ATCGGT TA AGG GA		
		C C_ _		
GAM3616	CSNK1G3 3'	GTCCTTGAAAATATACGTG	81749	C_
		GTTC GAAAATATACGTG		
		CAGG CTTTTATATGCAC		
		AA		
GAM3616	FUT6 5'	ATCCCGTCTGGATGCCCGTGA	81750	CC AAATATA
		ATCCCGTT GA CGTGA		
		TAGGGCAG CT GCACT		
		AC ACGG_____		
GAM3616	HTR2B 5'	ATCCCGTTCCGAACAGTG	81751	AATATAC
		ATCCCGTTCCGAA GTG		

			TAGGGCAAGGCTT	CAC	
			GT_____		
GAM3616	AMOTL1	3'	ATCCTGTTTAGAAAATAC	81752	C CC
			ATCC GTT GAAAATAT		
			TAGG CAA CTTTTATG		
			A AT		
GAM3616	C20orf130	3'	GTCCTGAAGGACACGTGA	81753	C AAT
			GTTC GAA ATACGTGA		
			CAGG CTT TGTGCACT		
			A CC_		
GAM3616	LOC254122	3'	ATCCTTTTCTTGACGTATACGT	81754	CG C_ AAA
	G		ATCC TTC GA TATACGTG		
			TAGG AAG CT ATATGCAC		
			AA AA GC_		
GAM3617	C7orf2	3'	TGAATAAGCTTCACTTAGTA	81757	T G_
			TG ATAAGCTTTA TAGTA		
			AC TATTCGAAGT ATCAT		
			T GA		
GAM3617	CLASP1	5'	TGTAGAAGCTCTAGATGT	81758	T TA
			TGTA AAGCTTTAG GT		
			ACAT TTCGAGATC CA		
			C TA		
GAM3617	FHL1	3'	TGTTAAGCTTCCAGAAGTA	81759	A _ T
			TGT TAAGCTTT AG AGTA		
			ACA ATTCGAAG TC TCAT		
			_ G T		
GAM3617	GNG5	3'	TGTACAGGCTTCAAATGTA	81760	A TA
			TGTATA GCTTTAG GTA		
			ACATGT CGAAGTT CAT		
			C TA		
GAM3617	ICA1	3'	TAAGCTCTTTAAAGTAGTA	81761	_____
			TAAGCTTT AGTAGTA		
			ATTCGAGA TCATCAT		
			AATT		
GAM3617	LBR	3'	TGCATAAGCTTAACAGTA	81762	TAG
			TGTATAAGCTT TAGTA		
			ACGTATTCGAA GTCAT		
			TT_		
GAM3617	PCDH7	3'	TGCATAGACACCAGTAGTA	81763	AG T
			TGTATA C TTAGTAGTA		

		ACGTAT G GGTCA	TCAT		
		CT T			
GAM3617	PCDHB9	3'	TGTATTAGCTTTAAAGTA	81764	A T
			TGTAT AGCTTTAG AGTA		
			ACATA TCGAAATT TCAT		
			A _		
GAM3617	FLJ10241	3'	TGTAAAGTGTGTCAGTAGTA	81765	T CT
			TGTA AAG TTAGTAGTA		
			ACAT TTC AGTCATCAT		
			_ AC		
GAM3617	FLJ12085	3'	TGTAAAGCTTTAATGTA	81766	T A
			TGTA AAGCTTTAGT GTA		
			ACAT TTCGAAATTA CAT		
			_ _		
GAM3617	FLJ20625	3'	TGTATAAGCCGCAGT	81767	TTA
			TGTATAAGCT GTAGT		
			ACATATTCGG CGTCA		
			_		
GAM3617	FLJ22794	3'	TGTATGGCTTTAGTAGTA	81768	AA
			TGTAT GCTTTAGTAGTA		
			ACATA CGAAATCATCAT		
			C_		
GAM3617	HERC3	3'	TGTATAGGCCTCAATGT	81769	A A
			TGTATA GCTTTAGT GT		
			ACATAT CGGAGTTA CA		
			C _		
GAM3617	KIAA1165	3'	TGTACCTTTTAGTAGTA	81770	AAGC
			TGTAT TTTAGTAGTA		
			ACATG AAATCATCAT		
			GA_		
GAM3617	MEF-2	3'	TGTATAAGCATGCAATA	81771	TTTA
			TGTATAAGC GTAGTA		
			ACATATTCG CGTTAT		
			TA_		
GAM3617	OSRF	3'	TATAAGCTCCAACAGTAGTA	81772	_
			TATAAGCTT TAGTAGTA		
			ATATTCGAG GTCATCAT		
			GTT		
GAM3617	RAP140	3'	TGTAAAAGCTTAGTAGTA	81773	T T
			TGTA AAGCTT AGTAGTA		

ACAT TTCGAA TCATCAT
 T _
 GAM3617 TRIM2 3' TGTATATTTAGTAGT 81774 AGC
 TGTATA TTTAGTAGT
 ||||| |||||
 ACATAT AAATCATCA
 _
 GAM3617 LOC113763 3' TGTACAAAGCCACGTAGTA 81775 _ TTA
 TGTATAA GCT GTAGTA
 ||||| || |||||
 ACATGTT CGG CATCAT
 T TG_
 GAM3617 LOC133418 3' TGTATGAGCCTCAATGGT 81776 A A
 TGTAT AGCTTTAGT GT
 ||||| ||||| ||
 ACATA TCGGAGTTA CA
 C C
 GAM3617 LOC145652 3' TGTATAAGCATGCAATA 81771 TTTA
 TGTATAAGC GTAGTA
 ||||| |||||
 ACATATTCG CGTTAT
 TA_
 GAM3617 LOC152580 5' TGTGAGCTCCAGCAGTA 81777 ATA
 TGT AGCTTTAGTAGTA
 || |||||
 ACA TCGAGGTCGTCAT
 C_
 GAM3617 LOC168346 5' TGTACAAGCTCCCTCAGT 81778 AG
 TGTATAAGCTTT TAGT
 ||||| |||||
 ACATGTTTCGAGG GTCA
 GA
 GAM3617 LOC200558 3' TGTAAGAGTCAGTAGTA 81779 T CT
 TGTA AAG TTAGTAGTA
 ||||| |||||
 ACAT TTC AGTCATCAT
 _ TC
 GAM3617 LOC254978 3' TGTTAAGCTTTATCAGTA 81780 A G
 TGT TAAGCTTTA TAGTA
 || ||||| |||||
 ACA ATTCGAAAT GTCAT
 _ A
 GAM3617 LOC256642 3' TGTAATGCTGTAGTAGTA 81781 TAA T
 TGTA GCT TAGTAGTA
 ||||| |||||
 ACAT CGA ATCATCAT
 TA_ C
 GAM3617 LOC81558 3' TGTGTAAGCTCTGCAGTA 81782 A A
 TGT TAAGCTTT GTAGTA
 || ||||| |||||

		ACA ATTCGAGA CGTCAT		
		C _		
GAM3617	LOC89919	3' TGTAGAAGCAACAATAGTA	81783	T TT
		TGTA AAGC TAGTAGTA		
		ACAT TTCG GTTATCAT		
		C TT		
GAM3617	LOC91137	3' GTATGGGCTTTAGTACCA	81784	AA G
		GTAT GCTTTAGTA TA		
		CATA CGAAATCAT GT		
		CC G		
GAM3618	MFAP3	3' TCAGTTAGGCAATCCCTG	81787	A A
		TCAGTTAG CGATC TTG		
		AGTCAATC GTTAG GAC		
		C G		
GAM3618	MYO1D	3' CCAGTTAGATGGTTCCACTA	81788	CGA__
		TCAGTTAGA TCATTG		
		GGTCAATCT GGTGAT		
		ACCAA		
GAM3618	RCN1	3' TCTAATCAGTGATCATTGAGG	81789	_ AC
		TC AGTTAG GATCATTGAGG		
		AG TTAGTC CTAGTAACTCC		
		A A_		
GAM3618	TDG	3' TCAGTTAGCAAAGTCTGAGG	81790	A TC
		TCAGTTAG CGA ATTGAGG		
		AGTCAATC GTT TGA CTCC		
		_ _		
GAM3618	VAT1	3' TCATTTAGACAATGAG	81791	G TCAT
		TCA TTAGACGA TGAG		
		AGT AATCTGTT ACTC		
		A _		
GAM3618	CABYR	3' TCAGTTAGACAATAAAGG	81792	CATT
		TCAGTTAGACGAT GAGG		
		AGTCAATCTGTTA TTCC		
		T_		
GAM3618	DKFZP434P0721	3' TCAGTTAGGAGACAAAGG	81793	AC CATT
		TCAGTTAG GAT GAGG		
		AGTCAATC CTG TTCC		
		CT T_		
GAM3618	DKFZp566D234	3' TCAATTGGTAGTTCATTGAGG	81794	AGACGA
		TCAGTT TCATTGAGG		

		AGTTAA AGTAACTCC		
		CCATCA		
GAM3618	FLJ10297 3'	CCAGTTAGGTGGATCCTGGG	81795	AC_ A A
		TCAGTTAG GATC TTG GG		
		GGTCAATC CTAG GAC CC		
		CAC _ _		
GAM3618	MGC21738 3'	TCAGTTAATGTCAGGGAGG	81796	ACGA TT
		TCAGTTAG TCA GAGG		
		AGTCAATT AGT CTCC		
		AC_ CC		
GAM3618	PRO2133 3'	TCAGTTAATGTTTTTACTGAG	81797	ACGATC_
	G	TCAGTTAG ATTGAGG		
		AGTCAATT TGA CTCC		
		ACCAAAAA		
GAM3618	LOC150157 3'	CCAGTAGTCATTGAG	81798	T ACGA
		TCAGT AG TCATTGAG		
		GGTCA TC AGTAACTC		
		_ _ _		
GAM3618	LOC91464 5'	CCAGTTAGATGATCCAAACAGG	81799	C ATTG_
		TCAGTTAGA GATC AGG		
		GGTCAATCT CTAG TCC		
		A GTTTG		
GAM3619	CCND1 3'	GGCACCGCCCCTTCCCCTCG	81802	G_ GCG
		GGCACCGCCC CCC CTCG		
		CCGTGGCGGG GGG GAGC		
		GAA _		
GAM3619	CNP 5'	GGGGCCGCCCCGCTGCGC	81803	CA C
		GG CCGCCCGCC GCGC		
		CC GGCGGGCGG CGCG		
		CC A		
GAM3619	DDX20 5'	GGCACCGCCCCGCTCTCG	81804	_ CGCG
		GGCACCGCCC GCC CTCG		
		CCGTGGCGGG CGG GAGC		
		G A_		
GAM3619	DVL1 5'	GGCGCTACCCGCCCGCCG	81805	ACC G T
		GGC GCCCGCCCGC C CG		
		CCG TGGGCGGGCG G GC		
		CGA _ _		
GAM3619	FGFR1 5'	AGCTGCCGCCCGCCGCCG	81806	A_ CGC T
		GGC CCGCCCGCC GC CG		

			TCG GGC GGG CGG CG GC			
			AC _ _			
GAM3619	FGFR1	5'	AGCTGCCGCCCGCCGCGG	81806	A_	CGC T
			GGC CCGCCCGCC GC CG			
			TCG GGC GGG CGG CG GC			
			AC _ _			
GAM3619	FGFR1	5'	AGCTGCCGCCCGCCGCGG	81806	A_	CGC T
			GGC CCGCCCGCC GC CG			
			TCG GGC GGG CGG CG GC			
			AC _ _			
GAM3619	FGFR1	5'	AGCTGCCGCCCGCCGCGG	81806	A_	CGC T
			GGC CCGCCCGCC GC CG			
			TCG GGC GGG CGG CG GC			
			AC _ _			
GAM3619	FGFR1	5'	AGCTGCCGCCCGCCGCGG	81806	A_	CGC T
			GGC CCGCCCGCC GC CG			
			TCG GGC GGG CGG CG GC			
			AC _ _			
GAM3619	GPR30	5'	AGGCACCGCCAGCCCCG	81807		C G
			AGGCACCGCC GCCC CG			
			TCCGTGGCGG CGGG GC			
			T _			
GAM3619	GSR	5'	GCGCCGCCCGCCGCCAGCTCG	81808	A	C _
			GC CCGCCCGCC GC GCTCG			
			CG GCGGGCGG CG CGAGC			
			C _ GT			
GAM3619	HS3ST3B1	5'	GCGCGACGACGCGCTCG	81809	ACC	C_ CC
			GGC GC CG CGCGCTCG			
			CCG CG GC GCGCGAGC			
			_ CT T_			
GAM3619	KCNS2	5'	AGGCGCCGCGCCCGCG	81810	A	C
			AGGC CCG CCGCCGCG			
			TCCG GGC GCGGGCGC			
			C C			
GAM3619	LRP3	5'	GCGCCGCCTCCTGCCCGC	81811	A	C_ G
			GGC CCGC GCCC CGC			

		CCG GGCGG CGGG GCG		
		C AGGA _		
GAM3619 MYBL2	5'	GGCCCCGGGCGCGCTCGA	81812	ACCG C_
		GGC CCG CCGCGCTCGA		
		CCG GGGC GGCGCGAGCT		
		____ CC		
GAM3619 NFIA	5'	AGCCGCCGCCGCTCGCG	81813	A_ C
		GGC CCGCCCGC CGCG		
		TCG GGCGGGCG GCGC		
		GC A		
GAM3619 NRG1	5'	GGTCCGGTCTCCCGCGCTCG	81814	CA CCG
		GG CCG CCCGCGCTCG		
		CC GGC GGGCGCGAGC		
		A_ CAGA		
GAM3619 PITX1	5'	GGCGCGCCCGCCGCCT	81815	AC C G
		GGC CGCCCGCC GC CT		
		CCG GCGGGCGG CG GA		
		C_ _ _		
GAM3619 PKD2	5'	GGTGCGCGGCGCCGCGCTCG	81816	CAC CC _
		GG CGC GC CCGCGCTCG		
		CC GCG CG GGCGCGAGC		
		AC_ C_ C		
GAM3619 PTMS	5'	AGGCGGTGCCGGCGCGCTCG	81817	ACC C CC
		AGGC GCC GC GCGCTCG		
		TCCG CGG CG CGCGAGC		
		CCA C _		
GAM3619 SULT1A3	5'	GGCACCGCCTCCCCGTCA	81818	CG G C
		GGCACCGCC CCC CG TCG		
		CCGTGGCGG GGG GC AGT		
		A_ _ _		
GAM3619 TARBP2	3'	AGGCACCGTGTGCACTCG	81819	CCCGCCC
		AGGCACCG GCGCTCG		
		TCCGTGGC CGTGAGC		
		ACA_		
GAM3619 TR2	5'	GGCATCGCCCGCCTTTCCCG	81820	C CGCG
		GGCA CGCCCGCC CTCG		
		CCGT GCGGGCGG GGGC		
		A AAA_		
GAM3619 UBE3A	5'	AGGCGCCGCCGCCCGCAGCCGA	81821	A C _ T
		AGGC CCGCC GCCCGC GC CGA		

TCCG GGCGG CGGGCG CG GCT
 C _ T _
 GAM3619 C11orf24 3' GGTCTGCCCCGCCACCC 81822 CA _ G
 GG CC GCCCGCCC CGCTC
 || || ||||| ||||
 CC GG CGGGCGGG GTGGG
 A_ A _
 GAM3619 C9orf12 5' GGGGCCGCCCGCCTCGCT 81823 CA CG
 GG CCGCCCGCC CGCT
 || ||||| |||
 CC GCGGGGCGG GCGA
 CC A_
 GAM3619 CENTG2 5' GCGCCGCCCGCCGACCT 81824 A C G
 GC CCGCCCGCC GC CT
 || ||||| ||
 CG GCGGGGCGG TG GA
 C C _
 GAM3619 DKFZp434O0320 3' AGGCACCAGCTTGGCTTCG 81825 CCC CC_ GC
 AGGCACCG GC GC TCG
 ||||| || || ||
 TCCGTGGT CG CG AGC
 _ AAC A_
 GAM3619 DKFZP566F2124 5' GGCCTCAGCGCCCGCGCTCG 81826 A_ CC
 GGC CCG CGCCCGCGCTCG
 ||| || |||||
 CCG GGT GCGGGCGCGAGC
 CA C_
 GAM3619 DKFZp761G0313 5' AGGCGCTGCCCTCCCGCCC 81827 ACC G G
 AGGC GCCC CCCGC CT
 |||| |||| |||| ||
 TCCG CGGG GGGCG GG
 CGA A _
 GAM3619 DNAJA3 3' AGGCACCGACTGTGCAGCTGCT 81828 _CC_ CC _
 AGGCACCG C GC GC GCT
 ||||| | || ||||
 TCCGTGGC G CG CG CGA
 T ACA T_ A
 GAM3619 DREV1 5' AGGCACCGCCGCCTCCG 81829 C CG
 AGGCACCGCC GCC CG
 ||||| ||| ||
 TCCGTGGCGG CGG GC
 _ AG
 GAM3619 DTX2 5' GGCACCACCGCGCTCG 81830 CGCCC
 GGCACCGCC GCGCTCG
 ||||| |||||
 CCGTGGTGG CGCGAGC
 _
 GAM3619 EFS2 5' GGGCGCTGGGCTGCGCTCGA 81831 CAC CC_ CC
 GG CGC GC GCGCTCGA
 || ||| || |||||

		CC GCG CG CGCGAGCT		
		C__ ACC A_		
GAM3619	ERGL	3' AGACACTGCTGCTTCCCA	81832	C C CCGCG
		AGGCAC GCC GC CTCG		
		TCTGTG CGG CG GGGT		
		A A AA__		
GAM3619	FBXO9	5' GGCGGCCTGCTGCGCTCGA	81833	ACC C CC
		GGC GCC GC GCGCTCGA		
		CCG CGG CG CGCGAGCT		
		C__ A A_		
GAM3619	FLJ20174	5' GGCGCCGCGCCCGGGCTCGA	81834	A CC C
		GGC CCGC GCCCG GCTCGA		
		CCG GGCG CGGGC CGAGCT		
		C _ C		
GAM3619	GBA2	5' AGGCACCGCCCCCGGGACCTCG	81835	G C__ G
		AGGCACCGCCC CC GC CTCG		
		TCCGTGGCGGG GG TG GAGC		
		_ CCC _		
GAM3619	HCAP-G	5' GACGAGTCCTGCCGCGCTCG	81836	ACCG C
		GGC CC GCCGCGCTCG		
		CTG GG CGGGCGCGAGC		
		CTCA A		
GAM3619	HUMZD58C02	5' GGCGCGGCGCGCGCTCG	81837	ACC CC C
		GGC GC GC CGCGCTCG		
		CCG CG CG GCGCGAGC		
		__ C_ C		
GAM3619	KIAA0237	5' GGCATCGCCCGCCACCACG	81838	C _
		GGCA CGCCCGCC CGCG		
		CCGT GCGGGCGG GTGC		
		A TG		
GAM3619	KIAA1766	5' GGCCGCCGCGCCGCGCTCG	81839	A_ C C
		GGC CCGCC GCC GCGCTCG		
		CCG GGCGG CGG CGCGAGC		
		GC _ _		
GAM3619	LGI3	5' GGCGCGCGCCCGCTCTCGA	81840	ACC C G
		GGC GC CGCCCGC CTCGA		
		CCG CG GCGGGCG GAGCT		
		__ C A		
GAM3619	LYSAL1	3' AGGCGTGAGCCACGCGCTCG	81841	ACC_ CGC
		AGGC GCC CCGCGCTCG		

		TCCG CGG GGCGCGAGC			
		CACT T__			
GAM3619	MGC2714	5' GGCCGCGCGCCCGCTCCCA	81842	AC C G	
		GGC CGCC GCCCGC CTCG			
		CCG GCGG CGGGCG GGGT			
		__ _ A			
GAM3619	MGC2803	5' GGCCGCTCCGGCCCCGCGCT	81843	AC _ _	
		GGC CGC CCG CCCGCGCT			
		CCG GCG GGC GGGCGCGA			
		__ A CG			
GAM3619	MGC29643	5' AGCCTGCATCGCCCCGCGCTCG	81844	ACC C_	
		GGC GC CGCCCGCGCTCG			
		TCG CG GCGGGCGCGAGC			
		GA_ TA			
GAM3619	NAKAP95	3' GGCTCCGCCCCGCCCGAGCTCG	81845	A _C	
		GGC CCGCCCCGCC G GCTCG			
		CCG GGCGGGCGGG C CGAGC			
		A GT			
GAM3619	PRAX-1	3' AGGCTCCGCCCCGCTGCCG	81846	A CGC	
		AGGC CCGCCCGCC GCTCG			
		TCCG GGCGGGCGG CGGGC			
		A A__			
GAM3619	PRO2964	3' AGGCGTGAGCCACGCGCTCG	81841	ACC_ CGC	
		AGGC GCC CCGCGCTCG			
		TCCG CGG GGCGCGAGC			
		CACT T__			
GAM3619	RNASE6PL	5' AGCCGCCGTCCGCCACG	81847	A_ C	
		GGC CCG CCGCCCGCG			
		TCG GGC GGCGGGTGC			
		GC A			
GAM3619	RNPC1	5' GGCCGCGGGAAGCCCGCGCTCG	81848	AC CCC_	
		GGC CG GCCCGCGCTCG			
		CCG GC CGGGCGCGAGC			
		GC CCTT			
GAM3619	SARM	5' AGGCACCGCCAGCCGCTCG	81849	C CGC	
		AGGCACCGCC GCC GCTCG			
		TCCGTGGCGG CGG CGAGC			
		T _			
GAM3619	SAST	5' AGGCACCGTTGCTTATGAGCTT	81850	CCC CCGC_ C	
	GA	AGGCACCG GC GCT GA			

		TCCGTGGC CG CGA CT	
		AA_ AATACT A	
GAM3619 SDS3	5'	GACACCGCGGCCACCCGCGCTC 81851	___
G		GGCACCGC CCGCCCGCGCTCG	
		CTGTGGCG GGTGGGCGCGAGC	
		CC	
GAM3619 SNTG1	5'	AGGCACCGCCTTTTAGCTGCGA 81852	CGCCCGC _
		AGGCACCGCC GCT CGA	
		TCCGTGGCGG CGA GCT	
		AAAAT__ C	
GAM3619 LOC123591	5'	AGCGCCGCTTCGCGCTCG 81853	A CCGCC
		GGC CCGC CGCGCTCG	
		TCG GGCG GCGCGAGC	
		C AA__	
GAM3619 LOC131583	5'	GACGCCGGGGACTCGCGCTCG 81854	A CCC C
		GGC CCG GC CGCGCTCG	
		CTG GGC TG GCGCGAGC	
		C CCC A	
GAM3619 LOC143384	5'	GGCACCGCTGCCTCCCCGA 81855	CC CGCG
		GGCACCGC GCC CTCGA	
		CCGTGGCG CGG GGGCT	
		A_ AG__	
GAM3619 LOC150538	3'	AGCTACCGCCCGCCGGGCGG 81856	_ C C T
		GGC ACCGCCCGCC G GC CG	
		TCG TGGCGGGCGG C CG GC	
		A _C _	
GAM3619 LOC158297	5'	GGCACGCCAGGCTCG 81857	CGCCC C
		GGCAC GCCCG GCTCG	
		CCGTG CGGGT CGAGC	
		_____ C	
GAM3619 LOC200269	3'	GGCACCTCCGCCACCG 81858	GC CGC T
		GGCACC CCGCC GC CG	
		CCGTGG GGCGG TG GC	
		A_ _ _	
GAM3619 LOC201522	5'	GGTCCGCCCGCCGTCCCG 81859	CA CGCG
		GG CCGCCCGCC CTCG	
		CC GGCGGGCGG GGGC	
		A_ CA__	
GAM3619 LOC219800	5'	AGGCATCGCCCTCCGCACCCG 81860	C GC
		AGGCA CGCCC CCGCGCTCG	

TCCGT GCGGG GCGGTGGGC
 A A_
 GAM3619 LOC253981 5' GGCGCCGCGTCCCGCGCTCG 81861 A CCG
 GGC CCGC CCCGCGCTCG
 ||| ||| |||||
 CCG GGCG GGGCGCGAGC
 C CA_
 GAM3619 LOC255413 3' AGGCACTGCGCGCTCG 81862 C CCGCCC
 AGGCAC GC GCGCTCG
 ||||| || |||||
 TCCGTG CG CGCGAGC
 A _____
 GAM3619 LOC90719 5' GGCGGGGAGCCGCCCGCGCTCG 81863 ACCGC_
 GGC CCGCCCGCGCTCG
 ||| |||||
 CCG GGCGGGCGCGAGC
 CCCCTC
 GAM3619 LOC92405 5' AGGCCCGCTCGCCCGCGCTCG 81864 A C
 AGGC CCGC CGCCCGCGCTCG
 ||| ||| |||||
 TCCG GGCG GCGGGCGCGAGC
 _ A
 GAM3620 HDGF 5' CGCGGTGGGTGCGCGCTCGTCTCG 81867 T TC C
 CGC GT GT CGCGCTCGTCTCG
 ||| || |||||
 GCG CA CA GCGCGAGCAGC
 C CC C
 GAM3620 C20orf21 3' CGCTGTCCAGGCGCTTGT 81868 TCC C
 CGCTGTTCG GCGCT GT
 ||||| |||||
 GCGACAGGT CGCGA CA
 C_ A
 GAM3620 LANO 5' CGCTGCCCTCTCCGCGCTCGT 81869 G_
 CGCTGTTC TCCGCGCTCGT
 ||||| |||||
 GCGACGGG AGGCGCGAGCA
 AG
 GAM3621 ATP1B1 3' TACACTAAATAAAATACACAA 81872 CTTGA_
 TACACTGAA GCACAA
 ||||| |||||
 ATGTGATTT TGTGTT
 ATTTA
 GAM3621 CYP51 3' TACCCTGAACCTATTTGGCA 81873 A A_
 TAC CTGAACCTG GCA
 ||| ||||| |||
 ATG GACTTGAAT CGT
 G AAAC
 GAM3621 DTR 3' CCGATTCTTGAGCACAA 81874 A_
 CTGA CTTGAGCACAA
 ||| |||||

			GGCT GAACTCGTGTT		
			AAG		
GAM3621	EGLN2	5'	TACACTGATGATGCAC 81875	ACT	_
			TACACTGA TGA GCAC		
			ATGTGACT ACT CGTG		
			___ A		
GAM3621	FAT	3'	TACACTGAAATGTACTAACAAA 81876	CT A	___
			TACACTGAA TG GC ACAA		
			ATGTGACTT AC TG TGTTT		
			T_ A AT		
GAM3621	FLRT2	3'	TACACTGATCACCTTCACA 81877	___	GA
			TACACTGA ACTT GCA		
			ATGTGACT TGGA TGT		
			AG AG		
GAM3621	HDAC5	3'	TACACTGAGCCTGGCCCCA 81878	A A A	_
			TACACTGA CTTG GC CA		
			ATGTGACT GGAC CG GT		
			C _ GG		
GAM3621	HLF	3'	CACACACATGAGCACAA 81879	TGA	T
			TACAC AC TGAGCACAA		
			GTGTG TG ACTCGTGTT		
			___ T		
GAM3621	HNF3B	3'	TACACCGAGTCACTCACAAA 81880	AC	AG
			TACACTGA TTG CACAAA		
			ATGTGGCT AGT GTGTTT		
			C_ GA		
GAM3621	IL22RA2	3'	CACTTGCCCTAAGCACAAA 81881	GAA	
			CACT CTTGAGCACAAA		
			GTGA GGATTCGTGTTT		
			AC_		
GAM3621	LPIN1	3'	CACATTGAACTTGACACA 81882	C	G
			TACA TGA ACTTGA CACA		
			GTGT ACTTGA ACT GTGT		
			A _		
GAM3621	LRP8	3'	TACACTGACCTTCGCCAAA 81883	A GA	A
			TACACTGA CTT GC CAAA		
			ATGTGACT GGA CG GTTT		
			_ AG _		
GAM3621	LRP8	3'	TACACTGACCTTCGCCAAA 81883	A GA	A
			TACACTGA CTT GC CAAA		

			ATGTGACT GGA CG GTTT	
			_ AG _	
GAM3621	MGAT4B	5'	TACACTGACACTAATGCTCA 81884	_ TGA A
			TACACTGA ACT GC CA	
			ATGTGACT TGA CG GT	
			G TTA A	
GAM3621	P53AIP1	3'	TACACTGAGACTCAGGCA 81885	_ GA
			TACACTGA ACTT GCA	
			ATGTGACT TGAG CGT	
			C TC	
GAM3621	PATE	3'	TACAGTGAAAGCACAA 81886	C ACTT
			TACA TGA GAGCACAA	
			ATGT ACT TTCGTGTT	
			C _	
GAM3621	PRKACB	3'	ACACTGAACTAAATGTGCA 81887	_ A
			ACACTGAACT TG GCA	
			TGTGACTTGA AC CGT	
			TTT A	
GAM3621	SH3GL2	3'	TAAACTGCTAAGCACAAA 81888	_
			TGAACT TGAGCACAAA	
			ATTTGA ATTCGTGTTT	
			CG	
GAM3621	SLC6A12	3'	ACACTGGCCTGAGCACAA 81889	AA
			ACACTG CTTGAGCACAA	
			TGTGAC GGA CTCTGTGTT	
			C_	
GAM3621	SP3	3'	TACACTAAACCACACA 81890	TGA
			TACACTGAACT GCACA	
			ATGTGATTTGG TGTGT	
			_	
GAM3621	TAF7L	3'	TACCTGAACAGAGACA 81891	A TT C
			TAC CTGAAC GAG ACA	
			ATG GACTTG CTC TGT	
			_ T_ _	
GAM3621	THBS1	3'	CACACTGATGCAAGCACACA 81892	ACT
			TACACTGA TGAGCACACA	
			GTGTGACT GTTCGTGT	
			AC_	
GAM3621	TRAM	3'	TACACTAAAAATGGCACAAA 81893	CT A
			TACACTGAA TG GCACAAA	

		ATGTGATTT AC CGTGTTT	
		TT _	
GAM3621 WRB	3'	ACACAAGTTGAGCACAAA 81894	TGAAC
		ACAC TTGAGCACAAA	
		TGTG AACTCGTGTTT	
		TTC__	
GAM3621 XK	3'	TACACCTGAACTGGGTGAG 81895	- ____
		TACAC TGAAC TGAG	
		ATGTG ACTTGA ACTC	
		G CCC	
GAM3621 YWHAB	3'	AACTGAACAGATCACAAA 81896	TT G
		AACTGAAC GA CACAAA	
		TGTGACTTG CT GTGTTT	
		T_ A	
GAM3621 YWHAB	3'	AACTGAACAGATCACAAA 81896	TT G
		AACTGAAC GA CACAAA	
		TGTGACTTG CT GTGTTT	
		T_ A	
GAM3621 ADMP	3'	TAACTGAATGAAAGTACAAA 81897	CTT C
		TAACTGAA GAG ACAA	
		ATGTGACTT TTC TGTTT	
		ACT A	
GAM3621 AKAP11	3'	TACACCGAGTGATAACACAAA 81898	ACTTG
		TAACTGA AGCACAAA	
		ATGTGGCT TTGTGTTT	
		CACTA	
GAM3621 AMOT	3'	CACTGATACAGCACAAA 81899	_ TTG
		CACTGA AC AGCACAAA	
		GTGACT TG TCGTGTTT	
		A ____	
GAM3621 AP3M2	3'	CACACTGAACTAGGACAAA 81900	TG C
		TAACTGAACT AG ACAA	
		GTGTGACTTGA TC TGTTT	
		_ C	
GAM3621 C6orf9	5'	CTGAGCCAAAAGCACAAA 81901	A T_
		CTGA CT GAGCACAAA	
		GACT GG TTCGTGTTT	
		C TT	
GAM3621 DJ328E19.C1.1	3'	AACTGAAGACACAA 81902	CTT G
		AACTGAA GA CACAA	

TGTGACTT CT GTGTT

GAM3621 DKFZp434F1719 3' TACACTGAGGCTTGATCA 81903 A_ G
TACACTGA CTTGA CA
||||||| ||||| ||
ATGTGACT GAACT GT
CC A

GAM3621 DKFZp434K114 3' TACACTGAGTGTCACCTAAA 81904 _____
TACACTGA ACTTGAG
||||||| |||||
ATGTGACT TGAATTT
CACAG

GAM3621 DKFZp761B0514 3' TACACTGAAAGGGCACAA 81905 CTTGA
TACACTGAA GCACAA
||||||| |||||
ATGTGACTT CGTGTT
TCC__

GAM3621 EML4 3' TACCTGAACTTTATCACAAA 81906 A GAG
TAC CTGAACTT CACAAA
||| ||||| |||||
ATG GACTTGAA GTGTTT
_ ATA

GAM3621 FBX30 3' CACACTGAGAGGCTCCACAAA 81907 ACTT _____
TACACTGA GAG CACAAA
||||||| ||| |||||
GTGTGACT CTC GTGTTT
_____ CGAG

GAM3621 FLJ13769 3' CACTGAACTTTGCCTCAAA 81908 GA A_
CACTGAACTT GC CAAA
||||||| || |||||
GTGACTTGAA CG GTTT
A_ GA

GAM3621 FLJ20086 3' CACACTGACAAAAAGCACAAA 81909 ACTT
TACACTGA GAGCACAAA
||||||| |||||
GTGTGACT TTCGTGTTT
GTTT

GAM3621 FLJ20445 3' ACACTGAAACACACAAA 81910 CTTGA
ACACTGAA GCACAAA
||||||| |||||
TGTGACTT TGTGTTT
TG__

GAM3621 FLJ31168 3' ACACTGAATCCCACAAA 81911 _ TGAG
ACACTGAA CT CACAAA
||||||| || |||||
TGTGACTT GG GTGTTT
A _____

GAM3621 HBP17 3' CACTCACTAAGCACAAA 81912 GA T
CACT ACT GAGCACAAA
||| ||| |||||

			GTGA TGA TTCGTGTTT		
			G_ _		
GAM3621	HEF1	3'	TGACTGAACCACTCACAAA	81913	C TGAG
			A ACTGAACT CACAAA		
			A TGACTTGG GTGTTT		
			C TGA_		
GAM3621	KIAA0097	3'	TACACTAAACTCATCCAC	81914	AG
			TACACTGAACTTG CAC		
			ATGTGATTTGAGT GTG		
			AG		
GAM3621	KIAA0140	3'	CACACTGAAAACACAA	81915	ACTT
			TACACTGA GAGCACAA		
			GTGTGACT TTTGTGTT		

GAM3621	KIAA0186	3'	TACACTGAAAACACAAA	81916	ACTT _
			TACACTGA GAGC ACAAA		
			ATGTGACT TTTG TGTTT		
			_____ A		
GAM3621	KIAA0217	3'	TACACTGAATGACACAAA	81917	CT G
			TACACTGAA TGA CACAAA		
			ATGTGACTT ACT GTGTTT		
			_____ _		
GAM3621	KIAA0895	3'	ACTGAACCAATAGCACAAA	81918	TG_
			ACTGAACT AGCACAAA		
			TGACTTGG TCGTGTTT		
			TTA		
GAM3621	KIAA1058	3'	ACTGGAACAGCACAAA	81919	_ TTG
			ACTG AAC AGCACAAA		
			TGAC TTG TCGTGTTT		
			C _____		
GAM3621	KIAA1243	3'	CACTGAACTGGCCAA	81920	T A A
			CACTGAACT G GC CAA		
			GTGACTTGA C CG GTT		

GAM3621	KIAA1332	3'	CATTGAAGGGAACACAAA	81921	C CTT
			CA TGAA GAGCACAAA		
			GT ACTT CTTGTGTTT		
			A CC_		
GAM3621	KIAA1649	3'	CACACTGAAAAACACAA	81922	CTT
			TACACTGAA GAGCACAA		

GTGTGACTT TTTGTGTT

GAM3621 KIAA1649 5' CACACTGAAAAACACAA 81922 CTT
TACACTGAA GAGCACAA
||||||| |||||
GTGTGACTT TTTGTGTT

GAM3621 KIAA1718 3' ACTGAACTACTACAAA 81923 TGA _
ACTGAACT GC ACAA
||||||| || |||||
TGA CTGA TG TGTTT

____ A
GAM3621 KIAA1829 3' TACACTGAAGCTAAACACA 81924 C
TACACTGAA TTGAGCACA
||||||| |||||
ATGTGACTT GATTTGTGT
C

GAM3621 KIAA1870 3' TACCTGATGAGCACAA 81925 A ACT
TAC CTGA TGAGCACAA
||| ||| |||||
ATG GACT ACTCGTGTT

— —
GAM3621 MBLR 3' TACACTGAAATTTTATGGCACA 81926 CT____ A
TACACTGAA TG GCACA
||||||| || |||||
ATGTGACTT AC CGTGT
TAAAAT _

GAM3621 MGC2488 3' CATTGAGTTTAAACACAAA 81927 C AC
CA TGA TTGAGCACAAA
|| ||| |||||
GT ACT AATTTGTGTTT
A CA

GAM3621 MGC30052 3' TAAACAACTGAGCACAAA 81928 _
TGAAC TTGAGCACAAA
||||| |||||
ATTTG GACTCGTGTTT
TT

GAM3621 NDP52 3' CATTGAACTTAGTTCACAAA 81929 C AG_
CA TGA ACTTG CACAAA
|| ||||| |||||
GT ACTTGAAT GTGTTT
A CAA

GAM3621 NLN 3' TGA CTGAACTTTAGACA 81930 C G C
A ACTGAACTT AG ACA
| ||||| || |||
A TGA CTTGAA TC TGT
C A _

GAM3621 P311 3' CACACTGAAGACACAA 81931 CTT G
TACACTGAA GA CACAA
||||||| || |||||

GTGTGACTT CT GTGTT

GAM3621 POPX1 3' ACACTGAACTTGGCCA 81932 A A
ACACTGAACTTG GC CA
||||||| ||
TGTGACTTGAAC CG GT

GAM3621 PRDM10 3' TACACTGAACATGTCAGCA 81933 T _
TACACTGAAC TG AGCA
||||||| || |||
ATGTGACTTG AC TCGT
T AG

GAM3621 PTPRN2 3' TACGCTGAACCCACACA 81934 A GA
TAC CTGAACTT GCACA
||| ||||| ||||
ATG GACTTGGG TGTGT
C G_

GAM3621 PTPRN2 3' TACGCTGAACCCACACA 81934 A GA
TAC CTGAACTT GCACA
||| ||||| ||||
ATG GACTTGGG TGTGT
C G_

GAM3621 SEPT3 3' ACACTGAACACGACACA 81935 T G
ACACTGAAC TGA CACA
||||||| ||| |||
TGTGACTTG GCT GTGT
T _

GAM3621 SLC2A12 3' ACACTGAAAAGAGAGCACA 81936 CTT_
ACACTGAA GAGCACA
||||||| |||||
TGTGACTT CTCGTGT
TTCT

GAM3621 Spir-1 3' ACGCTGACTCGTAGCACAAA 81937 A A _
AC CTGA CTTG AGCACAAA
|| ||| ||| |||||
TG GACT GAGC TCGTGTTT
C _ A

GAM3621 STAF65(gamma) 3' TACTCTGAACTTAATGCA 81938 A _
TAC CTGAACTTGA GCA
||| ||||| |||
ATG GACTTGAATT CGT
A A

GAM3621 VDAC3 3' ACTGAAACGTGGCACAAA 81939 _ T A
ACTGAA C TG GCACAAA
||||| | || |||||
TGA CTT G AC CGTGTTT
T C _

GAM3621 ZNF185 3' CACACACTGAGCACAAA 81940 TGA T
CAC ACT GAGCACAAA
||| ||| |||||

		GTG TGA CTCGTGTTT		
		TG_ _		
GAM3621	LOC134553 3'	TACACTTGAACCTATGTACAAA	81941	_ AGC
		TACACT GAACTTG ACAAA		
		ATGTGA CTTGGAT TGTTT		
		A ACA		
GAM3621	LOC145009 3'	TACCCTGAACTTATTTGGCA	81873	A A__
		TAC CTGAACTTG GCA		
		ATG GACTTGAAT CGT		
		G AAAC		
GAM3621	LOC149013 3'	ACACTGAAGACACAA	81902	CTT G
		ACACTGAA GA CACAA		
		TGTGACTT CT GTGTT		
		— —		
GAM3621	LOC149317 3'	ACACTGAAGACACAA	81902	CTT G
		ACACTGAA GA CACAA		
		TGTGACTT CT GTGTT		
		— —		
GAM3621	LOC149734 3'	TAACTGAACCTCACAA	81942	C GAG
		A ACTGAACTT CACAA		
		A TGA CTTGGA GTGTT		
		T —		
GAM3621	LOC150084 5'	CACATTGAACTTAACACA	81943	C G
		TACA TGA CTTGA CACA		
		GTGT ACTTGAATT GTGT		
		A —		
GAM3621	LOC151162 5'	ACACTGAATCCTCACAAA	81944	_ GAG
		ACACTGAA CTT CACAAA		
		TGTGACTT GGA GTGTTT		
		A —		
GAM3621	LOC155434 3'	ACACTGAACTCAAGCACAA	81945	TG
		ACACTGAACT AGCACAA		
		TGTGACTTGA TCGTGTT		
		GT		
GAM3621	LOC161734 3'	TACACTGAAATAATTAACAA	81946	CT GC_
		TACACTGAA TGA ACAA		
		ATGTGACTT ATT TGTT		
		T_ AAT		
GAM3621	LOC203377 5'	ACACTGAATCCTCACAAA	81944	_ GAG
		ACACTGAA CTT CACAAA		

		TGTGACTT GGA GTGTTT	
		A _	
GAM3621	LOC220638 3'	ACACTGAAGACACAA 81902	CTT G
		ACACTGAA GA CACAA	
		TGTGACTT CT GTGTT	
		_ _	
GAM3621	LOC221288 5'	TACACTAATTCTGTAACACAAA 81947	AC _
		TACACTGA TTG AGCACAAA	
		ATGTGATT GAC TTGTGTTT	
		AA A	
GAM3621	LOC255223 3'	CACTGGGTGCAGCACAAA 81948	AACT _
		CACTG TG AGCACAAA	
		GTGAC AC TCGTGTTT	
		CC_ G	
GAM3621	LOC257031 3'	ACACTGAAGACACAA 81902	CTT G
		ACACTGAA GA CACAA	
		TGTGACTT CT GTGTT	
		_ _	
GAM3621	LOC257471 3'	TACACTAAACCACACA 81890	TGA
		TACACTGAACT GCACA	
		ATGTGATTTGG TGTGT	
		_	
GAM3621	LOC51026 3'	TACACTTGAACAATGACA 81949	_ T_ G
		TACACT GAAC TGA CA	
		ATGTGA CTTG ACT GT	
		A TT _	
GAM3621	LOC91548 5'	ACACTGAACAGCAACAAA 81950	TTG _
		ACACTGAAC AGCA CAAA	
		TGTGACTTG TCGT GTTT	
		_ T	
GAM3622	ALS2 3'	TATAAAGTAGAGCAAAAACC 81953	A GTA
		TATAAAGTA AGTAAA GACC	
		ATATTTTCAT TCGTTT TTGG	
		C _	
GAM3622	FBXL5 3'	TAAAGTCCTCAAAGTAGA 81954	AAAG
		TAAAGT TAAAGTAGA	
		ATTTCA GTTTCATCT	
		GGA_	
GAM3622	FBXL5 3'	TAAAGTCCTCAAAGTAGA 81954	AAAG
		TAAAGT TAAAGTAGA	

		ATTTCA GTTTCATCT		
		GGA_		
GAM3622	PCDH11X 5'	TATAAAGTACAAGTAAGCAA 81955	_	A
		TATAAAGTA AAGTAA GTAG		
		ATATTTTCAT TTCATT CGTT		
		G _		
GAM3622	PCDH11X 5'	TATAAAGTACAAGTAAGCAA 81955	_	A
		TATAAAGTA AAGTAA GTAG		
		ATATTTTCAT TTCATT CGTT		
		G _		
GAM3622	PCDH11X 5'	TATAAAGTACAAGTAAGCAA 81955	_	A
		TATAAAGTA AAGTAA GTAG		
		ATATTTTCAT TTCATT CGTT		
		G _		
GAM3622	PCDH11Y 5'	TATAAAGTACAAGTAAGCAA 81955	_	A
		TATAAAGTA AAGTAA GTAG		
		ATATTTTCAT TTCATT CGTT		
		G _		
GAM3622	PCDH11Y 5'	TATAAAGTACAAGTAAGCAA 81955	_	A
		TATAAAGTA AAGTAA GTAG		
		ATATTTTCAT TTCATT CGTT		
		G _		
GAM3622	PIP5K1B 3'	TATAAAGTGAAGGCAGACC 81956	A	TAAA
		TATAAAGT AAG GTAGACC		
		ATATTTCA TTC CGTCTGG		
		C _		
GAM3622	STE 3'	GTTAAGTAAAGAAAGACC 81957	A	T_
		GT AAGTAAAG AGACC		
		CA TTCATTTTCTCTGG		
		A TT		
GAM3622	KIAA0532 5'	TATAAAATAAGACTTCATAGAC 81958		AG AAA
	CC	TATAAAGTAA T GTAGACCC		
		ATATTTTATT G TATCTGGG		
		CT AAG		
GAM3622	KIAA1908 3'	AGTAAAGCCATCATGGACCC 81959	AAA_	A
		AGTAAAGT GT GACCC		
		TCATTTTCG TA CTGGG		
		GTAG C		
GAM3622	SH3BGRL2 3'	TATGGAGCAAAGTGCAGCC 81960	AA	AAA A
		TAT AGTAAAGT GTAG CC		

		ATA TCGTTTCA CGTC GG	
		CC — —	
GAM3622	LOC146540 3'	GTGAAGTAAAGATAACACCC 81961	A — —
		GT AAGTAAAG TAG ACCC	
		CA TTCATTTC ATT TGGG	
		C T G	
GAM3622	LOC155435 3'	ATAAAGTAAGTCGGTAGGCC 81962	A AAA A
		ATAAAGTAA GT GTAG CC	
		TATTTTCATT CA CATC GG	
		— GC_ C	
GAM3622	LOC256568 3'	TATAAAGTAGAGCAATGT 81963	A A
		TATAAAGTA AGTAA GT	
		ATATTTTCAT TCGTT CA	
		C A	
GAM3623	ARNTL 3'	AGAACAAGGGAAACATTT 81966	CA T
		AGAACAAG GAAC ATTT	
		TCTTGTTT TTTG TAAA	
		CC —	
GAM3623	CCNC 3'	ACAGAAACAAGCTATTCATTTT 81967	— AGAAC
	CA	ACAGAA CAAGC TATTTTCA	
		TGTCTT GTTCG GTAAAAGT	
		T ATAA_	
GAM3623	EPB72 3'	ACAGAACAAGGAGGAATCATTT 81968	CA_ C
		ACAGAACAAG GAA TATTT	
		TGTCTTGTTT CTT GTAAA	
		CTC A	
GAM3623	GYG 3'	AGAACACACTGCTATTTTCA 81969	A AGAA
		AGAACA GC CTATTTTCA	
		TCTTGT TG GATAAAAGT	
		G AC_	
GAM3623	HPGD 3'	CAAAACCTCACAGCTATTTT 81970	AA_ AA
		CAGAAC GCAG CTATTTT	
		GTTTTG TGTC GATAAAA	
		GAG —	
GAM3623	IL13RA1 3'	CAGAACAAAGTAGAACATCT 81971	_C T
		CAGAACAA G AGAAC ATTT	
		GTCTTGTT C TCTTG TAGA	
		T A —	
GAM3623	MAB21L1 3'	AGAACAAGCAATATTT 81972	AAC
		AGAACAAGCAG TATTT	

TCTTGTTCGTT ATAAA

GAM3623 MCL1 3' CAGAACAAATCAGCAATTTCA 81973 G AACTAT
CAGAACAA CAG TTTCA
||||| ||| ||||
GTCTTGTGTT GTC AAAGT
A GTT__

GAM3623 MYO1D 3' ACAGATAAGCAGAACACCTT 81974 AC T
ACAGA AAGCAGAAC ATTTT
|||| ||||||| ||||
TGTCT TTCGTCTTG TGGAA
A_ _

GAM3623 NONO 3' ACAGAATACAGCAGACCCAGTT 81975 CA_ A _
TTTCA ACAGAA AGCAGA CTA TTTTCA
|||| |||||| ||| |||||
TGTCTT TCGTCT GGT AAAAGT
ATG G CA

GAM3623 NR3C2 3' ACAGAAAAAGTAGAAAGGTTTC 81976 C C CTAT
A ACAGAA AAG AGAA TTTCA
||||| ||| ||| ||||
TGTCTT TTC TCTT AAAGT
T A TCC_

GAM3623 PCDHA9 3' ACAGAACAAAGTGAATTCTC 81977 CA ACT
ACAGAACAAAG GA ATTTTC
||||||| || |||||
TGTCTTGTTC CT TAAGAG
A_ _

GAM3623 PEPD 3' AGAACAGCATTATTTTC 81978 A GAAC
AGAACA GCA TATTTTC
||||| ||| |||||||
TCTTGT CGT ATAAAAG
_ A_

GAM3623 PTPRC 3' AGAACAAGGAGGACATCTT 81979 C A T
AGAACAAG AG AC ATTTT
||||||| || || |||||
TCTTGTTC TC TG TAGAA
C C _

GAM3623 PTPRC 3' AGAACAAGGAGGACATCTT 81979 C A T
AGAACAAG AG AC ATTTT
||||||| || || |||||
TCTTGTTC TC TG TAGAA
C C _

GAM3623 RAD21 3' ACATAGCATCAACTATTTTCA 81980 _ G_
ACA AGCA AACTATTTTCA
||| ||| |||||||||
TGT TCGT TTGATAAAAGT
A AG

GAM3623 RPA2 3' ACAGAAGAGCAGTAAGTTTCA 81981 CA AACTAT
ACAGAA AGCAG TTTCA
||||| |||| |||||

			TGTCTT TCGTC AAAGT		
			C_ ATTC__		
GAM3623	SOD2	3'	ACAAAGCATTACTATTTTCA 81982	_	GA_
			ACAA GCA ACTATTTTCA		
			TGTT CGT TGATAAAAGT		
			T AAA		
GAM3623	SSRP1	3'	ACAGGACAAGCAGCAGCTA 81983	A	AA_
			ACAG ACAAGCAG CTA		
			TGTC TGTTTCGTC GAT		
			C GTC		
GAM3623	THY1	3'	ACAGAACAGGAAGAACCA 81984	AGC	
			ACAGAACCA AGAACTA		
			TGTCTTGT TCTTGGT		
			CCT		
GAM3623	ABCA8	3'	ACAGAACAAATGGAACCA 81985	GCA	
			ACAGAACAA GAACTA		
			TGTCTTGTT CTTGGT		
			AC_		
GAM3623	C21orf7	3'	AGAACAAGGAGAAATTGTTTCA 81986	C	CTAT
			AGAACAAG AGAA TTTCA		
			TCTTGTTT TCTT AAAGT		
			C TAAC		
GAM3623	CABP5	3'	ACAGGAGAAGAGACTATTTTCA 81987	AAC	C A
			ACAG AAG AGA CTATTTTCA		
			TGTC TTC TCT GATAAAAGT		
			CTC _ _		
GAM3623	CRIP1	3'	CAGAGCAGGGATTTATTTTCA 81989	ACAA	AAC__
			CAGA GCAG TATTTTCA		
			GTCT CGTC ATAAAAGT		
			____ CCTAA		
GAM3623	CRIP1	3'	ACAGAACTGAGAAATATTTTCA 81988	AAGC	C
			ACAGAAC AGAA TATTTTCA		
			TGTCTTG TCTT ATAAAAGT		
			AC__ T		
GAM3623	DDM36	3'	CAGGGCAAGCAGAAGCACT 81990	AA	C
			CAG CAAGCAGAA TATT		
			GTC GTTCGTCTT GTGA		
			CC C		
GAM3623	DKFZP564K2062	3'	AAACAAGCAGGACTTTCCA 81991	A	AT
			GAACAAGCAG ACT TTTCA		

TTTGTTTCGTC TGA AAGGT
 C _
 GAM3623 DKFZP586M0622 5' ACAGAAAAGCAGCCCGTTTCA 81992 C AA AT
 ACAGAA AAGCAG CT TTTCA
 ||||| ||||| || |||||
 TGTCTT TTCGTC GG AAAGT
 _ _ GC
 GAM3623 FIBL-6 3' ACAGAGTGTAGCACCATTTTCA 81993 ACA_ AGA
 ACAGA AGC ACTATTTTCA
 ||||| ||| |||||
 TGTCT TCG TGGTAAAAGT
 CACA _
 GAM3623 H2AV 3' ACAAATAAGCAGTTTTATTTTC 81994 AC AAC
 A
 ACAGA AAGCAG TATTTTCA
 ||||| ||||| |||||
 TGTCTT TTCGTC ATAAAAGT
 A_ AAA
 GAM3623 KIAA0408 3' ACAAAAACATCAAAAACATTTTT 81995 AGC
 CA
 ACAGAACA AGAACTATTTTCA
 ||||| |||||
 TGTCTTGT TTTTGATAAAAGT
 AGT
 GAM3623 KIAA0530 5' GAACAAGCAGGATTCCCA 81996 AACT TT
 GAACAAGCAG ATT CA
 ||||| ||| ||
 CTTGTTTCGTC TAA GT
 C_ GG
 GAM3623 KIAA0546 3' GAACAACAGACTATTTT 81997 G A
 GAACAA CAGA CTATTTT
 ||||| ||| |||||
 CTTGTT GTCT GATAAAA
 _ _
 GAM3623 KIAA0748 3' CAGCAACAGGCCATTTTC 81998 AACAA AA
 CAG GCAG CTATTTTC
 ||| ||| |||||
 GTC TGTC GGTAAAAG
 GT_ C_
 GAM3623 KIAA1054 3' CAGATAAGATGAAGCTATTTTC 81999 AC CA _
 A
 CAGA AAG GAA CTATTTTCA
 ||||| ||| ||| |||||
 GTCT TTC CTT GATAAAAGT
 A_ TA C
 GAM3623 KIAA1077 3' ACACAACAAGGATATTTTC 82000 G CA AC
 ACA AACAAG GA TATTTTC
 ||| ||||| || |||||
 TGT TTGTTC CT ATAAAAG
 G _ _
 GAM3623 KLF12 3' AGAAAAGCAGCTATTTTCA 82001 C AA
 AGAA AAGCAG CTATTTTCA
 ||||| ||||| |||||

			TCTT TTCGTC GATAAAAGT		
			— —		
GAM3623	MGC2963	3'	ACAGAACAAAGCAGCGAATTCA 82002		AACTATT
			ACAGAACAAAGCAG TTCA		
			TGTCTTGTTCGTC AAGT		
			GCTT__		
GAM3623	ODZ2	3'	CAGAACAAAGTGGGTCATATTTT 82003		CAGAAC_
			CAGAACAAAG TATTTT		
			GTCTTGTTT ATAAAA		
			ACCCAGT		
GAM3623	RNPC2	3'	CAGAACAAAGAGAACAGTTTT 82004		C TA
			CAGAACAAAG AGAAC TTTT		
			GTCTTGTTT TCTTG AAAA		
			— TC		
GAM3623	SEMA4F	3'	GAAGAATAAGCAGAACCA 82005	C C	
			A AGAA AAGCAGAACTA		
			C TCTT TTCGTCTTGGT		
			T A		
GAM3623	TRIM31	5'	ACAGAACAAACAGGGCTGTTTCA 82006		G AA AT
			ACAGAACAA CAG CT TTTCA		
			TGTCTTGTT GTC GA AAAGT		
			— CC C_		
GAM3623	ZNF396	3'	AGACAAGCAGTCATTTTCA 82007	A	AAC
			AGA CAAGCAG TATTTTCA		
			TCT GTTCGTC GTAAAAGT		
			— A_		
GAM3623	LOC127162	3'	AGAACAAGTAGAACACATTT 82008		C _
			AGAACAAG AGAAC TATTT		
			TCTTGTTT TCTTG GTAAA		
			A T		
GAM3623	LOC131870	3'	ACAAGAGCAAGTCTATTTTCA 82009		AACA AA
			ACAG AGCAG CTATTTTCA		
			TGTT TCGTT GATAAAAGT		
			C__ CA		
GAM3623	LOC133088	5'	GAACAAGCAGTGCTTTTCA 82010		AACTA
			GAACAAGCAG TTTTCA		
			CTTGTTTCGTC AAAAGT		
			ACG__		
GAM3623	LOC145652	3'	ACAAAGCAAGGAGCTCTATTTT 82011		A C AA
			ACAGA CAAG AG CTATTTT		

		TGTTT GTTC TC GATAAAA		
		C C GA		
GAM3623	LOC148280 5'	ACGAAACAAGCAGTTTTTC	82012	AG AACTA
		AC AACAAGCAG TTTTC		
		TG TTGTTGTC AAAAG		
		CT _____		
GAM3623	LOC150005 3'	ACAGACACAGGATATTTTC	82013	ACAA AAC
		ACAGA GCAG TATTTTC		
		TGTCT TGTC ATAAAAG		
		G__ CT_		
GAM3623	LOC150166 3'	ACAGAACAACGTAGGACCA	82014	GC_ A
		ACAGAACAA AG ACTA		
		TGTCTTGTT TC TGGT		
		GCA C		
GAM3623	LOC152300 3'	GAAGAACAAGCAGGTGTTATTT	82015	C AAC_
	T	A AGAACAAGCAG TATTTT		
		C TCTTGTTGTC ATAAAA		
		T CACA		
GAM3623	LOC153937 5'	GAACAAGCAGGATCCCA	81996	AACT TT
		GAACAAGCAG ATT CA		
		CTTGTTGTC TAA GT		
		C__ GG		
GAM3623	LOC201895 3'	CAAGGTGTTAACTATTTTCA	82016	CAG__
		CAAG AACTATTTTCA		
		GTTT TTGATAAAAGT		
		CACAA		
GAM3623	LOC202347 3'	AGAATAAAATAACTATTTTCA	82017	C CAG
		AGAA AAG AACTATTTTCA		
		TCTT TTT TTGATAAAAGT		
		A TA_		
GAM3623	LOC220883 3'	GAAAAGCAGAAGCACTTT	82018	C C
		GAA AAGCAGAA TATTTT		
		CTT TTCGTCTT GTGAAA		
		_ C		
GAM3623	LOC221421 3'	ACAGAACAGGCAGGCCAAGTTC	82019	A AA TT
	A	ACAGAACA GCAG CTA TTCA		
		TGTCTTGT CGTC GGT AAGT		
		C C_ TC		
GAM3623	LOC253716 3'	CAGGAACAGGCCATTTTC	82020	AACA AA
		CAG AGCAG CTATTTTC		

GTC TTGTC GGTAAG
 C__ C_
 GAM3623 LOC257608 5' ACAGAACAACAGGGCTGTTTCA 82006 G AA AT
 ACAGAACAA CAG CT TTTCA
 ||||| ||| || ||||
 TGTCTTGTT GTC GA AAAGT
 _ CC C_
 GAM3623 LOC90557 3' AAACAAGCTTTATTTTC 82021 AGAAC
 GAACAAGC TATTTTC
 ||||| |||||
 TTTGTTCG ATAAAG
 AA__
 GAM3623 LOC91115 3' ACAGAACAGGACAGGGATTTTC 82022 A_ AACT
 A ACAGAACA GCAG ATTTTCA
 ||||| ||| |||||
 TGTCTTGT TGTC TAAAGT
 CC CC__
 GAM3623 LOC91409 3' AAACAAGCTTTATTTTC 82021 AGAAC
 GAACAAGC TATTTTC
 ||||| |||||
 TTTGTTCG ATAAAG
 AA__
 GAM3624 PLAG1 3' GCATTGGCAATACTTATT 82025
 GCATTGGTAATACTTATT
 |||||
 CGTAACCGTTATGAATAA
 GAM3624 SIAT1 3' GCATTGGGCACAATTGTAATT 82026 TAA TT
 GCATTGG TAC ATTGTAATT
 ||||| ||| |||||
 CGTAACC GTG TAACATTAA
 C__ T_
 GAM3624 ESDN 3' GCATTGGTAATAAATACT 82027 CT
 GCATTGGTAATA TATT
 ||||| |||
 CGTAACCATTAT ATGA
 TT
 GAM3624 ZMPSTE24 3' GCGTTGGCAATGTTTAATGT 82028 A AC T
 GC TTGGTAAT TTA TGT
 || ||||| ||| |||
 CG AACCGTTA AAT ACA
 C CA T
 GAM3625 ACE2 3' GCCATTCTCAATCCTTGACAGCT 82031 _ C GAAA
 GC ATTC CGA TTGCAGCT
 || ||| ||| |||||
 CG TAAG GTT AACGTCGA
 G A AGG_
 GAM3625 NEBL 3' GCATTCCCAGGAATATAC 82032 A AT
 GCATTCCCG GAA TGC
 ||||| ||| |||

CGTAAGGGT CTT ATG
C AT

GAM3625 CAMKK2 3' GCATTCCCTGGAAGAAATC 82033 ____
GCATTCCC GAGAAATT
||||||| |||||||
CGTAAGGG TTCTTTAG
ACC

GAM3625 ChGn 3' TAGCATTCTAGAAACT 82034 CG
TAGCATTCC AGAAATT
||||||| |||||||
ATCGTAAGG TCTTTGA
A_

GAM3625 DKFZP761I2123 5' TAGCACTGAATTGCAGC 82035 CCC GAA
TAGCATT GA ATTGCAGC
||||||| || |||||||
ATCGTGA CT TAACGTCG
A_ _

GAM3625 FLJ12700 3' TAGCATTCCCAGAAAACAACT 82036 G TT
TAGCATTCCC AGAAA GCAGCT
||||||| ||||| |||||||
ATCGTAAGGG TCTTT TGTTGA

GAM3625 KIAA1199 3' TAGCACCAATGGGGAGTTGCAG 82037 CCC_ AAA
CT TAGCATT GAG TTGCAGCT
||||||| ||| |||||||
ATCGTGG CTC AACGTCGA
TTACCC _

GAM3625 KIAA1765 3' TTCCCGAGAAGCCAACT 82038 ATTG
TTCCCGAGAA CAGCT
||||||| |||||
AAGGGCTCTT GTTGA
CG_

GAM3625 RNF9 3' TAGCAGTTTCTGAGCCCACAGC 82039 _ CC AAA TG
T TAGCA TTC GAG T CAGCT
||||| ||| ||| | |||||
ATCGT AAG CTC G GTCGA
CA A_ G_ GT

GAM3625 ZNF313 3' GCTTCTCGGCATCTGCAGCT 82040 A C AGAAA
GC TTC CG TTGCAGCT
|| ||| || |||||||
CG AAG GC GACGTCGA
_ A CGTA_

GAM3625 LOC222112 5' TAGCATCCTGGGAGGCATCG 82041 CC_ AA
TAGCATTG GAG ATTG
||||||| ||| |||||
ATCGTAGG CTC TAGC
ACC CG

GAM3625 LOC254544 5' ATTCCCGAGCCGCGGC 82042 AAA A
ATTCCCGAG TTGC GC
||||||| ||||| ||

TAAGGGCTC GGCG CG
 ____ C
 GAM3626 AARS 3' TATCTATAGATGCGAGCGTGA 82045 AACT T C
 TGTCTATA CGA GCG GA
 ||||| ||| ||
 ATAGATAT GCT CGC CT
 CTAC _ A
 GAM3626 SLC21A2 3' TGTTCATAAACTCAGCTGA 82046 C AT GC
 TGT TATAAACTCG GC GA
 || ||||| || ||
 ACA GTATTTGAGT CG CT
 A ____ A_
 GAM3626 CAPN6 3' ACTGTCTAGGACTCATTG 82047 TAA A
 ACTGTCTA ACTCG TG
 ||||| |||| ||
 TGACAGAT TGAGT AC
 CC_ A
 GAM3626 DKFZP434L0117 3' ACTGGTTATAAACTTTATG 82048 TC CG
 ACTG TATAAACT ATG
 ||| ||||| ||
 TGAC ATATTTGA TAC
 CA AA
 GAM3626 FLJ20340 3' CTGCTATAAACAGTCATGTGCG 82049 T ____ G C
 A CTG CTATAAAC TC ATG GCGA
 || ||||| || ||| |||
 GAC GATATTTG AG TAC CGCT
 _ TC _ A
 GAM3626 TSPAN-5 3' ACTGTCCATAAATTCATG 82050 C G
 ACTGTCTATAAA TC ATG
 ||||| || |||
 TGACAGGTATTT AG TAC
 A _
 GAM3626 LOC150157 5' ACTTTCTATAAACCGTCCCG 82051 G T ATG
 ACT TCTATAAAC CG CG
 || ||||| || ||
 TGA AGATATTTG GC GC
 A _ AGG
 GAM3626 LOC201564 3' ACTGTCTAAAGATGGACA 82052 TAAACTC C
 ACTGTCTA GATG GCG
 ||||| ||| |||
 TGACAGAT CTAC TGT
 TT_____ C
 GAM3627 GTF2H1 3' TTCTGACAAAATTCTGCA 82055 A CTAC
 TTC TGACAAAATTC TGTA
 || ||||| |||
 AAG ACTGTTTAAAG ACGT
 _ _
 GAM3627 SEPP1 3' GACAAATCCGTACTGTAT 82056 AT _
 GACAAA TCC TACTGTAT
 ||||| || |||||

		CTGTTT AGG ATGACATA	
		— C	
GAM3627	SEPP1	3' GACAAATCCGTACTGTAT 82056	AT _
		GACAAA TCC TACTGTAT	
		CTGTTT AGG ATGACATA	
		— C	
GAM3627	KIAA1742	3' TCCATGACAGGGTTCCGCGCCC 82057	AAA TA__
		TGT TTCATGACA TTCC CTGT	
		AGGTACTGT AAGG GACA	
		CCC CGCGG	
GAM3627	LIN-7-C	3' ATGACAAAATCTGCA 82058	TCCTA
		ATGACAAAAT CTGTA	
		TACTGTTTGA GACGT	

GAM3627	RFX4	3' GACAAGGTCTCACTGTAT 82059	AAT C
		GACAA TC TACTGTAT	
		CTGTT AG GTGACATA	
		CC_ A	
GAM3627	LOC165771	5' TTCATGGAGCTCCTACTGT 82060	ACAAAA
		TTCATG TTCCTACTGT	
		AAGTAC GAGGATGACA	
		CTC__	
GAM3627	LOC203547	3' TTCATGTGAAATTCCTCAGT 82061	ACA ACT
		TTCATG AAATTCCT GT	
		AAGTAC TTAAAGGA CA	
		AC_ GT_	
GAM3627	LOC257449	3' TCCATGACAGGGTTCCGCGCCC 82057	AAA TA__
		TGT TTCATGACA TTCC CTGT	
		AGGTACTGT AAGG GACA	
		CCC CGCGG	
GAM3628	GNAS	3' CTGCTGTTTTATTTATTTTAC 82064	GTAAGT
		T TTGCTGTTT TTTTACT	
		GACGACAAA AAAAATGA	
		ATAAAT	
GAM3628	GNAS	3' CTGCTGTTTTATTTATTTTAC 82064	GTAAGT
		T TTGCTGTTT TTTTACT	
		GACGACAAA AAAAATGA	
		ATAAAT	
GAM3628	GNAS	3' CTGCTGTTTTATTTATTTTAC 82064	GTAAGT
		T TTGCTGTTT TTTTACT	

			GACGACAAA	AAAAATGA		
			ATAAAT			
GAM3628	GNAS	3'	CTGCTGTTTTATTTATTTTAC	82064	GTAAGT	
	T		TTGCTGTTT	TTTTACT		
			GACGACAAA	AAAAATGA		
			ATAAAT			
GAM3628	PUM1	3'	TTGTTTTTGTGTTGTTTTTACT	82065	CTG	AA
	A		TTG	TTTGT	GTTTTTACTA	
			AAC	AAACA	CAAAAAATGAT	
			AA_	AA		
GAM3628	AK000009	3'	TTCCTGTTTGTCTGATTTTTA	82066	G	AAGT
			TT	CTGTTTGT	TTTTTA	
			AA	GACAAACA	AAAAAT	
			G	GACT		
GAM3628	DREV1	3'	CTGTTTTTTTTTTTACT	82067	GTAAG	
			CTGTTT	TTTTTACT		
			GACAAA	AAAAAATGA		
			AAA_			
GAM3628	RIS1	3'	TGTTTTGTATTTTTTTTACTA	82068	_	AG
			TGTTT	GTA	TTTTTACTA	
			ACAAA	CAT	AAAAAATGAT	
			A	AA		
GAM3628	LOC253461	3'	TTGCTGTTTTTTTAC	82069	GTAAGTT	
			TTGCTGTTT	TTTTAC		
			AACGACAAA	AAAATG		
GAM3629	ABCA1	5'	CCGTGGCTGGTCATTAAGTGT	82072	CCA	CTA _
			CC	GCTG	TCAT	AACTGTT
			GG	CGAC	AGTA	TTGACAA
			CAC	C_	A	
GAM3629	ASH1	3'	CCTCAGCTACTGTTTCTGTT	82073	C	ATCATAA
			CC	CAGCTGCT	CTGTT	
			GG	GTCGATGA	GACAA	
			A	CAAA_		
GAM3629	ATP1A1	5'	CCCGGGCTGCTACCGCTGTT	82074	CA	ATAA
			CCC	GCTGCTATC	CTGTT	
			GGG	CGACGATGG	GACAA	
			CC	C_		
GAM3629	CD80	3'	GCCAGCCATCTTGTAAGTGT	82075	_	A_
			GCT	GCTATC	TAAGTGT	

CGG CGGTAG ATTGACAA
 T AAC
 GAM3629 G6PD 3' CCCAGCTGCTGCGTCTGCT 82076 ATCATAA
 CCCAGCTGCT CTGTT
 ||||| ||||
 GGGTCGACGA GACGA
 CGCA__
 GAM3629 ID4 3' CCACTAGCTATAACTGT 82077 G _ TCA
 CCA CT GCTA TAACTGT
 ||| || |||||
 GGT GA CGAT ATTGACA
 _ T _
 GAM3629 OPHN1 5' GCTCCTTCCTCAACTGTT 82078 G A A
 GCT CT TC TAACTGTT
 ||| || |||||
 CGA GA GG GTTGACAA
 G A A
 GAM3629 SCN3A 3' CAGGCACATAACTGTT 82079 CT TAT
 CAG GC CATAACTGTT
 ||| || |||||
 GTC CG GTATTGACAA
 _ T _
 GAM3629 TCF2 3' CAGTGTCCCATAACTGTT 82080 C CTA
 CAG TG TCATAACTGTT
 ||| || |||||
 GTC AC GGTATTGACAA
 _ AG_
 GAM3629 DKFZP667O116 3' CCCCAGCTGCTGTCTGCACT 82081 A ATA
 CCCCAGCTGCT TC ACT
 ||||| || |||
 GGGGTCGACGA AG TGA
 C ACG
 GAM3629 KIAA0014 3' ACCCCAAGTGCACAGGCTGTT 82082 TAT TAA
 ACCCCAGCTGC CA CTGTT
 ||||| || |||||
 TGGGGTTGACG GT GACAA
 T__ CC_
 GAM3629 KIAA0182 3' CCAGCTGCCAGCAAGCTGTT 82083 T TAA
 CCAGCTGCTA CA CTGTT
 ||||| || |||||
 GGTCGACGGT GT GACAA
 C TC_
 GAM3629 KIAA0565 5' CCTAAGCTGTCTATAACTGTT 82084 CC _ TCA
 CC AGCTG CTA TAACTGTT
 || |||| || |||||
 GG TCGAC GAT ATTGACAA
 AT A _
 GAM3629 KIAA1822 3' CCCTATTCTATGTAAGTGT 82085 AGCTG CA
 CCC CTAT TAACTGTT
 || |||| |||||

GGG GATA ATTGACAA
ATAA_ C_
GAM3629 TRIM6 3' CCTAGTACTGAGTAACTGTT 82086 C C ATCA
CC AG TGCT TAACTGTT
|| ||||| |||||
GG TC ATGA ATTGACAA
A _ CTC_
GAM3629 LOC123523 3' ACTCCAGCTGCTGGCACTGCC 82087 C ATCATA
AC CCAGCTGCT ACTGTT
|| ||||| |||||
TG GGTCGACGA TGACGG
A CCG_
GAM3629 LOC145902 3' ACTCCAGCTGCTGGCACTGCC 82087 C ATCATA
AC CCAGCTGCT ACTGTT
|| ||||| |||||
TG GGTCGACGA TGACGG
A CCG_
GAM3629 LOC150407 3' ACCCCAGCTGCGAGCTGT 82088 TATCATAA
ACCCCAGCTGC CTGT
||||||| |||
TGGGGTCGACG GACA
CTC____
GAM3629 LOC154739 5' CATTGCTATCACACAGTT 82089 GC ACT
CA TGCTATCATA GTT
|| ||||| |||
GT ACGATAGTGT CAA
A_ GT_
GAM3629 LOC253868 3' CCCAGCTGTCCAGCTGT 82090 _ TCATAA
CCCAGCTG CTA CTGT
||||||| ||| |||||
GGGTCGAC GGT GACA
A C____
GAM3629 LOC256207 5' CCTAAGCTGTCTATAACTGTT 82084 CC _ TCA
CC AGCTG CTA TAACTGTT
|| ||||| ||| |||||
GG TCGAC GAT ATTGACAA
AT A ____
GAM3629 LOC93587 3' ACCACAGCTGCTAAGAGCTGTT 82091 C TCATAA
ACC CAGCTGCTA CTGTT
||| ||||| ||| |||||
TGG GTCGACGAT GACAA
T TCTC_
GAM3630 GNAI1 3' ACAAGTATACATATAATC 82094 TTG
ACA GTACATATAATC
||| |||||
TGT TATGTATATTAG
TCA
GAM3630 GRM6 3' CACTGGAACATATAATTCA 82095 T C
CATTGG ACATATAAT CA
||||| ||||| ||| ||

GTGACC TGTATATTA GT
 T A
 GAM3630 MAN1A1 3' TAACTAGTATATAATCC 82096 C CA
 A ATTGGTA TATAATCC
 I I I I I I I I I I I I
 A TGATCAT ATATTAGG
 T _
 GAM3630 PCSK2 3' TGGCATTGGTAGTAAAATATCC 82097 A CATATA_
 A TG CATTGGTA ATCCA
 II I I I I I I I I I I
 AC GTAACCAT TAGGT
 C CATTTTA
 GAM3630 PIK3R1 3' ATTGATACAAATCCA 82098 TAT
 ATTGGTACA AATCCA
 I I I I I I I I I I I I
 TAACTATGT TTAGGT
 _
 GAM3630 SLC20A2 3' TGACATTGGAGACAAGGATCC 82099 T_ TATA
 TGACATTGG ACA ATCC
 I I I I I I I I I I I I
 ACTGTAACC TGT TAGG
 TC TCC_
 GAM3630 SLC4A4 3' TAACACAATAACATATAATTCA 82100 TGGT C
 TGACAT ACATATAAT CA
 I I I I I I I I I I I I
 ATTGTG TGTATATTA GT
 TTAT A
 GAM3630 BAG5 3' TGACATTGGTAACCCGTCTCCA 82101 _ATATAA
 TGACATTGGTA C TCCA
 I I I I I I I I I I I I
 ACTGTAACCAT G AGGT
 T GGCAG_
 GAM3630 CPSF2 3' TGCATTAACACTATAATC 82102 A GG A
 TG CATT TAC TATAATC
 II I I I I I I I I I I
 AC GTAA GTG ATATTAG
 _ TT _
 GAM3630 FLJ14440 3' ACAGGTTGATATATAATCCA 82103 _ CA
 ACA TTGGTA TATAATCCA
 III I I I I I I I I I I
 TGT AACTAT ATATTAGGT
 CC _
 GAM3630 FLJ14686 3' ACATGATATATAATCC 82104 T CA
 ACAT GGTA TATAATCC
 III I I I I I I I I I I
 TGTA CTAT ATATTAGG
 _ _
 GAM3630 FLJ20130 3' TGACATTGTGTGCATGCTCC 82105 _ A ATAA
 TGACATTG GT CAT TCC
 I I I I I I I I I I I I

ACTGTAAC CA GTA AGG
 A C CG__
 GAM3630 GDAP2 3' TAACAAGTCATATAATCCA 82106 TT A
 TGACA GGT CATATAATCCA
 |||| ||| |||||
 ATTGT TCA GTATATTAGGT

 — —
 GAM3630 KIAA0332 3' CAATTATACATATAATCCA 82107 TTG
 CA GTACATATAATCCA
 || |||||
 GT TATGTATATTAGGT
 TAA
 GAM3630 KIAA0493 5' GACATTGGTACATCC 82108 TATAA
 GACATTGGTACA TCC
 ||||| |||
 CTGTAACCATGT AGG

 —
 GAM3630 KIAA1309 3' TGTACATTTACTATAATCCA 82109 _ GG A
 TG ACATT TAC TATAATCCA
 || |||| ||| |||||
 AC TGTAATG ATG ATATTAGGT
 A _ _
 GAM3630 KIAA1432 5' TGACACTGGTGTAAATAATCCA 82110 ACATAT
 TGACATTGGT AATCCA
 ||||| |||||
 ACTGTGACCA TTAGGT
 CATTAT
 GAM3630 KIAA1500 3' TGAAGTAAATATAATCC 82111 AT TAC
 TGAC TGG ATATAATCC
 |||| ||| |||||
 ACTG ACT TATATTAGG
 _ T_
 GAM3630 KIAA1718 3' TGACATTGTAAATTATAATCCA 82112 GTACA
 TGACATTG TATAATCCA
 ||||| |||||
 ACTGTAAC ATATTAGGT
 ATTTA
 GAM3630 MGC5149 3' TGACATTAGTACAAGCAGTC 82113 TA A
 TGACATTGGTACA TA TC
 ||||| ||| |||
 ACTGTAATCATGT GT AG
 TC C
 GAM3630 NETO2 3' TGACAATGGTACATATATCCCA 82114 T A
 TGACA TGGTACATATA TCCA
 |||| ||||| |||||
 ACTGT ACCATGTATAT GGGT
 T A
 GAM3630 Rpo1-2 3' TGGCATTGGTACATGTTCC 82115 A ATAA
 TG CATTGGTACAT TCC
 || ||||| |||

AC GTAACCATGTA AGG
 C CA__
 GAM3630 LOC145837 5' CATGTTGGTACAGGTACTCCA 82116 TA A
 CAT TGGTACA TA TCCA
 ||| ||||| || ||||
 GTA ACCATGT AT AGGT
 CA CC G
 GAM3630 LOC151194 3' ACATTGGTATAATACC 82117 CATA _
 ACATTGGTA TAAT CC
 ||||| ||| ||
 TGTAAACCAT ATTA GG
 T
 GAM3630 LOC151465 3' GACATTGAACACTATGATC 82118 T _ A
 GACATTGG ACAT AT ATC
 ||||| ||| || |||
 CTGTAAC TGTG TA TAG
 _ A C
 GAM3630 LOC159250 5' ATTGGTACAGACACCA 82119 T AT
 ATTGGTACA ATA CCA
 ||||| ||| |||
 TAACCATGT TGT GGT
 C _
 GAM3630 LOC169026 3' ACTGATCAGTATATAATCCA 82120 AC__
 ATTGGT ATATAATCCA
 ||||| |||||
 TGA CTA TATATTAGGT
 GTCA
 GAM3630 LOC202050 3' TAACATTGGTACAAGTCTC 82121 TATAA
 TGACATTGGTACA TC
 ||||| ||| ||
 ATTGTAACCATGT AG
 TCAG_
 GAM3630 LOC256942 3' TGGCTCACGTATAATCCA 82122 _ A
 TGGT AC TATAATCCA
 ||| || |||||
 ACCG TG ATATTAGGT
 AG C
 GAM3630 LOC90693 3' CATAGGATATAATCCA 82123 T TAC
 CAT GG ATATAATCCA
 ||| || |||||
 GTA CC TATATTAGGT
 T _
 GAM3631 IL1A 3' TGTAACATTTCATTTAGAA 82126 C ATGCG
 TGTAACAA CATTTAGAA
 ||||| ||| |||||
 ACATT TGT GTAAATCTT
 _ AA_
 GAM3631 ITGA2 3' ACACAATGCAAATTAGAAT 82127 CAT
 ACACAATGCG TTAGAAT
 ||||| |||||

			TGTGTTACGT AATCTTA		
			TT_		
GAM3631	PAIP2	3'	TGTAACACAGTGACAAGA 82128	A C	TTT
			TGTAACACA TG GCA AGA		
			ACATTGTGT AC TGT TCT		
			C _ _		
GAM3631	SORCS1	3'	TGCAACACTTCTATATTTAGAA 82129	AATGCGC	
	T		TGTAACAC ATTTAGAAT		
			ACGTTGTG TAAATCTTA		
			AAGATA_		
GAM3631	ZNF10	3'	TGTGACCCAAAACAATTTAGAA 82130	A A T C	
	T		TGT AC CAA GCG ATTTAGAAT		
			ACA TG GTT TGT TAAATCTTA		
			C G T _		
GAM3631	FLJ13611	3'	GTAACACATGATTTAGA 82131	A CGC	
			GTAACACA TG ATTTAGA		
			CATTGTGT AC TAAATCT		
			_ _		
GAM3631	MDS029	3'	TGCAATATACCACATTTAGAAT 82132	CACA _	
			TGTAA ATGC GCATTTAGAAT		
			ACGTT TATG TGTAATCTTA		
			A_ G		
GAM3631	OMD	3'	TGGAACACAATAACATTGTTTA 82133	T C _	
	G		TG AACACAATG GCATT TAG		
			AC TTGTGTTAT TGTAATC		
			C _ CAA		
GAM3632	PMX1	3'	GCTTTAATGAAAACCTTCGT 82136	C CCATC	
			GCT TTAA AAAACCTTCGT		
			CGA AATT TTTTGAAGCA		
			_ AC_		
GAM3632	PMX1	3'	GCTTTAATGAAAACCTTCGT 82136	C CCATC	
			GCT TTAA AAAACCTTCGT		
			CGA AATT TTTTGAAGCA		
			_ AC_		
GAM3632	RAD50	3'	GCTCTTAATCTTACTCGT 82137	ACC AAA T	
			GCTCTTA ATC ACT CGT		
			CGAGAAT TAG TGA GCA		
			_ AA_ _		
GAM3632	RAD50	3'	GCTCTTAATCTTACTCGT 82137	ACC AAA T	
			GCTCTTA ATC ACT CGT		

CGAGAAT TAG TGA GCA
 ____ AA_ _
 GAM3632 KIAA1257 3' GCTTTCAATCATCAAAAC 82138 C C
 GCT TTAA CATCAAAAC
 ||| ||| |||||
 CGA AGTT GTAGTTTTG
 A A
 GAM3633 APBA1 3' TGGGTCAGTACCAGGTGGGTGC 82141 A _ T A A
 TGG TG GTCGG ATTA GTG GT CTGG
 || |||| ||| || || ||||
 AC CAGTC TGGT CAC CA GACC
 C A C C C
 GAM3633 C5orf4 3' TGAGTCGGGTATGTGAA 82142 AT
 TGAGTCGG TATGTGAG
 ||||| |||||
 ACTCAGCC ATACACTT
 C_
 GAM3633 C5orf4 3' TGAGTCGGGTATGTGAA 82142 AT
 TGAGTCGG TATGTGAG
 ||||| |||||
 ACTCAGCC ATACACTT
 C_
 GAM3634 STK18 3' TTCTATTTTATATCCACTATAT 82145 _
 TT TTTTATTTTATATT TTATATTT
 ||||| |||||
 AAGATAAAATATAG GATATAAA
 GT
 GAM3634 WNT5A 3' TTTTATTTTATATTCTAT 82146
 TTTTATTTTATATTTTAT
 ||||| |||||
 AAAATAAAATATAAGATA
 GAM3634 FLJ23516 3' TATTTTATTTTACATTTTATATT 82147 T
 T TATTTTATTT ATATTTTATATTT
 ||||| |||||
 ATAAAATAAA TGTAATATAAA
 _
 GAM3634 MGC4832 3' CATTTTATTTTACATTATAT 82148 T
 TATTTTATTTTATATT TAT
 ||||| ||||| |||
 GTAAAATAAAATGTAA ATA
 T
 GAM3635 F3 3' TAAAGTGCAGATTGTAAAGCA 82151 ATAC _
 TAAAGTGCA TGTAAGCG
 ||||| ||||| |||
 ATTCACGT ACATT CGT
 CTA_ T
 GAM3635 FCMD 3' AAGTGCAATGCCGCGA 82152 A GTAA
 AAGTGCAAT CT GCGA
 ||||| || ||||

TTCACGTTA GG CGCT
 C ____
 GAM3635 DRIL2 3' GTGAGCCGCAAGCGAAT 82153 CAATA
 GTG CTGTAAGCGAAT
 ||| |||||
 CAC GCGTTCGCTTA
 TC____
 GAM3636 P23 3' TGCCTTAGCTGACTTAAAAT 82156 C GT_
 TGCC TAGCTGAC GGGT
 ||||| |||||
 ACGG ATCGACTG TTTA
 A AAT
 GAM3636 SERPINF2 3' TGTCCCAGCTGACGTGGG 82157 C
 TG CCTAGCTGACGTGGG
 || |||||
 AC GGGTCGACTGCACCC
 A
 GAM3636 TCF3 3' TGCCCTAGTTCGTGTGGAAC 82158 CTGA _ T
 TGCCCTAG CGTG GG ACT
 ||||| |||||
 ACGGGATC GCAC CC TGA
 AA__ A T
 GAM3636 FLJ12787 3' CTTACTTAAACGGGTACT 82159 A _ CG
 CT GCT GA TGGGTACT
 || |||||
 GA TGA TT GCCCATGA
 A A TT
 GAM3636 MGC12981 3' TGCCCAGCTACTCAGGT 82160 T ACG
 TGCCC AGCTG TGGGT
 ||||| |||||
 ACGGG TCGAT GTCCA
 _ GA_
 GAM3636 STK29 3' TGTCCCTTGCCCGTTGGGTACTC 82161 C A GA _
 G TG CCT GCT CGT GGGTACTCG
 || |||||
 AC GGA CGG GCA CCCATGAGC
 A A _ A
 GAM3636 LOC144486 3' TGTCCCTAGTGATGGACACT 82162 C C CG GT
 TG CCTAG TGA TGG ACT
 || ||||| |||||
 AC GGATC ACT ACC TGA
 A _ _ TG
 GAM3636 LOC146745 5' GCCGCGACGTGGGTACT 82163 CTA T
 GCC GC GACGTGGGTACT
 ||| || |||||
 CGG CG CTGCACCCATGA

 GAM3636 LOC152084 3' GCTGCAGCTACGTGGGT 82164 CC A
 GC TAGCTG CGTGGGT
 || ||||| |||||

		CG GTCGAT GCACCCA		
		AC _		
GAM3636	LOC152924 3'	TGCCTTAGCTGACTTCAAAT	82165	C G_ GG
		TGCC TAGCTGAC T GT		
		ACGG ATCGACTG G TA		
		A AA TT		
GAM3636	LOC201243 5'	GCCGCGACGTGGGTACT	82163	CTA T
		GCC GC GACGTGGGTACT		
		CGG CG CTGCACCCATGA		
		— —		
GAM3636	LOC56920 3'	TGCCCTAGCTGGGTGGGT	82166	AC
		TGCCCTAGCTG GTGGGT		
		ACGGGATCGAC CACCCA		
		C_		
GAM3637	CYBB 3'	GAAGATAGAAAACCTTG	82169	TAAAT
		GAAGATA AGGATCTTG		
		CTTCTAT TTTTGAAC		
		C_		
GAM3637	IGFBP3 3'	GAAGACATAAACATTCTTCTTG	82170	GGA_
	G	GAAGATATAAATA TCTTGG		
		CTTCTGTATTTGT AGAACC		
		AAGA		
GAM3637	FLJ13189 3'	GAAGAATGAGTAGAATCTGG	82171	TATAAA T
		GAAGA TAGGATCT GG		
		CTTCT ATCTTAGA CC		
		TACTC_ —		
GAM3637	FLJ14054 3'	GAAGATTTTCAGATCTTGG	82172	ATAAATA
		GAAGAT GGATCTTGG		
		CTTCTA TCTAGAACC		
		AAAG_		
GAM3637	KIAA1571 3'	GAAGATCCAGGATCTTG	82173	ATAAA
		GAAGAT TAGGATCTTG		
		CTTCTA GTCCTAGAAC		
		G_		
GAM3637	MSTP028 3'	GAAAATATAAACTCGTTTTTGG	82174	AGGATC
		GAAGATATAAAT TTGG		
		CTTTTATATTTG AACC		
		AGCAAA		
GAM3638	BECN1 3'	ATAAAGTGGCTTTTGTGGA	82177	CTC C
		ATAAAGTGGCT GT GA		

			TATTTACCGA CA CT		
			AAA C		
GAM3638	CD8A	3'	AGGGGCTCTCCAACAAT 82178	T	GT
			AG GGCTCTC CGACAAT		
			TC CCGAGAG GTTGTTA		
			C _		
GAM3638	MEN1	5'	AAATGGCTTTTGCAAAACAAT 82179		CTC C_
			AAGTGGCT GT GACAAT		
			TTTACCGA CG TTGTTA		
			AAA TT		
GAM3638	T2BP	3'	TAAAGTGGCCCAAGAACA 82180		TCGTC
			TAAAGTGGCTC GACA		
			ATTTACCGGG TTGT		
			TTC_		
GAM3638	LOC200081	3'	TATAGAATGGCTCTACACA 82181	A	_ T
			TATA AGTGGCTCT CG CG		
			ATAT TTACCGAGA GT GT		
			C T _		
GAM3639	ASB3	3'	AGAAGTAACATCACAGTT 82184	TA_	
			AGA GACATCACAGTT		
			TCT TTGTAGTGTCAA		
			TCA		
GAM3639	B4GALT5	3'	CAGATCACAGTTCATCA 82185	CA	C
			TAGA TCACAGTTCA CA		
			GTCT AGTGTCAAGT GT		
			_ A		
GAM3639	CADPS	3'	AGACATGGACATCAGGAAATCA 82186	G A	CAGT_
			AGA AT GACATCA TCA		
			TCT TA CTGTAGT AGT		
			G C CCTTT		
GAM3639	DAAM2	3'	GAGATAGATAGTCACAGTTCCC 82187	CA_	A
	CA		GAGATAGA TCACAGTTC CCA		
			CTCTATCT AGTGTCAAG GGT		
			ATC G		
GAM3639	DNTT	3'	AGAGATAGACAGTATTTTCAGCT 82188		TCA_
			AGAGATAGACA CAGTT		
			TCTCTATCTGT GTCGA		
			CATAAA		
GAM3639	DUSP5	3'	AGAGACAGACATTGAACTGCC 82189		CACAGTTCA
	A		AGAGATAGACAT CCA		

			TCTCTGTCTGTA	GGT	
			ACTTTGAC_		
GAM3639	FACL3	3'	AGAGACAGACACAAGTT	82190	T C
			AGAGATAGACA CA AGTT		
			TCTCTGTCTGT GT TCAA		
			- -		
GAM3639	GNGT2	3'	AGAGAAGGTGACAGTTCAC	82191	T ACATC
			AGAGA AG ACAGTTCAC		
			TCTCT TC TGTCAAGTG		
			_ CAC_		
GAM3639	HDAC4	3'	AGAGAGACAGGCAGTTCAC	82192	TA TCA
			AGAGA GACA CAGTTCAC		
			TCTCT CTGT GTCAAGTG		
			_ CC_		
GAM3639	HTR2C	3'	AGGGACAGACATTGCAGTAAAT	82193	A CA TC_
	ACCA		AG GATAGACAT CAGT ACCA		
			TC CTGTCTGTA GTCA TGGT		
			C AC TTTA		
GAM3639	KCNA6	3'	AGAACAGTACATCACAGTT	82194	G _
			AGA ATAG ACATCACAGTT		
			TCT TGTC TGTAGTGTCAA		
			_ A		
GAM3639	MLLT2	3'	AGAGATAAGCATCGCTCCC	82195	GA ACA A
			AGAGATA CATC GTTC CC		
			TCTCTAT GTAG CGAG GG		
			TC _ _		
GAM3639	RNF28	3'	AGAGAAGACATCACCTCCCCA	82196	T AG A
			AGAGA AGACATCAC TTC CCA		
			TCTCT TCTGTAGTG AGG GGT		
			_ G_ _		
GAM3639	SACM1L	3'	AGAGATAGACTTTACATT	82197	ATC G
			AGAGATAGAC ACA TTC		
			TCTCTATCTG TGT AAG		
			AAA _		
GAM3639	SERPINE1	3'	GAGACAGATCTGGTTTACCA	82198	CA ACA C
			GAGATAGA TC GTT ACCA		
			CTCTGTCT AG CAA TGGT		
			_ AC_ A		
GAM3639	SIAT1	3'	AGAGATAGACCTTGCATCTACC	82199	ATCACA TC
	A		AGAGATAGAC GT ACCA		

			TCTCTATCTG	TA	TGGT		
			GAACG_	GA			
GAM3639	SLC26A4	3'	AGAGACAGTATTC	CCGCAGTT	82200	ACA__	A
			AGAGATAG	TC	CAGTT		
			TCTCTGTC	GG	GTCAA		
			ATAAG	C			
GAM3639	STAU2	3'	AGAGATAGATGCACCTAATCA		82201	CAT	AGT_
			AGAGATAGA	CAC	TCA		
			TCTCTATCT	GTG	AGT		
			AC_	GATT			
GAM3639	AKAP6	3'	AGGGATAGATGTCACCATGTCA		82202	A	CA AGT_
			AG	GATAGA	TCAC	TCA	
			TC	CTATCT	AGTG	AGT	
			C	AC	GTAC		
GAM3639	ARL8	3'	AGACAGTATCTTACAGTTCAC		82203	AC	__
			AGATAG	ATC	ACAGTTCAC		
			TCTGTC	TAG	TGTCAAGTG		
			A_	AA			
GAM3639	CL25084	3'	AGGGATAGACAGCACAGT		82204	A	T
			AG	GATAGACA	CACAGT		
			TC	CTATCTGT	GTGTCA		
			C	C			
GAM3639	DDX34	3'	AGGGATGCGGACGCAGTTCACC		82205	A	A__ ATCA
	A		AG	GAT	GAC	CAGTTCACCA	
			TC	CTA	CTG	GTCAAGTGGT	
			C	CGC	C__		
GAM3639	DKFZP434P211	3'	AGGTAGACATCATTTTCA		82206	A	CAG
			AG	TAGACATCA	TTCA		
			TC	ATCTGTAGT	AAGT		
			C	AA_			
GAM3639	FLJ10139	3'	AGAGATAGGTACTGAACAAACC		82207	__	ATC TTC
	A		AGAGATAG	AC	ACAG	ACCA	
			TCTCTATC	TG	TGTT	TGGT	
			CA	ACT	__		
GAM3639	FLJ20154	5'	GAGTTGGAGGTCGGTTCACCA		82208	ATA	CA ACA
			GAG	GA	TC	GTTCACCA	
			CTC	CT	AG	CAAGTGGT	
			AAC	CC	C__		
GAM3639	FLJ30046	5'	GAGATAGAATCATCCTCC		82209	C	CAG A
			GAGATAGA	ATCA	TTC	CC	

CTCTATCT TAGT AGG GG
 _ _ _ A
 GAM3639 IRAK3 3' GAGAGGACATTACAATCCA 82210 TA C
 GAGA GACAT ACAGTTCA
 |||| |||| ||||
 CTCT CTGTA TGTTAGGT
 C_ A
 GAM3639 KIAA0144 3' AGAAATACCACAGTT 82211 AGAC
 AGAGAT ATCACAGTT
 |||| ||||
 TCTTTA TGGTGTCAA
 _
 GAM3639 KIAA0212 3' AGAGATAGAGATGGCACGTT 82212 C _ A
 AGAGATAGA AT CAC GTT
 |||| || || ||
 TCTCTATCT TA GTG CAA
 C CC _
 GAM3639 KIAA1530 3' AGCAGATGACTGAACGGTTCAC 82213 _ A ATC A
 AG AGAT GAC AC GTTCAC
 || || || || || ||
 TC TCTA CTG TG CAAGTG
 G _ ACT C
 GAM3639 KLHL8 3' AGAAATAGACATTGAAGCC 82214 CAC
 AGAGATAGACAT AGTT
 |||| || ||
 TCTTTATCTGTA TCGG
 ACT
 GAM3639 LIPG 3' AGAGATAGACTTTGCCTCC 82215 ATCACA CA
 AGAGATAGAC GTT CC
 |||| || || ||
 TCTCTATCTG CGG GG
 AAA_ A_
 GAM3639 MEGF10 3' AGAGATAGAAAATTCA 82216 CATCAC
 AGAGATAGA AGTTCA
 |||| || || ||
 TCTCTATCT TTAAGT
 T_
 GAM3639 MGC13523 3' AGAGATAACATCACAATT 82217 A
 AGAGAT GACATCACAGTT
 |||| |||| ||||
 TCTCTA TTGTAGTGTTAA
 _
 GAM3639 NALP2 3' AGAGGAGTCACAGGCAGTTCAC 82218 AT A CA_
 CA AGAG AG CAT CAGTTCACCA
 || || || || || || || ||
 TCTC TC GTG GTCAAGTGGT
 C_ A TCC
 GAM3639 U5-100K 3' AAGATGGACACAGCCAGTTCAC 82219 A CA_
 C GAGAT GACAT CAGTTCACC
 |||| || || || || || ||

		TTCTA CTGTG GTCAAGTGG		
		C TCG		
GAM3639	LOC127733 3'	GAGAGAATCACAGTTCAC 82220	TA C	
		GAGA GA ATCACAGTTCAC		
		CTCT CT TAGTGTCAAGTG		
		— —		
GAM3639	LOC133634 5'	AGAGGGGGACATCACTCCC 82221	ATA AGT A	
		AGAG GACATCAC TC CC		
		TCTC CTGTAGTG AG GG		
		CCC — —		
GAM3639	LOC145624 5'	AGAGGAGGTATCACCCACC 82222	AT AC AGT	
		AGAG AG ATCAC TCACC		
		TCTC TC TAGTG GGTGG		
		C_ CA —		
GAM3639	LOC148229 5'	GAGAGGACATCACGCT 82223	TA A	
		GAGA GACATCAC GTT		
		CTCT CTGTAGTG CGA		
		C_ —		
GAM3639	LOC202934 3'	AGAGAAAGGCATCAAATC 82224	T A C	
		AGAGA AG CATCA AGTT		
		TCTCT TC GTAGT TTAG		
		T C —		
GAM3639	LOC221322 5'	AGGATAGGATAACAAGTTCACC 82225	A ACAT_ C	
	A	AG GATAG CA AGTTCACCA		
		TC CTATC GT TCAAGTGGT		
		— CTATT —		
GAM3639	LOC221810 3'	AGAGAAGACATTACATCA 82226	T C GT	
		AGAGA AGACAT ACA TCA		
		TCTCT TCTGTA TGT AGT		
		— A —		
GAM3639	LOC253044 3'	GAAATAGATATCTCAC 82227	C ACAGT	
		GAGATAGA ATC TCAC		
		CTTTATCT TAG AGTG		
		A —		
GAM3639	LOC255465 3'	AGAGAAAGGCATCAAGTC 82228	T A C	
		AGAGA AG CATCA AGTT		
		TCTCT TC GTAGT TCAG		
		T C —		
GAM3639	LOC51696 3'	GAGATAGTTAATTCACC 82229	ACATCAC	
		GAGATAG AGTTCACC		

		CTCTATC TTAAGTGG		
		AA_____		
GAM3639	LOC90231	3' GAGATGGACATCACCGCC 82230	A	A
		GAGAT GACATCAC GTT		
		CTCTA CTGTAGTG CGG		
		C G		
GAM3640	FLJ13910	3' CAGTGTGTGTACACTAAC 82233	CA	
		TAGTGTG TACACTAAT		
		GTCACAC ATGTGATTG		
		AC		
GAM3640	KIAA1505	5' TAGTGTGCACACATAACTT 82234	C	
		TAGTGTGCATACA TAATTT		
		ATCACACGTGTGT ATTGAA		
		—		
GAM3640	OR51E2	3' GTGTACATTCAAAATTTTTGA 82235	A CT	C
		GTGTGCAT CA AATTTT GA		
		CACATGTA GT TTAAAA CT		
		A T_ A		
GAM3641	CERD4	3' TGTACTTGAAGCCCCCACC 82238	_ T_	
		TGT CTTGG CTTCCACC		
		ACA GAACT GGGGGTGG		
		T TC		
GAM3641	KCNE3	3' TGTCTTGGTCTTCCACCG 82239		
		TGTCTTGGTCTTCCACC G		
		ACAGAACCAGAAGGTGG C		
GAM3641	MAT1A	3' TGCCTTAATTTCCTTTCACC 82240	___ C	
		TGTCTTGGT CTT CACC		
		ACGGAATTA GAA GTGG		
		AAG A		
GAM3641	RDS	3' TGCCTTGGTCTGGTCACC 82241	TC_	
		TGTCTTGGTCT CACC		
		ACGGAACCAGA GTGG		
		CCA		
GAM3641	TNXB	5' TGTCCTGCCGAGCCCACC 82242	G T_	
		TGTCTTG TC TCCACC		
		ACAGGAC GG GGGTGG		
		_ CTC		
GAM3641	FLJ22031	3' TGCCAGCCCCTTTCCACC 82243	TT _	
		TGTC GGTCT TCCACC		

		ACGG TCGGG AGGTGG		
		— GAA		
GAM3641	FLJ23185	3' TGCCCCGAGTCTTCTACC	82244	— C
		TGTCTTG GTCTTC ACC		
		ACGGGGC CAGAAG TGG		
		T A		
GAM3641	KIAA0628	3' TGCTAGTCCCTTTCCACC	82245	CT —
		TGT TGGTCT TCCACC		
		ACG ATCAGG AGGTGG		
		— GAA		
GAM3641	KIAA1029	3' TGCCTTGGCCAAAGCCACC	82246	TT—
		TGTCTTGGTC CCACC		
		ACGGAACCGG GGTGG		
		TTTC		
GAM3641	KIAA1056	3' TGTCTGGCCCTCTTCCACC	82247	T —
		TGTCT GGTCT TCCACC		
		ACAGA CCGGG AGGTGG		
		— AGA		
GAM3641	KIAA1719	5' GTCTTGACTATTTCCACC	82248	T —
		GTCTTGG CT TCCACC		
		CAGAACT GA AGGTGG		
		— TAA		
GAM3641	PRO1598	5' TGTCTAGGCCCTCTTCCAC	82249	—
		TGTCTTGG TCTTCCAC		
		ACAGGATC AGAAGGTG		
		CGGG		
GAM3641	TNFSF13	5' TGCCTTGAGACCCTCCACC	82250	—
		TGTCTTG G TCTTCCACC		
		ACGGAAC C GGGAGGTGG		
		T T		
GAM3641	LOC125268	3' TGCCTTGGTTCCCTCACC	82251	— TC
		TGTCTTGGT CT CACC		
		ACGGAACCA GG GTGG		
		A GA		
GAM3641	LOC142954	3' TATCCTAACGTTTCCACC	82252	TC—
		TGTCTTGG TTCCACC		
		ATAGGATT AAGGTGG		
		GCA		
GAM3641	LOC143310	5' TGTCTTGATGGTTCTTCCACC	82253	—
		TGTCTTGG TCTTCCACC		

ACAGAACT AGAAGGTGG
 ACCA
 GAM3641 LOC148887 5' TGTCTGGCCTGATCTGCC 82254 ___ CA
 TGTCTTGGTCT TC CC
 ||||| || ||
 ACAGGACCGGA AG GG
 CT AC
 GAM3641 LOC255338 5' TGTCTCGGGTAGGCTCCACC 82255 TC___
 TGTCTTGG TTCCACC
 ||||| |||||
 ACAGAGCC GAGGTGG
 CATCC
 GAM3641 LOC255736 5' TGTCTCCAGCCTTTCCACC 82256 ___ -
 TGTCTT GGTCTT CCACC
 |||| |||| ||||
 ACAGGA TCGGAA GGTGG
 GG A
 GAM3641 LOC257407 5' TGTCTTAGTAAGCCCCAC 82257 C___
 TGTCTTGGT TTCCAC
 ||||| |||||
 ACAGAATCA GGGGTG
 TTC
 GAM3641 LOC91548 5' TGTCTGGTGGGTTCCACC 82258 C___
 TGTCTTGGT TTCCACC
 ||||| |||||
 ACAGGACCA AAGGTGG
 CCC
 GAM3641 LOC92299 3' TGTCTCGATCTCTTCACC 82259 C_
 TGTCTTGGTCTT CACC
 ||||| |||||
 ACAGAGCTAGAG GTGG
 AA
 GAM3642 GALNT7 3' TCTGCTTCACTCTTTAATT 82262 _ T
 TCT TTTTA CTCTTTAATT
 || |||| |||||
 AGA GAAGT GAGAAATTAA
 C _
 GAM3642 HD 3' TCCATTTTTTCCCTTTAATTT 82263 C TA
 TCTAT TTTT TCTCTTTAATTT
 |||| ||| |||||
 AGGTA AAAA AGGGAAATTAAA
 - -
 GAM3642 KCNJ16 3' TCCTAATATCTCTTTGATT 82264 TT A
 TCTT TATCTCTTT ATT
 ||| ||||| |||
 AGGA ATAGAGAAA TAA
 TT C
 GAM3642 PRKCN 5' TCAGTCTGTACTTGTCTCTTTA 82265 TA T__ A
 ATTT TC TCT TTT TCTCTTTAATTT
 || ||| ||| |||||

AG AGA GAA AGAGAAATTAAA
 TC CAT C
 GAM3642 FLJ10508 3' TCTCTTTATCTCTTTAATTT 82266
 TCTTTTTATCTCTTTAATTT
 |||||
 AGAGAAATAGAGAAATTAAA

GAM3642 KIAA1762 3' TCTTCTTTTTATCTTCTTT 82267 A _
 TCT TCTTTTTATCT CTTT
 ||| ||||| ||||
 AGA AGAAAAATAGA GAAA
 _ A

GAM3642 LOC145693 5' TATCTTCCCTCTTTA 82268 TTA
 TATCTTT TCTCTTTA
 ||||| |||||
 ATAGAAG GGAGAAAT

GAM3642 LOC222193 3' TCTCTCTCTTTAATTT 82269 TTTA
 TCTT TCTCTTTAATTT
 ||| |||||
 AGAG AGAGAAATTAAA

GAM3642 LOC54505 5' TCTTTCTTTTTATCTTTCTCT 82270 A _
 TCT TCTTTTTATC TCTTT
 ||| ||||| ||||
 AGA AGAAAAATAG AGAGA
 A AA

GAM3643 ADD1 3' AGCACACGGTTCAGGCTCCA 82273 ATACA T A
 AGCACACG CA GT TCCA
 ||||| || |||||
 TCGTGTGC GT CG AGGT
 CAA_ C _

GAM3643 ADD1 3' AGCACACGGTTCAGGCTCCA 82273 ATACA T A
 AGCACACG CA GT TCCA
 ||||| || |||||
 TCGTGTGC GT CG AGGT
 CAA_ C _

GAM3643 AHCY 3' AAGCACACAGGTATAAGTCCA 82274 ATACAC TA
 AAGCACACG ATG TCCA
 ||||| ||| ||||
 TTCGTGTGT TAT AGGT
 CCA_ TC

GAM3643 CCRL1 3' AAGCATCATTTCATATGTATCCA 82275 _ CGATA C
 AAGCA CA CA ATGTATCCA
 ||||| || |||||
 TTCGT GT GT TACATAGGT
 A AA_ A

GAM3643 CKTSF1B1 3' AAACACACACACTATGT 82276 GAT _
 AAGCACAC ACAC ATGT
 ||||| ||| ||||

			TTTGTGTG TGTG TACA		
			____ A		
GAM3643	CRI1	3'	AAGCACACGTGATACATAT 82277	ATAC	
			AAGCACACG ACATGT		
			TTCGTGTGC TGTATA		
			ACTA		
GAM3643	GRM6	3'	ACATTACACACGTGTATC 82278	CG A	
			ACA ATACAC TGTATC		
			TGT TGTGTG ACATAG		
			AA C		
GAM3643	GTF2IRD1	3'	GCATCGATACATATCC 82279	CA CATG	
			GCA CGATACA TATCC		
			CGT GCTATGT ATAGG		
			A_ ____		
GAM3643	HELLS	3'	AAGTACACATCAGCCTGTATCC 82280	C ATACACA	
	A		AAG ACACG TGTATCCA		
			TTC TGTGT ACATAGGT		
			A AGTCGG_		
GAM3643	MJD	3'	AGCACACGGTATACAGT 82281	A C T	
			AGCACACG TA ACA GT		
			TCGTGTGC AT TGT CA		
			C A _		
GAM3643	MJD	3'	AGCACACGGTATACAGT 82281	A C T	
			AGCACACG TA ACA GT		
			TCGTGTGC AT TGT CA		
			C A _		
GAM3643	MS4A8B	3'	AGCACACGAATGTGTGTGTGCC 82282	TACACA AT_	
	A		AGCACACGA TGT CCA		
			TCGTGTGCT ACA GGT		
			TACAC_ CAC		
GAM3643	NT5C2	3'	AGTACAGATACACAAAACCA 82283	C C TGTAT	
			AG ACA GATACACA CCA		
			TC TGT CTATGTGT GGT		
			A _ TTT_		
GAM3643	NTSR1	3'	AAGCACACGGAATGCGCACCC 82284	ATACACA	
			AAGCACACG TGTATCC		
			TTCGTGTGC GCGTGGG		
			CTTAC_		
GAM3643	PLAG1	3'	AAGTACACGATATACATG 82285	C C	
			AAG ACACGATA ACATG		

		TTC TGTGCTAT TGTAC		
		A A		
GAM3643	PRAME	3' AAGCATTGTGATATGTGCACCCA 82286	CAC	CACA
		AAGCA GATA TGTATCCA		
		TTCGT CTAT ACGTGGGT		
		AAA AC__		
GAM3643	RB1	3' AAGCACACAGTATATCAGATTC 82287	A CA_ T A	
	CA	AAGCACACG TA CA GT TCCA		
		TTCGTGTGT AT GT TA AGGT		
		C ATA C _		
GAM3643	SCN4A	3' AAGCACACATACATGT 82288	ATAC	
		AAGCACACG ACATGT		
		TTCGTGTGT TGTACA		
		A__		
GAM3643	TPP2	3' GCACTTACACATGTATTCA 82289	ACGA	C
		GCAC TACACATGTAT CA		
		CGTG ATGTGTACATA GT		
		A__ A		
GAM3643	APOA5	3' AGCACACAGTATGCTCCC 82290	ATACAC	A
		AGCACACG ATGT TCC		
		TCGTGTGT TACG GGG		
		CA__ A		
GAM3643	BTBD3	3' AAGCACA CTGATGCACAAGT 82291	_ A T	
		AAGCACAC GAT CACA GT		
		TTCGTGTG CTA GTGT CA		
		A C T		
GAM3643	CAMKK1	3' AGCACGCGACATGCACCC 82292	A TACA	
		AGCAC CGA CATGTATCC		
		TCGTG GCT GTACGTGGG		
		C _		
GAM3643	CHUK	3' AAGCACAGATACACAATCC 82293	C TGT	
		AAGCACA GATACACA ATCC		
		TTCGTGT CTATGTGT TAGG		
		- -		
GAM3643	FCGBP	3' AGCACATGATGCATCC 82294	C TACACA	
		AGCACA GA TGTATCC		
		TCGTGT CT ACGTAGG		
		A _		
GAM3643	FLJ10350	3' AGCACACGAATGCAC 82295	TACAC	
		AGCACACGA ATGTAT		

TCGTGTGCT TACGTG

GAM3643 FLJ23309 3' AAGCACATCATACACATG 82296 CG
AAGCACA ATACACATG
||||| |||||||
TTCGTGT TATGTGTAC
AG

GAM3643 FLJ32762 3' AAGCAATACCATGTATC 82297 CACG A
AAGCA ATAC CATGTATC
|||| ||| |||||||
TTCGT TATG GTACATAG

GAM3643 IMAGE145052 3' AACATACGATACAATC 82298 C CATGT
AGCA ACGATACA ATC
||| ||||||| |||
TTGT TGCTATGT TAG
A

GAM3643 KIAA0390 3' AAGCACACGATCACCC 82299 A ATGTA
AAGCACACGAT CAC TC
||||||||| ||| ||
TTCGTGTGCTA GTG GG

GAM3643 KIAA0672 3' ACAACGATTTGTACATGTAT 82300 C AC__
GCA ACGAT ACATGTAT
||| ||||| |||||||
TGT TGCTA TGTACATA
_ AACA

GAM3643 KIAA1078 3' AAGCACACCATACACTGTAC 82301 G A
AAGCACAC ATACAC TGTAT
||||||| ||||||| |||||
TTCGTGTG TATGTG ACATG
G

GAM3643 KIAA1449 3' AAGCACACTGTTGTATCC 82302 GATACACA
AAGCACAC TGTATCC
||||||| |||||||
TTCGTGTG ACATAGG
ACA__

GAM3643 LCE 3' AAACATTGACACATGTAT 82303 CACGAT
AAGCA ACACATGTAT
||||| |||||||||
TTTGT TGTGTACATA
AAC__

GAM3643 MAPK11 3' AAGCACATGTACACACATGT 82304 CG_
AAGCACA ATACACATGT
||||||| |||||||||
TTCGTGT TGTGTGTACA
ACA

GAM3643 PSMD1 3' GCAACGATACATGCAT 82305 C CA
GCA ACGATACA TGTAT
||| ||||||| |||||

CGT TGCTATGT ACGTA

GAM3643 RTP801 3' ACATGCTACACACACATCCA 82306 CGA TG
ACA TACACA TATCCA
||| ||||| |||||
TGT ATGTGT GTAGGT
ACG GT

GAM3643 SYTL4 3' AAGCACACATACATGT 82288 ATAC
AAGCACACG ACATGT
||||||| |||||
TTCGTGTGT TGTACA

A____
GAM3643 TRAF3 3' AAGCACACAGTGTGCGCCCCCA 82307 ATACACA AT
AAGCACACG TGT CCA
||||||| ||| |||
TTCGTGTGT GCG GGT
CACAC__ GG

GAM3643 LOC123855 5' AAGCACACGAACGTCTCC 82308 TACAC A
AAGCACACGA ATGT TCC
||||||| ||| |||
TTCGTGTGCT TGCA AGG
____ G

GAM3643 LOC143310 5' AGCCACGATACATACGT 82309 A C
AGC CACGATACA ATGT
||| ||||| |||||
TCG GTGCTATGT TGCA
____ A

GAM3643 LOC148918 5' GCACACGAAACCACATCCA 82310 T A GT
GCACACGA AC CAT ATCCA
||||||| || ||| |||||
CGTGTGCT TG GTG TAGGT
____ T _ _

GAM3643 LOC149465 5' AGCAGACCACGCATGTATCCA 82311 C GA A
AGCA AC TAC CATGTATCCA
||| || ||| ||||| |||||
TCGT TG GTG GTACATAGGT
C _ C

GAM3643 LOC150577 3' AGCACATCACATGTATC 82312 CGATA C
AGCACA CACATGTAT C
||||| ||||| |||
TCGTGT GTGTACATA G
A____ A

GAM3643 LOC157507 5' AGCACACATACACAGC 82313 G T
AGCACAC ATACACA GT
||||| ||||| |||
TCGTGTG TATGTGT CG

GAM3643 LOC159199 5' AAGCACACGAATGCATGT 82314 TACA
AAGCACACGA CATGT
||||||| |||||

		TTCGTGTGCT	GTACA		
		TAC_			
GAM3643	LOC220513	3'	AAGTACACATCAGCCTGTATCC	82280	C ATACACA
		A	AAG ACACG TGTATCCA		
			TTC TGTGT ACATAGGT		
			A AGTCGG_		
GAM3643	LOC92305	3'	AGCGCACGGTGCACACATCCA	82315	A ATA GT
			AGC CACG CACAT ATCCA		
			TCG GTGC GTGTG TAGGT		
			C CAC _		
GAM3643	LOC93622	3'	AAGCACACGAGTATACTTCCA	82316	TACAC TA
			AAGCACACGA ATG TCCA		
			TTCGTGTGCT TAT AGGT		
			CA_ GA		
GAM3644	ACAT1	3'	CACTGATTACAGCAGGCCT	82319	A TT T
			CACTGATTG CA G GCCT		
			GTGACTAAT GT T CGGA		
			_ CG C		
GAM3644	CABC1	3'	ACTGGTGACACCTGTGCCTC	82320	AT _
			ACTG TGACAT TGTGCCTC		
			TGAC ACTGTG ACACGGAG		
			C_ G		
GAM3644	CACNA2D2	3'	CACTGTTTGACATTGAGC	82321	A GT
			CACTG TTGACATT GC		
			GTGAC AACTGTAA CG		
			A GT		
GAM3644	CDS1	3'	ACTGACTTCCTATTGTGCCT	82322	GAC_
			ACTGATT ATTGTGCCT		
			TGACTGA TAACACGGA		
			AGGA		
GAM3644	DBT	3'	CAGTGACAAATATTGTGCCT	82323	C T C
			CA TGAT GA ATTGTGCCT		
			GT ACTG TT TAACACGGA		
			C T A		
GAM3644	EMX2	3'	TGATTGACAGCTCCCC	82324	TT G
			TGATTGACA GT CCTC		
			ACTAACTGT CG GGGG		
			_ A		
GAM3644	GPR81	3'	CATTGATTGACTGAGCCC	82325	C AT T
			CA TGATTGAC TG GCCT		

		GT ACTAACTG AC CGGG		
		A _ T		
GAM3644	HIVEP3	5' CTGCTGGGTTTGTGCCTC	82326	A ACA
		CTG TTG TTGTGCCTC		
		GAC GAC AACACGGAG		
		_ CCA		
GAM3644	IL17E	5' CACTGACTGACAGGCCTC	82327	TTGT
		CACTGATTGACA GCCTC		
		GTGACTGACTGT CGGAG		
		C _		
GAM3644	LAMP2	3' CAGTGCCATGCATTGTGCTTC	82328	C AT_ A C
		CA TG TG CATTGTGC TC		
		GT AC AC GTAACACG AG		
		C GGT _ A		
GAM3644	LRAT	3' ACTGATTGGCCCCGCCC	82329	ACA G
		ACTGATTG TT TGCCT		
		TGACTAAC GG GCGGG		
		C _ G		
GAM3644	MAP3K7IP1	3' CACTGATTGTGTGGCT	82330	ACAT C
		CACTGATTG TGTG CT		
		GTGACTAAC ACAC GA		
		_ C		
GAM3644	MPP3	3' TGATGGTGAAGTGTGCCTC	82331	_ CAT
		TGAT TGA TGTGCCTC		
		ACTA ACT ACACGGAG		
		CC TC_		
GAM3644	PDE1B	3' CTGATGACATCAAACACT	82332	T T _
		CTGAT GACATTG GC CT		
		GACTA CTGTAGT TG GA		
		_ T T		
GAM3644	RAD52	5' CTGGTTGACCTGCGCCTC	82333	A A
		CTG TTGAC TTGTGCCTC		
		GAC AACTG GACGCGGAG		
		C _		
GAM3644	RAD52	5' CTGGTTGACCTGCGCCTC	82333	A A
		CTG TTGAC TTGTGCCTC		
		GAC AACTG GACGCGGAG		
		C _		
GAM3644	RAD52	5' CTGGTTGACCTGCGCCTC	82333	A A
		CTG TTGAC TTGTGCCTC		

			GAC AACTG GACGCGGAG		
			C _		
GAM3644	RAD52	5'	CTGGTTGACCTGCGCCTC	82333	A A
			CTG TTGAC TTGTGCCTC		
			GAC AACTG GACGCGGAG		
			C _		
GAM3644	TGFB1	3'	CACTGGTCCCCTGTGCCT	82334	A GACA
			CACTG TT TTGTGCCT		
			GTGAC AG GACACGGA		
			C GG_		
GAM3644	UBE3A	3'	CACTGATCACGTGCCT	82335	ACAT
			CACTGATTG TGTGCCT		
			GTGACTAGT GCACGGA		

GAM3644	UBE3A	3'	CACTGATCACGTGCCT	82335	ACAT
			CACTGATTG TGTGCCT		
			GTGACTAGT GCACGGA		

GAM3644	UBE3A	3'	CACTGATCACGTGCCT	82335	ACAT
			CACTGATTG TGTGCCT		
			GTGACTAGT GCACGGA		

GAM3644	WNT5A	5'	TGATTGACTGCGCTTC	82336	AT C
			TGATTGAC TGTGC TC		
			ACTAACTG ACGCG AG		
			_ A		
GAM3644	ZNF26	5'	CACGGATGGATTTGTGCCT	82337	T T CA
			CAC GAT GA TTGTGCCT		
			GTG CTA CT AACACGGA		
			C C A_		
GAM3644	CSMD1	3'	TGCTGGGCATTGTGCTTC	82338	A A_ C
			TG TTG CATTGTGC TC		
			AC GAC GTAACACG AG		
			_ CC A		
GAM3644	DKFZP434E2135	3'	ACTGACTCGGTATGTGCCTC	82339	GACAT
			ACTGATT TGTGCCTC		
			TGACTGA ACACGGAG		
			GCCAT		
GAM3644	DKFZP434P0721	3'	ACTGATGACTGTGCCTC	82340	T AT
			ACTGAT GAC TGTGCCTC		

TGACTA CTG ACACGGAG

GAM3644 DKFZp761O0113 5' CACTGTTGACATTCTTGC 82341 A G_
CACTG TTGACATT TGC
||||| ||||| ||
GTGAC AACTGTAA ACG
GA
GAM3644 FLJ10521 3' CATTGAGTGAGACCATGCCT 82342 C T C TG
CA TGA TGA AT TGCCT
|| ||| || |||||
GT ACT ACT TG ACGGA
A C C GT
GAM3644 FLJ12355 3' TGATTCCCATTTGTGCCTC 82343 GA _
TGATT CATT GTGCCTC
||||| ||| |||||
ACTAA GTAA CACGGAG
GG A
GAM3644 FLJ12891 3' TAATTGACACATGACTGTGC 82344 _____
TGATTGACAT TGTGC
||||||| |||||
ATTAAGTGTG ACACG
TACTG
GAM3644 FLJ14327 3' CACTGATTCACAGCTACT 82345 G TT GC
CACTGATT ACA GT CT
||||||| ||| || ||
GTGACTAA TGT CG GA
G _ AT
GAM3644 FLJ20079 5' TGATGGTGAGATGTGCCTC 82346 _ CAT
TGAT TGA TGTGCCTC
||||| ||| |||||
ACTA ACT ACACGGAG
CC CT_
GAM3644 FLJ20298 3' TGATGCATTGTGCTTC 82347 T A C
TGAT G CATTGTGC TC
||||| ||||| ||
ACTA C GTAACACG AG
_ _ A
GAM3644 GADD45A 5' CACTAATTGGGCCGCTGCCTC 82348 ACA _
CACTGATTG TTG TGCCTC
||||||| ||| |||||
GTGATTAAC GGC ACGGAG
CC_ G
GAM3644 KIAA0537 3' CTGAAAAGTATTGTGCCT 82349 TT _
CTGA GAC ATTGTGCCT
||||| ||| |||||
GACT TTG TAACACGGA
T_ AC
GAM3644 KIAA1463 3' CACTGATTAGCATGCTGGTCCT 82350 A _ TG
CACTGATTG CAT TG CCT
||||||| ||| || |||

			GTGACTAAT GTA AC GGA		
			C CG CA		
GAM3644 KIAA1492	3'	AATTGATGCATTTTGTGCCT	82351	—	—
		GATTGA CAT TGTGCCT			
		TTAACT GTA ACACGGA			
		AC AA			
GAM3644 KIAA1548	3'	ACTGCTGTGCTGTGCCT	82352	A	ACA
		ACTG TTG TTGTGCCT			
		TGAC GAC GACACGGA			
		— AC—			
GAM3644 LSFR2	3'	CACCAAAACATTGTGCTTC	82353	TG TT	C
		CAC A GACATTGTGC TC			
		GTG T TTGTAACACG AG			
		GT — A			
GAM3644 MGC21654	3'	CACTGATTGCAAATAGGTCTC	82354	A TT	C—
		CACTGATTG CA GTG CTC			
		GTGACTAAC GT TAT GAG			
		— TT CCA			
GAM3644 NXPH3	3'	CTGCTGGCATTGTGCCT	82355	A A	—
		CTG TTG CATT GTGCCT			
		GAC GAC GTAA CACGGA			
		— C A			
GAM3644 RAP2B	3'	CACTGTATTGGCATCAGTG	82356	— A	—
		CACTG ATTG CATT GTG			
		GTGAC TAAC GTAG CAC			
		A C T			
GAM3644 SEMA4F	3'	CACTGATTGCAAACGTATCT	82357	A T—	C
		CACTGATTG CA TGTG CT			
		GTGACTAAC GT GCAT GA			
		— TT A			
GAM3644 ST6GalNAcI	3'	CACTGTATCCTGTGCCT	82358	—	GACA
		CACTG ATT TTGTGCCT			
		GTGAC TAG GACACGGA			
		A ———			
GAM3644 LOC143188	5'	CACTAATTGATGTCCAGCCT	82359	CA	GT
		CACTGATTGA TT GCCT			
		GTGATTAAC AG CGGA			
		AC GT			
GAM3644 LOC143915	3'	CACTATCTTGCTGTGCCT	82360	A—	ACA
		CACTG TTG TTGTGCCT			

	GTGAT AAC GACACGGA	
	AG ____	
GAM3644 LOC144571 3'	CTGATTGATGTCTGATGTCTC 82361	CA_ _ C
	CTGATTGA TTG TG CTC	
	GACTAACT GAC AC GAG	
	ACA T A	
GAM3644 LOC147178 3'	ACTGAGTGACATTGCCTC 82362	T TG
	ACTGA TGACAT TGCCTC	
	TGACT ACTGTA ACGGAG	
	C ____	
GAM3644 LOC147991 5'	ACTGATTAAATGATGCCT 82363	C T
	ACTGATTGA AT GTGCCT	
	TGACTAATT TA TACGGA	
	_ C	
GAM3644 LOC148304 3'	ACTGATCTACAGCATTGTGCCT 82364	GA____
	ACTGATT CATTGTGCCT	
	TGACTAG GTAACACGGA	
	ATGTC	
GAM3644 LOC150271 3'	CACTCAGAACTTGTGCCTC 82365	GATT A
	CACT GAC TTGTGCCTC	
	GTGA TTG AACACGGAG	
	GTC_ _	
GAM3644 LOC151657 3'	CTGATTCACCACACCTC 82366	GA TG
	CTGATT CAT TGCCTC	
	GACTAA GTG GTGGAG	
	_ GT	
GAM3644 LOC153114 5'	CACTGATTGGTGCCT 82367	ACATT
	CACTGATTG GTGCCT	
	GTGACTAAC CACGGA	

GAM3644 LOC153232 5'	ACTGAAACAGTTTGTGCCT 82368	TT ____
	ACTGA GACA TTGTGCCT	
	TGACT TTGT AACACGGA	
	_ CA	
GAM3644 LOC155081 3'	CCCCTGCATTGTGCCT 82369	GA A
	CT TTG CATTGTGCCT	
	GG GAC GTAACACGGA	
	G_ _	
GAM3644 LOC159184 3'	AATTGATGTCTGTGCCTC 82370	CA_
	GATTGA TTGTGCCTC	

TTAACT GACACGGAG
ACA
GAM3644 LOC160954 5' CACTGATCGGTGTTTCGCGTGCC 82371 ACAT____
T CACTGATTG TGTGCCT
||||||| |||||
GTGACTAGC GCACGGA
CACAAGC
GAM3644 LOC161846 5' CATTGGGTAACCTGTGCCTC 82372 C AT A
CA TG TGAC TTGTGCCTC
|| || |||| |||||
GT AC ATTG GACACGGAG
A CC _
GAM3644 LOC199858 5' CACTAGGCATTGTGCCT 82373 ATTGA
CACTG CATTGTGCCT
|||| |||||
GTGAT GTAACACGGA
CC____
GAM3644 LOC200853 5' CACTGATTTCAAAGTGTCTC 82374 GA TT C
CACTGATT CA GTG CTC
|||||| || |||
GTGACTAA GT CAC GAG
A_ TT A
GAM3644 LOC201411 3' CACTGATTGATAAAATATCT 82375 CATT C
CACTGATTGA GTG CT
||||||| |||
GTGACTAACT TAT GA
ATTT A
GAM3644 LOC202802 3' CCCCTGCATTGTGCCT 82369 GA A
CT TTG CATTGTGCCT
|| ||| |||||
GG GAC GTAACACGGA
G_ _
GAM3644 LOC203078 3' CACTGATTAAGTATTGTGCCT 82376 C_
CACTGATTGA ATTGTGCCT
||||||| |||||
GTGACTAATT TAACACGGA
CA
GAM3644 LOC220394 5' TGTTTCGTCAAGTGTGCCTC 82377 A A T
TG TTG CA TGTGCCTC
|| ||| || |||||
AC AGC GT ACACGGAG
A A C
GAM3644 LOC221354 3' CACAGTACATTGTGCCTC 82378 TGATTG
CAC ACATTGTGCCTC
||| |||||
GTG TGTAACACGGAG
TCA____
GAM3644 LOC222228 3' CCCCTGCATTGTGCCT 82369 GA A
CT TTG CATTGTGCCT
|| ||| |||||

		GG GAC GTAACACGGA		
		G_ _		
GAM3644	LOC222233 3'	CCCCTGCATTGTGCCT	82369	GA A
		CT TTG CATTGTGCCT		
		GG GAC GTAACACGGA		
		G_ _		
GAM3644	LOC222256 3'	CAGTGATTGACAGGCCCTC	82379	C TT G
		CA TGATTGACA GT CCTC		
		GT ACTAACTGT CG GGAG		
		C C_ G		
GAM3644	LOC254020 3'	ACTAATTGGCATCTGGCTC	82380	A G C
		ACTGATTG CATT TG CTC		
		TGATTAAC GTAG AC GAG		
		C _ C		
GAM3644	LOC254413 5'	TAACTAAGCATTGTGCTTC	82381	_ C
		TGATTGA CATTGTGC TC		
		ATTGATT GTAACACG AG		
		C A		
GAM3644	LOC255520 3'	CACTGATTGTCCACTAGC	82382	A_ T
		CACTGATTG CATTG GC		
		GTGACTAAC GTGAT CG		
		AG _		
GAM3644	LOC256113 5'	CTTATTGATTGCCCTC	82383	G CA G
		CT ATTGA TTGT CCTC		
		GA TAACT AACG GGAG		
		A _ G		
GAM3644	LOC89919 5'	ACTGAATGTTTGTGCCT	82384	T ACA
		ACTGA TG TTGTGCCT		
		TGACT AC AACACGGA		
		T A_		
GAM3644	LOC91974 5'	ACTGACTGGCTGACCC	82385	ACA T
		ACTGATTG TTG GCCT		
		TGACTGAC GAC TGGG		
		C_ _		
GAM3644	LOC96597 5'	CTGATCCAACCTGTGCCTC	82386	GAC
		CTGATT ATTGTGCCTC		
		GACTAG TGACACGGAG		
		GT_		
GAM3645	ARNT2 3'	TGGAAGAAAGTGTTCATGG	82389	T GGTGA
		TGGAAGAA GTGT ATGG		

			ACCTTCTT CACA TACC		
			T AAG__		
GAM3645	CYP8B1	3'	TGGGAGATGGGGTGAATGG 82390	A	ATG T
			TGG AGA TG GGTGAATGG		
			ACC TCT AC CCACTTACC		
			C __ C		
GAM3645	GAS7	3'	TGGAGAATGTGTTTGCTGTGG 82391	A	GG AA_
			TGGA GAATGTGT TG TGG		
			ACCT CTTACACA AC ACC		
			_ A_ GAC		
GAM3645	ITGA11	3'	TGGGGGAATGTGTGAGTTGC 82392	AA	TGAATG
			TGG GAATGTGTGG GC		
			ACC CTTACACACT CG		
			CC CAA__		
GAM3645	MMP19	3'	TGGGAGCATGTGAATAAAATGG 82393	A A	TGGT
	CA		TGG AG ATGTG GAATGGCA		
			ACC TC TACAC TTTACCGT		
			C G TTAT		
GAM3645	MMP19	3'	TGGGAGCATGTGAATAAAATGG 82393	A A	TGGT
	CA		TGG AG ATGTG GAATGGCA		
			ACC TC TACAC TTTACCGT		
			C G TTAT		
GAM3645	MPV17	3'	GAAGAGTGGGGATGAGTGGCA 82394	AT T _ A	
			GAAGA GTG GG TGA TGGCA		
			CTTCT CAC CC ACT ACCGT		
			_ C T C		
GAM3645	NSF	3'	TGGAAGAAGTGTGTGGAGGG 82395	_	TGAAT
			TGGAAGAA TGTGTGG GG		
			ACCTTCTT ACACACC CC		
			C TC__		
GAM3645	USH3A	5'	TGGAGCCTGGTGAATGG 82396	AGAAT G	
			TGGA GT TGGTGAATGG		
			ACCT CG ACCACTTACC		
			_ G		
GAM3645	VAX2	3'	GGAAGAGTGTGTGGCTGC 82397	A	GAATG
			GGAAGA TGTGTGGT GC		
			CCTTCT ACACACCG CG		
			C A__		
GAM3645	C20orf175	3'	TGGGGGATGTGCGGGGATGGCA 82398	AA A	T A
			TGG GA TGTGTGG GA TGGCA		

ACC CT ACACGCC CT ACCGT
 CC _ C _
 GAM3645 DKFZp762A227 5' TGGAAGAATGTCAGAAGAATGG 82399 GT T
 CA TGGAAGAATGT GG GAATGGCA
 ||||| || |||||
 ACCTTCTTACA CT CTTACCGT
 GT T
 GAM3645 FLJ13052 3' GAGGAATGTGTGGGTCCGTGGC 82400 A TGAA_
 GA GAATGTGTGG TGGC
 || ||||| |||
 CT CTTACACACC ACCG
 C CAGGC
 GAM3645 FOXP1 3' TGGTAGAATGTGGTGGCA 82401 A _
 TGG AGAATGTG TGGTG
 || ||||| |||
 ACC TCTTACAC ACCGT
 A C
 GAM3645 KIAA0795 3' TGGGAGAATGTGTGTGA 82402 A G
 TGG AGAATGTGTG TGA
 || ||||| |||
 ACC TCTTACACAC ACT
 C _
 GAM3645 KIAA1026 3' TGAGGGAATTAATGAATGG 82403 AA GTG
 TGG GAAT TGGTGAATGG
 || ||| |||||
 ACT CTTA ATTACTTACC
 CC _
 GAM3645 KIAA1145 3' GAAGGCGGTGAATGG 82404 AATGT
 GAAG GTGGTGAATGG
 ||| |||||
 CTTC CGCCACTTACC
 _
 GAM3645 KIAA1243 5' TGGTGGAATGTATTGGTG 82405 AA _
 TGG GAATGTGT GGTG
 || ||||| |||
 ACC CTTACATA CCAC
 AC A
 GAM3645 KIAA1318 3' TGTAAGAATGTAGTGAGATGG 82406 G AT _
 TG AAGA GTGTGGTGA ATGG
 || ||| ||||| |||
 AC TTCT TACATCACT TACC
 A _ C
 GAM3645 KIAA1644 3' GGACAGTGTCTGAATGG 82407 AGAAT G
 GGA GTGT GTGAATGG
 || ||| |||||
 CCT CACA CACTTACC
 GT _ G
 GAM3645 MGC4251 3' TGGAGGACTGTGTGGTCTGG 82408 A A GAA
 TGGA GA TGTGTGGT TGG
 ||| || ||||| |||

ACCT CT ACACACCA ACC
 C G G__
 GAM3645 RAI 3' TGGGGGATGTGATGATGG 82409 AA ATG A
 TGG GA TGTGGTGA TGG
 ||| || ||||| |||
 ACC CT ACACTACT ACC
 CC ____ _
 GAM3645 TBC1D2 3' TGGGAAGAGGTGACGAAAGGGTG 82410 ATGT GT ____
 GCA GGAAGA GTG GAA TGGCA
 ||||| ||| ||| |||||
 CCTTCT CAC CTT ACCGT
 C__ TG TCCC
 GAM3645 LOC125488 3' TGGGAAAATGTGTCCCTGGCA 82411 A GGTGAA
 TGG AGAATGTGT TGGCA
 ||| ||||| |||||
 ACC TTTTACACA ACCGT
 C GGG__
 GAM3645 LOC132617 3' TGGAAAATGTGTATGGTG 82412 A_
 TGGGAAGA TGTGTGGTG
 ||||| |||||
 ACCTTTT ACATACCAC
 AC
 GAM3645 LOC147694 3' TGGTGGGAATGTAAAATGGCA 82413 AA_ TGGT
 TGG GAATGTG GAATGGCA
 ||| ||||| |||||
 ACC CTTACAT TTTACCGT
 ACC ____
 GAM3645 LOC148014 3' TGGACGGATGTTTGAATGGC 82414 AGAAT GG
 TGGGA GTGT TGAATGGC
 |||| ||| |||||
 ACCT TACA ACTTACCG
 GCC__ A_
 GAM3645 LOC155376 5' TGGAGATCCTGGGTGAATGG 82415 A ATG T
 TGGGA GA TG GGTGAATGG
 |||| || |||||
 ACCT CT AC CCACTTACC
 _ AGG _
 GAM3645 LOC157931 3' TGGGGGAGGGTGGCAAACATGG 82416 AA ATGT TG ____
 CA TGG GA GTGG A ATGGCA
 ||| || ||| | |||||
 ACC CT CACC T TACCGT
 CC CC__ GT TG
 GAM3645 LOC222233 5' TGGAGATCCTGGGTGAATGG 82415 A ATG T
 TGGGA GA TG GGTGAATGG
 |||| || |||||
 ACCT CT AC CCACTTACC
 _ AGG _
 GAM3645 LOC253532 5' TGGAGATCCTGGGTGAATGG 82415 A ATG T
 TGGGA GA TG GGTGAATGG
 |||| || |||||

ACCT CT AC CCACTTACC
 _ AGG _
 GAM3645 LOC253805 3' TGTGAGAATGTGTGGCTGA 82417 GA _
 TG AGAATGTGTGG TGA
 || ||||| |||
 AC TCTTACACACC ACT
 AC G
 GAM3645 LOC254747 5' TGGAGAGGTCTGTGAGTGGC 82418 A AT G G A
 TGGA GA GT TG TGA TGGC
 ||| || || || |||
 ACCT CT CA AC ACT ACCG
 _ C_ G _ C
 GAM3645 LOC254875 5' TGGAGATCCTGGGTGAATGG 82415 A ATG T
 TGGA GA TG GGTGAATGG
 ||| || || |||||
 ACCT CT AC CCACTTACC
 _ AGG _
 GAM3645 LOC256537 3' GGAAGAATGTTCGGTTGAATGG 82419 G _
 C GGAAGAATGT TGGT GAATGGC
 ||||| ||| |||||
 CCTTCTTACA GCCA CTTACCG
 A A
 GAM3646 DKFZP434A043 3' GTGACAGATTTTAAAATCG 82422 ATCAC
 GTGATAGATTT GTCG
 ||||| |||
 CACTGTCTAAA TAGC
 ATTT_
 GAM3646 IL1RAPL1 3' ATCGGATAGATTTGTCCA 82423 T A A
 ATCG GATAGATTT TC CG
 ||| ||||| || ||
 TAGC CTATCTAAA AG GT
 _ C _
 GAM3647 RECQL5 3' TAAAACAGATGCGTTGA 82426 TGTA
 TAAAACAG GCGTTGA
 ||||| |||||
 ATTTTGTC CGCAACT
 TA_
 GAM3647 FLJ12595 3' TAAAACAGAGTAGGGGTT 82427 T C_
 TAAAACAG GTAG GTT
 ||||| ||| |||
 ATTTTGTC CATC CAA
 T CC
 GAM3647 FLJ20558 5' AAAACAGTGTAACTGAATT 82428 G
 AAAACAGTGTAGC TTGAATT
 ||||| |||||
 TTTTGTCACATTG GACTTAA
 _
 GAM3647 GTF2A2 3' TATAGCACAGTGTAGTCATT 82429 AA _
 TATA ACAGTGTAG CGTT
 ||| ||||| |||

		ATAT TGTCACATC GTAA	
		CG A	
GAM3647 KIAA1577	3'	TATAAACAGTGATTTAGTT 82430	TAGC_
		TATAAACAGTG GTT	
		ATATTTTGTCAC CAA	
		TAAAT	
GAM3647 KIAA1915	5'	TAAACAGTGCGGCTTCCAATT 82431	TA G G
		TAAACAGTG GC TT AATT	
		ATTTTGTCAC CG AG TTAA	
		GC A G	
GAM3647 LOC150848	3'	AAACAGTGTAATAAAT 82432	CGT
		AAACAGTG TAG TGAAT	
		TTTGTCACATT ATTTA	
		—	
GAM3647 LOC157317	3'	TAAGACAGTGTAGGAAT 82433	A CGTT
		TAA ACAGTGTAG GAAT	
		ATT TGTCACATC CTTA	
		C —	
GAM3648 ANXA9	3'	GGATGACCCAGGTACAGATA 82436	CATA _
		GGA GATC GGTACAGATA	
		CCT CTGG CCATGTCTAT	
		A_ GT	
GAM3648 CENTD2	3'	TAGGGTAAAATATACAGATA 82437	ACA TCG
		TAGG TAGA GTACAGATA	
		ATCC ATTT TATGTCTAT	
		C_ TA_	
GAM3648 CENTD2	3'	TAGGGTAAAATATACAGATA 82437	ACA TCG
		TAGG TAGA GTACAGATA	
		ATCC ATTT TATGTCTAT	
		C_ TA_	
GAM3648 P53AIP1	3'	TAGGACATACTACGTACAG 82438	GAT G
		TAGGACATA CG TACAG	
		ATCCTGTAT GC ATGTC	
		GAT _	
GAM3648 ARHGEF3	3'	GGACAAAGGTACAGATAC 82439	TAGATC
		GGACA GGTACAGATAC	
		CCTGT CCATGTCTATG	
		TT_	
GAM3648 CARD6	3'	GGATATAACACTTACAGATA 82440	C ATCGG
		GGA ATAG TACAGATA	

CCT TATT ATGTCTAT
 A GTGA_
 GAM3648 DIS3 3' GGACATGGCTACAGATA 82441 AGATC _
 GGACAT GGT ACAGATA
 ||||| || |||||
 CCTGTA CCG TGTCTAT
 _____ A
 GAM3648 DKFZP434J214 3' AGACATCAGTACAGATA 82442 TAGA
 GGACA TCGGTACAGATA
 |||| | |||||
 TCTGT AGTCATGTCTAT

 GAM3648 H2AFY2 3' TAGGAGTAGTTACAGATA 82443 CA ATCGG
 TAGGA TAG TACAGATA
 |||| || |||||
 ATCCT ATC ATGTCTAT
 C_ A____
 GAM3648 KIAA0280 3' TAGGGCACAGACACAGAT 82444 A TCG
 TAGG CATAGA GTACAGAT
 ||| ||||| |||||
 ATCC GTGTCT CGTGTCTA
 C _____
 GAM3648 KIAA1786 3' GACGTAAGCATACAGATAC 82445 A ATCG
 GAC TAG GTACAGATAC
 ||| || |||||
 CTG ATT TATGTCTATG
 C CG____
 GAM3648 KIAA1904 3' CAGGACGTGGGACACAGAT 82446 ATAGATC _
 TAGGAC GG TACAGAT
 |||| | |||||
 GTCCTG CC GTGTCTA
 CAC_____ T
 GAM3648 LMOD1 3' TAGGGCACACAGATATGGGT 82447 _ C____
 TAGG ACATAGAT GGT
 ||| ||||| |||
 ATCC TGTGTCTA CCA
 CG TAC
 GAM3648 MAP3K2 3' TAGGATCTAAAGAATACAGATA 82448 CA TC
 TAGGA TAGA GGTACAGATA
 |||| ||| |||||
 ATCCT ATTT TTATGTCTAT
 AG C_
 GAM3648 LOC147429 5' GGAGTAAAGTTGTACAGATAC 82449 CA TCG
 GGA TAGA GTACAGATAC
 || |||| | |||||
 CCT ATTT CATGTCTATG
 C_ CAA
 GAM3648 LOC158654 3' GGA CTGGCAGGACAGATAC 82450 ATAGAT T
 GGAC CGG ACAGATAC
 ||| || |||||

			CCTG	GTC TGTCTATG		
			ACC__	C		
GAM3648	LOC255146	3'	TAGGGCTAGGCCACAGATA	82451	ACA	AT GGT
			TAGG TAG C ACAGATA			
			ATCC ATC G TGTCTAT			
			CG_ CG __			
GAM3649	AMH	5'	TGCCCGGCGCCCCCACTCC	82454		_
			TGCCTGGCGCCCCCAC CC			
			ACGGGCCGCGGGGGTG GG			
			A			
GAM3649	BCR	3'	GCTTGGGGCGCCCTCGGGT	82455	C C	CCCCA
			GC TGG GC CCCTCGGGT			
			CG ACC CG GGGAGCCCA			
			A C C__			
GAM3649	BCR	3'	GCTTGGGGCGCCCTCGGGT	82455	C C	CCCCA
			GC TGG GC CCCTCGGGT			
			CG ACC CG GGGAGCCCA			
			A C C__			
GAM3649	CHES1	3'	TGCCTGGTGCCACAAGCTTGGG	82456	C CC CC	C
	T		TGCCTGG GCC CA CT GGGT			
			ACGGACC CGG GT GA CCCA			
			A T_ TC A			
GAM3649	CHST1	5'	GCCGGCTCCATCCTCGGG	82457	T GCCC	C
			GCC GGC CCA CCTCGGG			
			CGG CCG GGT GGAGCCC			
			_ A__ A			
GAM3649	PKP1	5'	CCTGGCGCTTCCACCCTGG	82458	CC	C
			CCTGGCGC CCACCCT GG			
			GGACCGCG GGTGGGA CC			
			AA _			
GAM3649	PTPN7	3'	TGCTTGGGCAGGACCTCGGGT	82459	C C	CCCCAC
			TGC TGG GC CCTCGGGT			
			ACG ACC CG GGAGCCCA			
			A _ TCCT__			
GAM3649	PTPN7	3'	TGCTTGGGCAGGACCTCGGGT	82459	C C	CCCCAC
			TGC TGG GC CCTCGGGT			
			ACG ACC CG GGAGCCCA			
			A _ TCCT__			
GAM3649	PTPN7	3'	TGCTTGGGCAGGACCTCGGGT	82459	C C	CCCCAC
			TGC TGG GC CCTCGGGT			

		ACG ACC CG GGAGCCCA	
		A _ TCCT__	
GAM3649 SIAT4C	5'	TGCCTCGGGCCACCTTTGGGT 82460	_ C CCC CTC
		TGCCT GG GCC ACC GGGT	
		ACGGA CC CGG TGG CCCA	
		G _ ____ AAA	
GAM3649 VCY	5'	TGCCTGGCCTCCCTGTGTACCC 82461	G_ CC_____ CTCG
	GAG	CCTGGC CCC ACC G	
		GGACCG GGG TGG C	
		GA ACACAI GCTC	
GAM3649 BIRC8	5'	TGCATGGCGGGGCTCCTCGGGT 82462	C CCCCCAC
		TGC TGGCG CCTCGGGT	
		ACG ACCGC GGAGCCCA	
		T CCCGA__	
GAM3649 CHST3	5'	TGCCTGGCGCCCTCCCCG 82463	CCAC
		TGCCTGGCGCCC CCTCG	
		ACGGACCGCGGG GGGGC	
		A__	
GAM3649 FLJ14249	3'	TGCCTGGCCTCCCTGGGGGT 82464	GC ACCCTC
		TGCCTGGC CCCC GGGT	
		ACGGACCG GGGG CCCA	
		GA ACC__	
GAM3649 FLJ20967	5'	TGCTGGGCGCCCCTGGGCAGGG 82465	CT CACCCTC
	T	TGC GGCGCCCC GGGT	
		ACG CCGCGGGG CCCA	
		AC ACCCGT_	
GAM3649 KIAA0310	5'	TACCTGAAGCTTCATCCTCGGG 82466	C CCC C
	T	TGCCTGG GC CA CCTCGGGT	
		ATGGA CT CG GT GGAGCCCA	
		T AA_ A	
GAM3649 KIAA1940	5'	TGCCTGGGCCCGGGCATTGGG 82467	C CACCCTC
	T	TGCCTGG GCCC GGGT	
		ACGGACC CGGGG CCCA	
		_ CCCGTAA	
GAM3649 MGC15873	3'	GCCTGGCGCTCCTGTCAGAT 82468	C CACCC
		GCCTGGCGC CC TCGGGT	
		CGGACCGCG GG AGTCTA	
		A AC__	
GAM3649 NCKX3	3'	TGCCTGGCACCTCATGGATGGG 82469	CC CCCTC
	T	TGCCTGGCGCC CA GGGT	

ACGGACCGTGG GT CCCA
 A_ ACCTA
 GAM3649 NMT1 3' TGTCTGCCACTGTCTCGGGT 82470 C G CCCAC
 TG CTG CGC CCTCGGGT
 || ||| ||| |||||
 AC GAC GTG GGAGCCCA
 A G ACA__
 GAM3649 PCBP3 3' CCTGGCGCTCCCCATGGG 82471 _ CCCTC
 CCTGGCGC CCCCA GGG
 ||||| ||| |||
 GGACGCG GGGGT CCC
 A A__
 GAM3649 RAI16 3' TGCCTGGCGCCGCCGTGTACC 82472 _ C_____ CTCG
 CGAGGG TGGCGCC CC ACC GG
 ||||| || ||| ||
 ACCGCGG GG TGG CC
 C GCAC||| GCTC
 GAM3649 RIN3 3' TGCTTGCGCCCTGGCGTACCC 82473 C CC_____ CTCG
 GAG C TGGCGCCC ACC G
 | ||||| ||| |
 G ACCGCGG TGG C
 A ACCGCA||| GCTC
 GAM3649 LOC125058 3' TGTCTGGCTGCCCTCGAG 82474 C GCCCCCA
 TG CTGGC CCCTCGGG
 || ||| |||||
 AC GACCG GGGAGCTC
 A AC____
 GAM3649 LOC145501 3' TGCCGGCGCCCTTGCCACGGGT 82475 T CCAC T
 TGCC GGCGCCC CC CGGGT
 ||| ||||| || |||
 ACGG CCGCGGG GG GCCCA
 _ AAC_ T
 GAM3649 LOC146272 5' GCCTGGCGCCTCCACCCCC 82476 C
 GCCTGGCGCC CCACCCTC
 ||||| |||||
 CGGACGCGG GGTGGGG
 A
 GAM3649 LOC148930 3' TGCCTGGCCCTCTGCTCCAC 82477 _____ C
 TGCCTGGC GC CCCAC
 ||||| || |||
 ACGGACCG CG GGGTG
 GGAGA A
 GAM3649 LOC149664 5' GCCTGGCGCTCCCGCACGGT 82478 _ _ CCTCG
 GCCTGGCGC CCC CAC GGT
 ||||| ||| ||| |||
 CGGACGCG GGG GTG CCA
 A C _____
 GAM3649 LOC150372 5' TGCTAGGCGCCCCTGCAGGGT 82479 CT CACCCTC
 TGC GGCGCCCC GGGT
 || ||||| |||

		ACG CCGCGGGG	CCCA	
		AT ACGT__		
GAM3649	LOC151188 5'	TACCTGGCGCTCTCGCGG	82480	CCCCACC _
		TGCCTGGCGC	CTCG GG	
		ATGGACCGCG	GAGC CC	
		A_____ G		
GAM3649	LOC157543 5'	CCTGGCGCTCCTGCGAGG	82481	CCCCAC _ _
		CCTGGCGC	CCT CG GG	
		GGACCGCG	GGA GC CC	
		A_____ C T		
GAM3649	LOC200081 3'	TGCCTGGCTGTCCCTGGGG	82482	GCCCCCA C
		TGCCTGGC	CCCT GGG	
		ACGGACCG	GGA CCC	
		ACA_____ C		
GAM3649	LOC51162 3'	TGCCTGGCCTTCCGCTCAG	82483	GCCCCCA _
		TGCCTGGC	CC CTCGG	
		ACGGACCG	GG GAGTC	
		GAA_____ C		
GAM3649	LOC51162 3'	TGCCTGGCCTTCCGCTCAG	82483	GCCCCCA _
		TGCCTGGC	CC CTCGG	
		ACGGACCG	GG GAGTC	
		GAA_____ C		
GAM3650	FASN 3'	TTGCATGGCGGGGGTGGGG	82486	TGTTAAA
		TTGCATGGCG	TGGGG	
		AACGTACCGC	ACCCC	
		CCCC__		
GAM3650	LOC153196 5'	TCACATTGTAAATGGGG	82487	TG GGCG
		T CAT TGTTAAATGGGG		
		A GTA ACAATTTACCCC		
		GT _____		
GAM3650	LOC200830 3'	TTACATGGTGGCAGAATGGGG	82488	CGT TA
		TTGCATGG	GT AATGGGG	
		AATGTACC	CG TTACCCC	
		AC_ TC		
GAM3651	ARG2 3'	CATGTCAGTGACAGTGT	82491	CA TG
		TATGTCAG	GC AGTGT	
		GTACAGTC	CG TCACA	
		A_ TG		
GAM3651	CA1 3'	TATGTCAGAAGCAGGGCTGTGT	82492	C TGA__
		TATGTCAG	AGC GTGT	

			ATACAGTC TCG	CACA	
			T TCCCGA		
GAM3651	CASP10	3'	TGCAGAGCAGCTGAGTGT	82493	C_
			TGT AGCAGCTGAGTGT		
			ACG TCGTCGACTCACA		
			TC		
GAM3651	CASP10	3'	TGCAGAGCAGCTGAGTGT	82493	C_
			TGT AGCAGCTGAGTGT		
			ACG TCGTCGACTCACA		
			TC		
GAM3651	CASP2	3'	TATGCCAGCTGGAAGTGT	82494	AGCT
			TATGTCAGC GAGTGT		
			ATACGGTCG TTCACA		
			ACC_		
GAM3651	CASP2	3'	TATGCCAGCTGGAAGTGT	82494	AGCT
			TATGTCAGC GAGTGT		
			ATACGGTCG TTCACA		
			ACC_		
GAM3651	CHES1	3'	TGTAAAACAGCTGAGTGT	82495	C_
			TGT AGCAGCTGAGTGT		
			ACA TTGTCTGACTCACA		
			TT		
GAM3651	HBD	5'	TATGTCAGAAGAAAGTGT	82496	C CT
			TATGTCAG AG GAGTGT		
			ATACAGTC TC TTCACA		
			T T_		
GAM3651	ICAM1	3'	CATGACCGCTGAGTGT	82497	TCA A
			TATG GC GCTGAGTGT		
			GTAC TG CGACTCACA		
			_ G		
GAM3651	PCMT1	3'	ATCTGAACAGCTGAGTGT	82498	_
			GTC AGCAGCTGAGTGT		
			TAG TTGTCTGACTCACA		
			AC		
GAM3651	SLC22A5	3'	TATGTAGCCTCTGAGTGT	82499	C AG
			TATGT AGC CTGAGTGT		
			ATACA TCG GACTCACA		
			_ GA		
GAM3651	TEK	3'	TATATCAGTGCAAAGTGT	82500	CA T
			TATGTCAG GC GAGTGT		

		ATATAGTC CG TTCACA	
		A_ T	
GAM3651	TRPS1	3' TATGTCAAAAAAGGAGTGT 82501	C CT
		TATGTCAG AG GAGTGT	
		ATACAGTT TT CTCACA	
		T TC	
GAM3651	CGI-01	3' CATGTAGCTGAGTGT 82502	CAGC
		TATGT AGCTGAGTGT	
		GTACA TCGACTCACA	

GAM3651	CSMD1	3' TATGCCAGTAGACAAGGT 82503	C C T
		TATGTCAG AG TGAG GT	
		ATACGGTC TC GTTC CA	
		A T _	
GAM3651	DKFZP434I092	3' CATGTCAGCAGAATCTGGT 82504	___ A
		TATGTCAGCAG CTG GT	
		GTACAGTCGTC GAC CA	
		TTA _	
GAM3651	FLJ12649	3' TATCTCAAGCCTGAGTGT 82505	G _ AG
		TAT TCA GC CTGAGTGT	
		ATA AGT CG GACTCACA	
		G T _	
GAM3651	KIAA0337	3' TATGTCAACGGGCAATGT 82506	A_ TG
		TATGTCAGC GC AGTGT	
		ATACAGTTG CG TTACA	
		CC _	
GAM3651	KIAA0905	3' TATATCAGCAGAAATAGTGT 82507	CTG_
		TATGTCAGCAG AGTGT	
		ATATAGTCGTC TCACA	
		TTTA	
GAM3651	KIAA1841	3' TACGTGTAAACTGAGTGT 82508	CAGC
		TATGT AGCTGAGTGT	
		ATGCA TTGACTCACA	
		CAT_	
GAM3651	KIAA1958	5' CATGTCAAACAGGGTGT 82509	_ CTGA
		TATGTCAG CAG GTGT	
		GTACAGTT GTC CACA	
		T C_	
GAM3651	KIAA1958	3' TATGTCAATGACTAGTGT 82510	CA G
		TATGTCAG GCT AGTGT	

			ATACAGTT TGA TCACA		
			AC _		
GAM3651	MDS033	3'	ATGTCAGCAGAGAACGT 82511	CT	
			ATGTCAGCAG GAGTGT		
			TACAGTCGTC CTTGCA		
			T_		
GAM3651	MGC14859	3'	TATGGCAGCGGCCACTGT 82512	T A AG	
			TATG CAGC GCTG TGT		
			ATAC GTCG CGGT ACA		
			C C G_		
GAM3651	MGC4368	3'	TATGCTGAAGCTGAGTGT 82513	CAGC	
			TATGT AGCTGAGTGT		
			ATACG TCGACTCACA		
			ACT_		
GAM3651	TBC1D2	5'	ATGTCAGCATGATGT 82514	GC G	
			ATGTCAGCA TGA TGT		
			TACAGTCGT ACT ACA		
			— —		
GAM3651	LOC120114	3'	TATGTCATCAGAACTGT 82515	G CT G	
			TATGTCA CAG GA TGT		
			ATACAGT GTC TT ACA		
			A T_ G		
GAM3651	LOC151304	3'	TATGTCAGCATGCCGAGT 82516	_	
			TATGTCAGCA GCTGAGT		
			ATACAGTCGT CGGCTCA		
			A		
GAM3651	LOC158314	3'	CATGTCAGCAGCGTGT 82517	TGA	
			TATGTCAGCAGC GTGT		
			GTACAGTCGTCG CACA		
			—		
GAM3651	LOC222865	3'	TATGTCAGTGGCTGGACTGT 82518	CA _ G	
			TATGTCAG GCTG A TGT		
			ATACAGTC CGAC T ACA		
			AC C G		
GAM3651	LOC90321	3'	TATGCCAGCAGTTAAATGT 82519	C	
			TATGTCAGCAG TGAGTGT		
			ATACGGTCGTC ATTTACA		
			A		
GAM3651	LOC92080	3'	TATGCCAGAAATGAGTGT 82520	C C	
			TATGTCAG AG TGAGTGT		

			ATACGGTC TT ACTCACA		
			— T		
GAM3652	COX15	3'	AGGTCACAGAACTT 82523	CCAT CT	
			AGG TC GCAGAACTT		
			TCC AG TGTCTTTGAA		
			— —		
GAM3652	TAX1BP1	3'	CAAGGTCAACAGAACTT 82524	C TTCCT	
			TAAGG CA GCAGAACTT		
			GTTCC GT TGTCTTTGAA		
			A —		
GAM3652	UPF3B	3'	TAAGGCCATCTGGACT 82525	TC CAGAA	
			TAAGGCCAT CTG ACT		
			ATTCCGGTA GAC TGA		
			— C —		
GAM3652	UPF3B	3'	TAAGGCCATCTGGACT 82525	TC CAGAA	
			TAAGGCCAT CTG ACT		
			ATTCCGGTA GAC TGA		
			— C —		
GAM3652	ZNF217	5'	TAAGGCCACTTGTAAGA 82526	CC C	
			TAAGGCCATT TG AGA		
			ATTCCGGTGA AT TCT		
			AC _		
GAM3652	CTPS2	3'	TAAGGCCAGTTCCTGGAA 82527	_ CA	
			TAAGGCCA TTCCTG GAA		
			ATTCCGGT AAGGAC CTT		
			C —		
GAM3652	DKFZP564C1940	3'	TAAGGCCACTTTTGGGTAGA 82528	CC C_	
			TAAGGCCATT TG AGA		
			ATTCCGGTGA AC TCT		
			AA CCA		
GAM3652	FLJ10846	3'	TAAGACCATTTCAGCCAAGA 82529	CT _	
			TAAGGCCATTC GC AGA		
			ATTCTGGTAAG CG TCT		
			T_ GT		
GAM3652	FLJ12700	3'	CAAGGCCATCCGGAGACTT 82530	CTGCA A	
			TAAGGCCATTC GA ACTT		
			GTTCCGGTAGG CT TGAA		
			C_ C		
GAM3652	FLJ14564	3'	GGCCATGCAGAAAGGACTT 82531	TTCC _	
			GGCCA TGCAGAA ACTT		

		CCGGT ACGTCTT TGAA		
		_____ TCC		
GAM3652	FLJ25415	3' AGGTTTATTCCTGCATTCTT	82532	CC_ GAAA
		AGG ATTCCTGCA CTT		
		TCC TAAGGACGT GAA		
		AAA AA_		
GAM3652	MAEA	3' CAAGGCCTCTGCAGAAA	82533	ATTC
		TAAGGCC CTGCAGAAA		
		GTTCCGG GACGTCTTT		
		A_		
GAM3652	RNF29	3' GGCTATTTTTGCAGAAATCCT	82534	C CC _
		GGC ATT TGCAGAAA CTT		
		CCG TAA ACGTCTTT GGA		
		A AA A		
GAM3652	LOC150406	3' AGGCTATACAGGACAGAAACTT	82535	C TCCT_
		AGGC AT GCAGAAACTT		
		TCCG TA TGTCTTTGAA		
		A TGTCC		
GAM3653	LAMP1	3' TCTCTACTGTTGTAATGT	82538	AACATAA
		TCTCTAT TTGTAATGT		
		AGAGATG AACATTACA		
		AC_		
GAM3653	CDC14A	3' TCTCCATAACATAGTTTCAGTG	82539	A GTAAT
		TCTCTATAACATA TT GTG		
		AGAGGTATTGTAT AA CAC		
		C AGT_		
GAM3653	CYorf15B	3' TCTTTAAACATAATTGTA	82540	C T
		TCT TA AACATAATTGTA		
		AGA AT TTGTATTAACAT		
		A _		
GAM3653	KIAA1155	3' TCCATAATTCTGTAATGTG	82541	CATAA
		TCTATAA TTGTAATGTG		
		AGGTATT GACATTACAC		
		AA_		
GAM3653	LOC163404	3' TCTTTTAACATAATTGCAATG	82542	CTA
		TCT TAACATAATTGTAATG		
		AGA ATTGTATTAACGTTAC		
		AA_		
GAM3654	ADCY7	3' CTGCTGCTCCCCGCCTTCTTGC	4733	A_ CC C
		TTGCTGCT CTGCC TCT GC		

GACGACGA GGCGG AGA CG
 GG A_ A
 GAM3654 BMP1 3' TCCTGCTGACATTCCTCTTGC 82545 CT TGC C
 TCTTGCTG AC CCCTCT GC
 ||||| || ||||| ||
 AGGACGAC TG GGGAGA CG
 _ TAA A
 GAM3654 CASP4 5' TCCTGCCATACGTTGCTTCTCT 82546 C _ CC C
 TGC TCTTGCTG TAC TGC CTCT GC
 ||||| || || ||||| ||
 AGGACGGT ATG ACG GAGA CG
 _ CA AA A
 GAM3654 CREBL2 5' TCTGGCTGCCTCCTCTCTCGC 82547 T ACTG _
 TCT GCTGCT CC CCTCTCGC
 || ||||| || ||||| ||
 AGA CGACGG GG GGAGAGCG
 C A_ A
 GAM3654 DBCCR1 5' TCTCGCTGTTGCTCGCTCG 82548 CTAC CCCT
 TCTTGCTG TGC CTCG
 ||||| || ||||| ||
 AGAGCGAC ACG GAGC
 A_ AGC_
 GAM3654 ERBB2IP 3' TCTTGCTGTCTTCCCGCT 82549 CTA G T
 TCTTGCTG CT CCCC CT
 ||||| || ||||| ||
 AGAACGAC GA GGGG GA
 A_ A C
 GAM3654 IHPK2 5' TTGTCCGTGTGTCCCTCTCG 82550 _ CTAC C
 TTG CTG TG CCCTCTCG
 || || || ||||| ||
 AAC GGC AC GGGAGAGC
 A AC_ A
 GAM3654 LDHB 5' TCTGGCTGCTGGCCCCTCTTGC 82551 T ACT C
 TCT GCTGCT GCCCCTCT GC
 || ||||| ||||| ||
 AGA CGACGA CGGGGAGA CG
 C C_ A
 GAM3654 MDS1 5' TCTTTTGCTCTCCCTCTCG 82552 GC A GC
 TCTT TGCT CT CCCTCTCG
 || || || || ||||| ||
 AGAA ACGA GA GGGAGAGC
 A_ _ _
 GAM3654 PCDH7 5' TCCTGCTGCTGCTGCTACT 82553 A CC
 TCTTGCTGCT CTGC CT
 ||||| || || ||||| ||
 AGGACGACGA GACG GA
 C AT
 GAM3654 PCDH7 5' TCCTGCTGCTGCTGCTACT 82553 A CC
 TCTTGCTGCT CTGC CT
 ||||| || || ||||| ||

AGGACGACGA GACG GA
 C AT
 GAM3654 PCDH7 5' TCCTGCTGCTGCTGCTACT 82553 A CC
 TCTTGCTGCT CTGC CT
 ||||| ||| ||
 AGGACGACGA GACG GA
 C AT
 GAM3654 S100B 3' CCTTGCTGTCTGCTTTCTTGC 82554 CTA CCC C
 TCTTGCTG CTGC TCT GC
 ||||| ||| ||| ||
 GGAACGAC GACG AGA CG
 A__ AA_ A
 GAM3654 ST3GALVI 5' TCCAGCCGGCTGCTGCCTCTCT 82555 T _ A C
 CGC TCT GCTG CT CTGCC CTCTCGC
 ||| ||| || ||||| |||||
 AGG CGGC GA GACGG GAGAGCG
 T C C A
 GAM3654 DKFZP566D1346 5' TCTTCCTCTTGCTCCTCTCGC 82556 G G AC C
 TCTT CT CT TGC CCTCTCGC
 ||| || || ||| |||||
 AGAA GA GA ACG GGAGAGCG
 G _ _ A
 GAM3654 EPB41L1 3' TCTTGCTGCTGTGACTTCTCTT 4742 ACT CC C
 GC TCTTGCTGCT GC CTCT GC
 ||||| || ||| ||
 AGAACGACGA TG GAGA CG
 CAC AA A
 GAM3654 FLJ10846 5' TCTGCTGCTGCTGCTTCTGC 82557 T A CCC C
 TCT GCTGCT CTGC TCT GC
 ||| ||||| ||| ||| ||
 AGA CGACGA GACG AGA CG
 _ C A__ _
 GAM3654 FLJ13964 5' TCTTGCTGTTACTTCCC 82558 C GC
 TCTTGCTG TACT CCC
 ||||| ||| |||
 AGAACGAC ATGA GGG
 A A_
 GAM3654 KIAA0040 5' TCTGGCTGCTGGCCCCTCTTGC 82551 T ACT C
 TCT GCTGCT GCCCCTCT GC
 ||| ||||| ||||| ||
 AGA CGACGA CGGGGAGA CG
 C C__ A
 GAM3654 KIAA0446 3' TTGCTGCTCCTGCTCCCT 4748 A _
 TTGCTGCT CTGC CCCT
 ||||| ||| |||
 AACGACGA GACG GGGA
 G A
 GAM3654 KIAA0844 5' TTGCTGCTGCTGCAGCCGC 82559 A CCCTC
 TTGCTGCT CTGC TCGC
 ||||| ||| |||

AACGACGA GACG GGCG
 C TC___
 GAM3654 KIAA1028 3' TCTGCTGCTGTTGCTGATTCT 82560 T AC CCC_
 TCT GCTGCT TGC TCT
 ||| ||||| ||| |||
 AGA CGACGA ACG AGA
 _ CA ACTA
 GAM3654 SYNE-2 5' TTGCTCGCTCTCCCTCTCGC 82561 _ A GC
 TTGCT GCT CT CCCTCTCGC
 ||||| ||| || |||||
 AACGA CGA GA GGGAGAGCG
 G _ _
 GAM3654 LOC201771 5' TGCTTCTGGCTCCTCTCGC 82562 A _ C
 TGCT CTG C CCTCTCGC
 ||||| ||| || |||||
 ACGA GAC G GGAGAGCG
 A C A
 GAM3654 LOC202284 5' CTGCTGCTGTGGAGTCTTGC 82563 AC CCCC C
 TTGCTGCT TG TCT GC
 ||||| || ||| ||
 GACGACGA AC AGA CG
 C_ CTC_ A
 GAM3654 LOC221954 3' TCTTGCTGTGTTGCCCACT 82564 CTAC CT_
 TCTTGCTG TGCCC CT
 ||||| ||||| ||
 AGAACGAC ACGGG GA
 ACA_ TGT
 GAM3654 LOC90495 3' TCTTTTGCTCACTGCCCTCT 82565 GC _ C
 TCTT TGCT ACTGCCC TCT
 ||||| ||||| ||||| |||
 AGAA ACGA TGACGGG AGA
 A_ G _
 GAM3654 LOC91960 5' CTGCTGGACGGCCTCCTCTCGC 82566 CT T _
 TTGCTG AC GCC CCTCTCGC
 ||||| || ||| |||||
 GACGAC TG CGG GGAGAGCG
 C_ C A
 GAM3655 ADAMTS5 3' AATATACTTAGATTTTTTA 82569 GA
 AATAT ACTTAGATTTTTTA
 ||||| |||||
 TTATA TGAATCTAAAAAAT
 _
 GAM3655 EGFL5 5' TAAAATATGACATGATTTTTT 82570 ACTTA
 TAAAATATGA GATTTTTT
 ||||| |||||
 ATTTTATACT CTAAAAA
 GTA_
 GAM3655 ARHGAP11A 3' TAAAATATAAATTTAGACAGAT 82571 C TT_
 TTA TAAAATATGAA TTAGAT TTTA
 ||||| ||||| ||||| |||

		ATTTTATATTT AATCTG AAAT	
		A TCT	
GAM3655 KIAA0826	5'	AATATGAACTGATTTTT 82572	TA
		AATATGAACT GATTTTT	
		TTATACTTGA CTAAAAA	
		—	
GAM3655 LOC149086	3'	AAATATGTCTAGATTTTTTA 82573	AAC
		AAATATG TTAGATTTTTTA	
		TTTATAC GATCTAAAAAAT	
		A_	
GAM3656 AP1B1	3'	TGAGGAATGTATCACAGGCAGT 82576	A A CAA
		TGAGGAAT TA TATAG CAGT	
		ACTCCTTA AT GTGTC GTCA	
		C A C_	
GAM3656 COPA	3'	TGAGAAATATGAGAACAATAGT 82577	AATAT C
		TGAGGAATAT AGCAA AGT	
		ACTCTTTATA TTGTT TCA	
		CTC_ A	
GAM3656 OLIG2	3'	TGAGGAATGCACACAGC 82578	ATA
		TGAGGAAT ATATAGC	
		ACTCCTTA TGTGTCG	
		CG_	
GAM3656 PAIP2	3'	TGAGAAATATGCTTAACAG 82579	AATATA _
		TGAGGAATAT GC AACAG	
		ACTCTTTATA CG TTGTC	
		_____ AA	
GAM3656 TCTA	3'	GAGGAATATGAGTAGGACAGT 82580	AATA CA
		GAGGAATAT TAG ACAGT	
		CTCCTTATA ATC TGTCA	
		CTC_ C_	
GAM3656 FLJ10517	3'	TGAAGAATGTAATGAACAG 82581	A ATAGC
		TGAGGAAT TAAT AACAG	
		ACTTCTTA ATTA TTGTC	
		C C_	
GAM3656 FLJ23550	3'	TGAGGAATATTAATACGATGAC 82582	_ AGCA
	AGT	TGAGGAATAT AATAT ACAGT	
		ACTCCTTATA TTATG TGTCA	
		A CTAC	
GAM3656 PRO0149	5'	TGAGGAACTGTAATAAATAG 82583	— —
		TGAGGAAT ATAATA TAG	

		ACTCCTTG TATTAT ATC	
		ACAT T	
GAM3656	LOC170063 3'	TGAGGAATATGCTTCAACAGT 82584 TGAGGAATAT CAACAGT ACTCCTTATA GTTGTCA CGAA__	AATATAG
GAM3656	LOC51191 3'	TAAGGAATATGATGTAGGCA 82585 TGAGGAATAT AT TAG CA ATTCCTTATA TA ATC GT C C C	A A _
GAM3657	DKFZp761K1824 3'	ATTATTGGTGATAAATCATTA 82588 ATTATTG ATAAATCATTGA TAATAAC TATTAGTAATT CAC	ATA
GAM3657	KIAA1043 3'	TACTATTGATAATAAAACCA 82589 TATTATTGATAATAAA TCA ATGATAACTATTATTT GGT T	_
GAM3657	RERG 3'	TAATGATCAATAGATCATTGA 82590 TA TGAT AATA ATCATTGA AT ACTA TTAT TAGTAACT T G C	T _ A
GAM3658	ADAM11 3'	GGGTGGGGACGTGGGCAGGGG 82593 GGG GGAC GGGCAGGGG CCC CCTG CCCGTCCCC ACC CA_	GAA ATG
GAM3658	ADCY6 3'	CAGGGGAAGGGCATGGCTGG 82594 TAGGGGAAGG CATGG GG GTCCCCTTCC GTACC CC C GA__	A GGCAG
GAM3658	ADCY6 3'	CAGGGGAAGGGCATGGCTGG 82594 TAGGGGAAGG CATGG GG GTCCCCTTCC GTACC CC C GA__	A GGCAG
GAM3658	AR 5'	GGGGAAGGCAGGGTGGGGG 82595 GGGGAAGG CA GGG GGGG CCCCTTCC GT CCC CCCC _ _ AC_	A T GCA
GAM3658	ARHG 3'	GGGGGGAGGGCAGGG 82596 GGGG GGA GGGCAGGG 	AA CATG

CCCC CCT CCCGTCCC

GAM3658 ARHG 3' GGGGGGAGGGCAGGG 82596 AA CATG
GGGG GGA GGGCAGGG
|||| ||| |||||||
CCCC CCT CCCGTCCC

GAM3658 ARHG 3' GGGGGGAGGGCAGGG 82596 AA CATG
GGGG GGA GGGCAGGG
|||| ||| |||||||
CCCC CCT CCCGTCCC

GAM3658 ATRN 3' TAGGGTGACACGGGGGTGGGG 82597 GAAG CA
TAGGG GACATGGGG GGGG
|||| ||||||| |||
ATCCC CTGTGCCCC CCCC
A__ CA

GAM3658 AVP 5' TAGGAGCTGTGGGGCAGGG 82598 AAGGACA
TAGGGG TGGGGCAGGG
|||| |||||||
ATCCTC ACCCGTCCC
GAC__

GAM3658 BRF1 3' GGAGGAGGCAGGGGTGGGG 82599 A A T CA
GGGG AGG CA GGGG GGGG
|||| ||| || ||| |||
CCTC TCC GT CCCC CCCC
C _ _ AC

GAM3658 CALM3 3' AGGGGAAGCAGGGGGTGGGG 82600 GA T CA
AGGGGAAG CA GGGG GGGG
|||||| || ||| |||
TCCCCTTC GT CCCC CCCC
_ C AC

GAM3658 CARKL 5' CAGGGGGGCGGGGCAGGG 82601 AA ACA
TAGGGG GG TGGGGCAGGG
|||| || |||||||
GTCCCC CC GCCCGTCCC

GAM3658 CENTD2 5' GGGGGAGGGTGGACAGGG 82602 A ACATG
GGGG AGG GGGCAGGG
|||| ||| |||||||
CCCC TCC CCTGTCCC
C CA__

GAM3658 CLTCL1 3' TAGGGGAAGCTGGCAGGG 82603 GACATGG
TAGGGGAAG GGCAGGG
|||||| |||||
ATCCCCTTC CCGTCCC
GA__

GAM3658 COL5A3 3' GGGGAGGTGAGGGGCAGGG 82604 A ACAT
GGGGA GG GGGGCAGGG
|||| || |||||||

		CCCCT CC CCCC GTCCCC		
		_ ACT_		
GAM3658	DOK1	3' AGGGAAGG GATGGCTTTGGGG	82605	AC GGCA
		GGGGAAGG ATGG GGGG		
		TCCCTTCC TACC CCCC		
		C_ GAAA		
GAM3658	DRPLA	3' GGGGGAGGAGAAAAGCAGGGG	82606	A CAT
		GGGG AGGA GGGGCAGGGG		
		CCCC TCCT TTTCGTCCCC		
		C CT_		
GAM3658	DVL3	3' AGGGCAGGCATGGGGCAGGGG	82607	A A
		GGGG AGG CATGGGGCAGGGG		
		TCCC TCC GTACCCCGTCCCC		
		G _		
GAM3658	EGR3	3' AGGGGAAGGAGTGGGAGGGCAG	82608	CAT__
	GGG	AGGGGAAGGA GGGGCAGGGG		
		TCCCCTTCT TCCCGTCCCC		
		CACCC		
GAM3658	ELAVL3	3' GGGGGCAGGAGGATGGGGCGGG	82609	A_ C_ A
	GGC	GGG AGGA ATGGGGC GGGG C		
		CCC TCCT TACCCCG CCCC G		
		CG CC C		
GAM3658	ENTPD2	3' GGGGGAGGGATGGGGCAG	82610	A AC
		GGGG AGG ATGGGGCAG		
		CCCC TCC TACCCCGTC		
		C C_		
GAM3658	FE65L2	3' CAGGGGGAGGGGCAGG	82611	AAG CAT
		TAGGGG GA GGGGCAGG		
		GTCCCC CT CCCC GTCC		
		— —		
GAM3658	FE65L2	3' CAGGGGGAGGGGCAGG	82611	AAG CAT
		TAGGGG GA GGGGCAGG		
		GTCCCC CT CCCC GTCC		
		— —		
GAM3658	FXR2	3' GGGAGGAGGGATAGCAGGGG	82612	A CAT _
		GGGA GGA GGG GCAGGGG		
		CCCT CCT CCC CGTCCCC		
		_ _ TAT		
GAM3658	JTB	5' GGAGGAAGGGCCGGCGGGG	82613	_ ACATGG A
		GG GGAAGG GGC GGGG		

			CC CCTTCC CCG CCCC		
			T CGG__ C		
GAM3658	JUNB	3'	AGGGGAGGGCAGGGGGCGGGGG 82614	A A T A	
			AGGGGA GG CA GGGGC GGGG		
			TCCCCT CC GT CCCC G CCCC		
			C _ C C		
GAM3658	KCNJ4	3'	GGGGAAGGGTGGTGGATCCGGG 82615	ACA_ GCA	
	G		GGGGAAGG TGGG GGGG		
			CCCCTTCC ACCT CCCC		
			CACC AGG		
GAM3658	KRT17	3'	GGGGAAGGGACTGAAGCAGGGG 82616	_ A	
			GGGGAAGG AC TGGGGCAGGGG		
			CCCCTTCC TG ACTTCGTCCCC		
			C _		
GAM3658	LAMB2	3'	GGGGTAGGCCTTGGGCAGGGG 82617	A ACATG	
			GGGG AGG GGGCAGGGG		
			CCCC TCC CCGTCCCC		
			A GGAA_		
GAM3658	LYAAT1	3'	GGGGACACATGGGGCAGGGG 82618	AGG	
			GGGGA ACATGGGGCAGGGG		
			CCCCT TGTACCCCGTCCCC		
			G_		
GAM3658	MB	3'	GGGGGTGGGAGCGGCAGGGG 82619	AA ACAT _	
			GGGG GG GG GGCAGGGG		
			CCCC CC TC CCGTCCCC		
			CA C__ G		
GAM3658	MPP2	3'	GGGGAGGGGTGGCAGGG 82620	A ACAT _	
			GGGGA GG GG GGCAGGG		
			CCCCT CC CC CCGTCCC		
			_ _ _ A		
GAM3658	MSI1	3'	GGGGGCAGCAGGGCAGGG 82622	AA A TG	
			GGGG GG CA GGGCAGGG		
			CCCC TC GT CCGTCCC		
			CG _ _		
GAM3658	MSI1	3'	GGGGCAAGGGCGAAGAGGGG 82621	_ ACA C	
			GGGG AAGG TGGGG AGGGG		
			CCCC TTCC GCTTC TCCCC		
			G C__ _		
GAM3658	NEFH	3'	GGGGAGGGCATGGGGGCAGGGG 82623	A A _	
			GGGGA GG CATGGGG CAGGGG		

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CCCCT CC GTACCCC GTCCCC
  C _ C
GAM3658 NGFR 3' GGGGTGGGGGGCAAGAG 82624 AA ACAT
      GGGG GG GGGGCAGGGG
      ||| || |||||
      CCCC CC CCCC GTTCTC
      A _
GAM3658 NHLH1 3' GGGAAAGGATATGGTGTGG 82625 C GGCAG
      GGGGAAGGA ATGG GG
      ||||| ||| ||
      CCCTTTCCT TACC CC
      A ACA_
GAM3658 NKX2H 5' AGGGGAAGGAGGCGGGG 82626 CATGG A
      AGGGGAAGGA GGC GGG
      ||||| ||| |||
      TCCCCTTCCT CCG CCC
      _ C
GAM3658 PACSIN1 3' GGAGGAAGGGAAGCAGGGCAGG 82627 _ ACAT_
      GG GG GGAAGG GGGGCAGGGG
      || ||| |||||
      CC CCTTCC TCCCGTCCCC
      T CTTCG
GAM3658 PKM2 3' GGGGAAGGGGGTGGGACAGGGG 82628 ACA
      GGGGAAGG TGGGGCAGGGG
      ||||| |||||
      CCCCTTCC ACCCTGTCCCC
      CCC
GAM3658 PLA2G2D 3' GGGAGAGGTGGGGCAGGGG 82629 GA ACA
      GGG AGG TGGGGCAGGGG
      ||| ||| |||||
      CCC TCC ACCCGTCCCC
      TC _
GAM3658 POU3F1 3' GGGGGGGCAGGGGCGGGG 82630 AA A T A
      GGGG GG CA GGGGC GGG
      ||| ||| ||| |||
      CCCC CC GT CCCC G CCC
      C _ _ C
GAM3658 PRKACG 3' AGGAAGGCATGGGGCGGGG 82631 A A
      GGGAAGG CATGGGGC GGGG
      ||||| ||||| |||
      TCCTTCC GTACCCCG CCCC
      _ C
GAM3658 PTGDS 3' GGGGAGCCGGGGCAGGGG 82632 AGGACA
      GGGGA TGGGGCAGGGG
      ||| |||||
      CCCCT GCCCGTCCCC
      CG_
GAM3658 PTPRG 5' AGGGGAGGGGAGAGGCAGGGG 82633 A ACAT
      AGGGGA GG GGGGCAGGGG
      ||||| ||| |||||

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			TCCCCT CC CTCCGTCCCC		
			C CT__		
GAM3658	RAB4A	5'	GGGGAAGGCCTGGGGCGGGGG 82634	ACA	A
			GGGGAAGG TGGGGC GGGG		
			CCCCTTCC ACCCCG CCCC		
			CGG C		
GAM3658	S100A5	3'	AGGGAGAGGAGGGCAGGGG 82635	GA	CATG
			AGGG AGGA GGGCAGGGG		
			TCCC TCCT CCCGTCCCC		
			TC ____		
GAM3658	SDC4	3'	AGGGGAAGGGCACTGGGG 82636	A	_
			AGGGGAAGG CA TGGGG		
			TCCCCTTCC GT ACCCC		
			C G		
GAM3658	SLC8A2	3'	TAGGGGAAGGGAGACTTTGGGG 82637	ACAT	A__
			TAGGGGAAGG GGGGC GGGG		
			ATCCCCTTCC CTCTG CCCC		
			____ AAA		
GAM3658	SNRP70	3'	GGGGGAGGGGATGACAGCAAGG 82638	A	AC _
	G		GGGG AGG ATGG GGCAGGGG		
			CCCC TCC TACT TCGTTCCC		
			C CC G		
GAM3658	SOLH	3'	AGGGGAAGGAGGGGGGCGGGGG 82639	CAT	A
			AGGGGAAGGA GGGGC GGGG		
			TCCCCTTCCT CCCC G CCCC		
			CC_ C		
GAM3658	SOX10	3'	GGGGGCAGGGGCTGGGCGGGGG 82640	A_	ACATG A
			GGGG AGG GGGC GGGG		
			CCCC TCC CCG CCCC		
			CG CCGA_ C		
GAM3658	TAF4	3'	AGGGGAGGGGAGGGCAGGGG 82641	A	ACAT
			AGGGGA GG GGGCAGGGG		
			TCCCCT CC TCCGTCCCC		
			C C__		
GAM3658	UBE2L3	3'	GGAGGAGGGGGTTCAGCAGGGG 82642	A	ACAT ____
			GGGG AGG GGG GCAGGGG		
			CCTC TCC CCC CGTCCCC		
			C ____ AGT		
GAM3658	VASP	3'	AGGGGAGTCCCTGGGGTGGGGG 82643	A	GACA CA
			AGGGGA G TGGGG GGGG		

TCCCCT C ACCCC CCCC
_ AGGG AC
GAM3658 VTN 3' GGGGAAGGAGATGGGAGG 82644 C GC
GGGGAAGGA ATGGG AGG
||||||| ||||| |||
CCCCTTCCT TACCC TCC
C _
GAM3658 YWHAE 3' AGGGGAAGGAGGTAGGG 82645 CATG GC
AGGGGAAGGA GG AGGG
||||||| || |||||
TCCCCTTCCT CC TCCC
_ _ A_
GAM3658 7h3 3' GGGGGGGGGGCAAGG 82646 AA ACAT
GGGG GG GGGGCAGGG
|||| || |||||||
CCCC CC CCCCCGTTCC
_ _
GAM3658 APELIN 3' GGGGAATGGTGCAGCAGGGG 82647 _ ACA G
GGGGAA GG TG GGCAGGGG
||||| || || |||||||
CCCCTT CC AC TCGTCCCC
A _ G
GAM3658 BCL2L1 3' GGAACAAGTGTGGGGTGGGGG 82648 G CA_ CA
GGAA GA TGGGG GGGG
|||| || ||||| |||||
CCTT TT ACCCC CCCC
G CAC AC
GAM3658 C21orf57 5' GGGGAGGGACAGGAGAGGGG 82649 A T C
GGGGA GGACA GGGG AGGGG
||||| ||||| ||||| |||||
CCCCT CCTGT CCTC TCCCC
C _ _
GAM3658 C22orf4 3' GGGGTGGGGACACGGAAGGCAG 82650 AA_ _
GGG GGGG GGACATGG GGCAGGGG
|||| ||||||| |||||||
CCCC CCTGTGCC CCGTCCCC
ACC TT
GAM3658 Cab45 5' GGGAGGGGGCAGGGGCAGGGG 82651 A A T
GGGA GG CA GGGGCAGGGG
|||| || || |||||||
CCCT CC GT CCCCCGTCCCC
C C _
GAM3658 Cab45 5' GGGAGGGGGCAGGGGCAGGGG 82651 A A T
GGGA GG CA GGGGCAGGGG
|||| || || |||||||
CCCT CC GT CCCCCGTCCCC
C C _
GAM3658 CASKIN1 3' GGGGGTGCGGTGGGGCAGGGG 82652 AA_ ACA
GGGG GG TGGGGCAGGGG
|||| || |||||||

CCCC CC ACCCCGTCCCC
 CACG ____
 GAM3658 CBX8 3' AGGGGCTGGTGGGGTGGGGG 82653 AA ACA CA
 AGGGG GG TGGGG GGGG
 |||| || |||| ||||
 TCCCC CC ACCCC CCCC
 GA ____ AC
 GAM3658 CENTG1 3' GGGGAAGGGGCAGGG 82654 GGACAT
 GGGGAA GGGGCAGGG
 ||||| |||||
 CCCCTT CCCCCGTCCC

 GAM3658 CIC 3' GGGGAAGGGGGCAAGGGCAGGG 82655 ACAT_
 G GGGGAAGG GGGGCAGGGG
 ||||| |||||
 CCCCTTCC TCCCGTCCCC
 CCCGT
 GAM3658 CNNM2 3' GGGAGGAGGAGCAGG 82656 A CAT
 GGGA GGA GGGGCAGG
 ||| ||| |||||
 CCCT CCT CCTCGTCC

 GAM3658 CNTNAP1 3' GGGGAGAGGCAGGACTGGGG 82657 _ A TG A
 GGGGA AGG CA GGGC GGGG
 |||| ||| || |||||
 CCCCT TCC GT CCTG CCCC
 C _ _ A
 GAM3658 DKFZp547M072 3' TAGGGCAGGGGCACTGAGAGGC 82658 GA A_ _
 AGGGG AGGG AGG CAT GGGGCAGGGG
 ||| ||| ||| |||||
 TCCC TCC GTG CTCCGTCCCC
 G_ CC ACT
 GAM3658 DKFZP564O0423 3' GGAGGAGGGACAGGGCGTGGGG 82659 _ A TG A_
 GG GGA GGACA GGGC GGGG
 || ||| |||| ||| ||||
 CC CCT CCTGT CCCG CCCC
 T C _ CA
 GAM3658 DKFZP586G1122 3' TAGGGGAGAGGGAAAGGCAGGG 82660 _ ACAT
 G TAGGGGA AGG GGGGCAGGGG
 ||||| ||| |||||
 ATCCCCT TCC TTCCGTCCCC
 C CT_
 GAM3658 DKFZP586G1122 3' AGGGGAGGACCGTGGGTGGGGG 82661 A ATG CA
 AGGGGA GGAC GGG GGGG
 ||||| |||| ||| ||||
 TCCCCT CCTG CCC CCCC
 _ GCA AC
 GAM3658 DKFZP586N0721 5' GGGGAGCCCAGGGCAGGGG 82662 A GA TG
 GGGGA G CA GGGCAGGGG
 ||||| ||| |||||

CCCCT C GT CCCGTCCCC
 _ GG _
 GAM3658 DMRTB1 3' TAGAGGAGGGGCAAG 82663 AGGACAT
 TAGGGGA GGGGCAGG
 ||||| |||||
 ATCTCCT CCCCCTTC

 GAM3658 DNAL4 3' GGGGAAGGGGTTTCTGAGGGG 82664 ACAT GGC____
 GGGGAAGG GG AGGGG
 ||||| || |||||
 CCCCTTCC CC TCCCC
 _____ AAAGAC

GAM3658 DUSP9 3' GGGTGGGGGTGGGGCAGGGG 82665 GAA ACA
 GGG GG TGGGGCAGGGG
 ||| || |||||
 CCC CC ACCCCGTCCCC
 AC_ CC_

GAM3658 EPB41L1 3' AGGGTGAAGGGTGTGGGGTGGG 82666 _ ACA CA
 GG AGGG GAAGG TGGGG GGGG
 ||| |||| |||| ||||
 TCCC CTTCC ACCCC CCCC
 A CAC AC

GAM3658 EPB41L1 3' GGGGAAGGGGGAAGGG 82667 ACAT C
 GGGGAAGG GGGG AGGG
 ||||| |||||
 CCCCTTCC CCCT TCCC

_____ _
 GAM3658 FEM-2 3' GAGGAAGGGGAGGGCAGGGG 82668 ACAT
 GGGGAAGG GGGGCAGGGG
 ||||| |||||
 CTCCTTCC TCCCGTCCCC
 CC_

GAM3658 FLJ10374 3' GGGGGCAGGAGCAGCAGGGG 82669 A_ CATGG
 GGGG AGGA GGCAGGGG
 ||| ||| |||||
 CCCC TCCT TCGTCCCC
 CG CG_

GAM3658 FLJ10759 5' AGGGGGGCCCCAGGGGCAGGGG 82670 AA ACAT_
 AGGGG GG GGGGCAGGGG
 |||| || |||||
 TCCCC CC CCCCCTCCCC
 _ GGGCT

GAM3658 FLJ10829 3' GGGGAGGGGGCAGGG 82671 A ACATG
 GGGGA GG GGGCAGGG
 |||| || |||||
 CCCCT CC CCCGTCCC

 GAM3658 FLJ11078 3' GGGGAAGGAGGGCACCCCAGGG 82672 CATG _____
 G GGGGAAGGA GGGCA GGGG
 ||||| |||| ||||

		CCCCTTCCT CCGT CCCC	
		_____ GGGGT	
GAM3658	FLJ12747 3'	AGAGGGATTGGGGGCAGGGG 82673	A CAT
		GGA GGA GGGGCAGGGG	
		TCTCCT CCGGTCCCC	
		C AAC	
GAM3658	FLJ14054 3'	GGGTGGAGGGGCAGAAG 82674	AA CAT
		GGG GGA GGGGCAGGGG	
		CCC CCT CCGGTCTTC	
		A_ _____	
GAM3658	FLJ14326 3'	GGGGAAGGGTGGGCACACAGGG 82675	ACA _____
	G	GGGGAAGG TGGG GCAGGGG	
		CCCCTTCC ACCC TGTCCCC	
		C_ GTG	
GAM3658	FLJ14596 3'	GGGGTGGGGCAAAGTCAGGGG 82676	AA A T GG
		GGGG GG CA GG CAGGGG	
		CCCC CC GT TC GTCCCC	
		AC C T A_	
GAM3658	FLJ14721 3'	TAGGGGAAGGAGGAACAGGGG 82677	CAT
		TAGGGGAAGGA GGGGCAGGGG	
		ATCCCCTTCCT CCTTGTCCCC	

GAM3658	FLJ21324 5'	GGGGAAGGTAGCGGGGTGGGGG 82678	ACA CA
		GGGGAAGG TGGGG GGGG	
		CCCCTTCC GCCCC CCCC	
		ATC AC	
GAM3658	FLJ22127 3'	AGGGAAGGATATGTTGTGGG 82679	C GGGCA
		GGGGAAGGA ATG GGG	
		TCCCTTCCT TAC CCC	
		A AACA_	
GAM3658	FLJ23168 3'	GGGAAAGGGTAGTTTTGGCAGG 82680	ACATGG_
	GG	GGGGAAGG GGCAGGGG	
		CCCTTTCC CCGTCCCC	
		CATCAAAA	
GAM3658	FN3K 3'	CAGGGGAAGGGAGGGCAGGGG 82681	ACAT
		TAGGGGAAGG GGGGCAGGGG	
		GTCCCCTTCC TCCCGTCCCC	
		C_	
GAM3658	FOXO3A 5'	AGGGGGAGGGGCGCCCGGGG 82682	A ACAT G A_
		AGGGG AGG GG GC GGGG	

			TCCCC TCC CC CG CCCC		
			C ____ G GG		
GAM3658	FUK	3'	GGGGCAAGGAAGGTGGGG 82683	_	CAT GCA
			GGGG AAGGA GGG GGG		
			CCCC TTCCT TCC CCC		
			G ____ AC_		
GAM3658	GBTS1	3'	GGGGGGAGAGGGGGCAGGGG 82684	AA	CAT
			GGGG GGA GGGGCAGGGG		
			CCCC CCT CCCC GTCCCC		
			____ CTC		
GAM3658	GIT2	3'	GGGGAAGGGTGGCATATGGGG 82685	ACATGG	____
			GGGGAAGG GGCA GGGG		
			CCCCTTCC CCGT CCCC		
			CA____ ATA		
GAM3658	GIT2	3'	GGGGAAGGGTGGCATATGGGG 82685	ACATGG	____
			GGGGAAGG GGCA GGGG		
			CCCCTTCC CCGT CCCC		
			CA____ ATA		
GAM3658	GIT2	3'	GGGGAAGGGTGGCATATGGGG 82685	ACATGG	____
			GGGGAAGG GGCA GGGG		
			CCCCTTCC CCGT CCCC		
			CA____ ATA		
GAM3658	GTPBG3	3'	TAGGGGAAGGGGAAGG 82686	GGACAT	C
			TAGGGGAA GGGG AGG		
			ATCCCCTT CCCC TCC		
			____ T		
GAM3658	HMT-1	3'	GGGAAGGACAGCAGGG 82687	TGGG	
			GGGAAGGACA GCAGGG		
			CCCTTCCTGT CGTCCC		

GAM3658	HOMER-2B	3'	GGGGGGGCGGGGGGCAGGGG 82688	AA ACAT	
			GGGG GG GGGGCAGGGG		
			CCCC CC CCCC GTCCCC		
			C_ GCC_		
GAM3658	KIAA0057	3'	GGGCGGGCAAGGGGTAGGGG 82689	AA A T	C
			GGG GG CA GGGG AGGGG		
			CCC CC GT CCCC TCCCC		
			GC _ T A		
GAM3658	KIAA0227	3'	GGGGAAGGAGGCAGGG 82690	CATGG	
			GGGGAAGGA GGCAGGG		

CCCCTTCCT CCGTCCC

GAM3658 KIAA0284 3' TAGGGGGCGAGGCAGGGGTGGG 82691 A__ A T CA
GG TAGGGG AGG CA GGGG GGGG

||||| ||| || ||| |||
ATCCCC TCC GT CCCC CCCC
CGC _ _ AC

GAM3658 KIAA0545 3' GGGGGTGAGGGTGGGGGCAGGG 82692 A__ ACAT
G GGGG AGG GGGGCAGGGG

||| ||| |||||
CCCC TCC CCCCCTCCCC
CAC CAC_

GAM3658 KIAA0557 3' AGGGGGGGGGAGCAGGTGG 82693 AA ACAT _
AGGGG GG GGGGCAGG GG

||||| || ||||| ||
TCCCC CC CCTCGTCC CC
C_ _ _ A

GAM3658 KIAA0595 3' TAGGGGAAGGGGGTGGAG 82694 ACAT GCA
TAGGGGAAGG GGG GGG

||||||| ||| |||
ATCCCCTTCC CCC CTC
_ _ AC_

GAM3658 KIAA0939 3' GGGGATGGGATGGGGCAGGGG 82695 A AC
GGGGA GG ATGGGGCAGGGG

||||| || |||||
CCCCT CC TACCCCGTCCCC
A C_

GAM3658 KIAA1054 3' AGGGGAGGGGGAGGCAGGGG 82696 A ACAT
AGGGGA GG GGGGCAGGGG

||||| || |||||
TCCCCT CC CTCCGTCCCC
C C_

GAM3658 KIAA1110 3' GGGGAAGGACATGGTCAGG 82697 GG
GGGGAAGGACATGG CAGG

||||||| |||
CCCCTTCCTGTACC GTCC
A_

GAM3658 KIAA1238 5' GGGGAAGGAGAGGAGGG 82698 CAT C
GGGGAAGGA GGGG AGGG

||||||| ||| |||
CCCCTTCCT CTCC TCCC

GAM3658 KIAA1543 3' GGGGGAGGACAGACAAGGG 82699 A TGG
GGGG AGGACA GGCAGGGG

||| ||||| |||||
CCCC TCCTGT CTGTTCCC
C _

GAM3658 KIAA1706 3' GGGGAAGGGGGCGGGG 82700 ACATG A
GGGGAAGG GGGC GGG

||||||| ||| |||

CCCCTTCC CCG CCC
 _____ C
 GAM3658 KIAA1719 3' GGGGAAAGGGTAGAGGG 82701 ACAT _ C
 GGGGAAGG GG GG AGGG
 ||||| || ||||
 CCCCTTTC CC TC TCCC
 _____ A _
 GAM3658 KIAA1813 5' GGGGAAGGGACTTCTTAGGGG 82702 _ ATGGGGC
 GGGGAAGG AC AGGGG
 ||||| || ||||
 CCCCTTCC TG TCCCC
 C AAGAA_
 GAM3658 KIAA1887 5' GGGGGACAGGAGCAGGG 82703 AA T
 GGG GGACA GGGGCAGGG
 || |||| |||||
 CCC CCTGT CCTCGTCCC

 GAM3658 KIAA1938 3' GGGGAGGGAAGCAGAGGGGCGG 82704 A _ T_ A
 GGG GGGGA GGA CA GGGGC GGGG
 |||| || || |||| ||||
 CCCCT CCT GT CCCC CCCC
 C TC CT C
 GAM3658 KIAA1940 3' AGGGGCTGGTGGGGCAGGGG 82705 AA ACA
 AGGGG GG TGGGCAGGGG
 |||| || |||||
 TCCCC CC ACCCGTCCCC
 GA _
 GAM3658 MGC10882 3' AGGGGAGTGGGATGGGGTGGGG 82706 A_ CA CA
 G AGGGGA GGA TGGGG GGGG
 |||| || |||| ||||
 TCCCCT CCT ACCCC CCCC
 CAC _ AC
 GAM3658 MGC10924 3' AGGGGGGTGGGGGTGGGG 82707 AA ACA CA
 AGGGG GG TGGGG GGGG
 |||| || |||| ||||
 TCCCC CC ACCCC CCCC
 _ _ CA
 GAM3658 MGC14832 3' TAGGGGAAAGAGGCAGGG 82708 CATGG
 TAGGGGAAGGA GGCAGGG
 ||||| |||||
 ATCCCCTTTCT CCGTCCC

 GAM3658 MGC21621 3' GGGTGGGGGAGCCGGGCAGGGG 82709 GAA_ CATG
 GGG GGA GGGCAGGGG
 || || |||||
 CCC CCT CCCGTCCCC
 ACCC CGG_
 GAM3658 MIDORI 3' AGGGGAGGTTCGGGTGGGGG 82710 A ACA GCA
 AGGGGA GG TGGG GGGG
 |||| || |||| ||||

			TCCCCT CC GCCC CCCC		
			_ AAG AC_		
GAM3658	NCKX3	3'	GGGGAGCGAGGATGGGGCAGGG 82711	___	CA
	G		GGGGA AGGA TGGGGCAGGGG		
			CCCCT TCCT ACCCCGTCCCC		
			CGC _		
GAM3658	NOL4	5'	GGGGAAGGGATGGGAAGAGGGG 82712	AC	C_
			GGGGAAGG ATGGGG AGGGG		
			CCCCTTCC TACCCT TCCCC		
			C_ TC		
GAM3658	P5CR2	5'	TAGGGGAAGGGCGGACAGCGCA 82714	AC_	G
	GGGG		TAGGGGAAGG ATGG GCAGGGG		
			ATCCCCTTCC TGTC CGTCCCC		
			CGCC G		
GAM3658	P5CR2	3'	GGTGGGAGCGGGGCAGGG 82713	GAA	CA
			GG GGA TGGGGCAGGG		
			CC CCT GCCCGTCCC		
			AC_ C_		
GAM3658	PAK7	5'	TAGGGGCAAGGGGGGCGGGGG 82715	_	ACAT A
			TAGGGG AAGG GGGGC GGGG		
			ATCCCC TTCC CCCCCG CCCC		
			G _ _ C		
GAM3658	PDK2	3'	TAGGGGAAGGGTGGGGGCATTC 82716	ACAT	___
	AGGG		TAGGGGAAGG GGGGCA GGGG		
			ATCCCCTTCC CCCCCG TCCC		
			CAC_ AAG		
GAM3658	RIS1	3'	GGGGAAGGAGTCGGGCAGGGG 82717	CATG	
			GGGGAAGGA GGGCAGGGG		
			CCCCTTCCT CCCGTCCCC		
			CAG_		
GAM3658	SCAM-1	3'	GGGGAAGGAGGATGTGGGCGGG 82718	C_ _	A
	GG		GGGGAAGGA ATG GGGC GGGG		
			CCCCTTCCT TAC CCCC CCCC		
			CC A C		
GAM3658	SCYA22	3'	GGGGGGGGGGGTGGGGAGAGG 82719	AA ACA	C
			GGGG GG TGGGG AGGGG		
			CCCC CC ACCCC TCTCC		
			CC CC_ _		
GAM3658	SEMA4G	5'	GGGAGAAGGGTATGGAGTGGGG 82720	_	AC CA
	G		GGG GAAGG ATGGGG GGGG		

CCC CTTCC TACCTC CCCC
 T CA AC
 GAM3658 STX5A 3' GGGGGGAGGACAGGG 82721 AA CATG
 GGGG GGA GGGCAGGG
 |||| || |||||
 CCCC CCT CCTGTCCC

 GAM3658 SUCLG2 5' AGGGCGGGCGCGGCAGGGG 82722 AA ACATG
 GGGG GG GGGCAGGGG
 |||| || |||||
 TCCC CC CCCGTCCCC
 GC GCG__
 GAM3658 TADA3L 3' AGGGGAGACAGGGGTAGGGG 82723 AG T C
 AGGGGA GACA GGGG AGGGG
 |||| |||| ||||
 TCCCCT CTGT CCCC TCCCC
 __ _ A
 GAM3658 TBC1D1 5' GGGGCGGGTTGGGGCGGGGG 82724 AA ACA A
 GGGG GG TGGGGC GGGG
 |||| || |||| ||||
 CCCC CC ACCCCG CCCC
 GC A__ C
 GAM3658 TEB4 3' GAGGATGTGGGTGTGGGGTGGG 82725 A__ ACA CA
 GG GGGGA GG TGGGG GGGG
 |||| || |||| ||||
 CTCCT CC ACCCC CCCC
 ACA CAC AC
 GAM3658 THG-1 5' GGGAGGGGGGAGCAGGGG 82726 A ACAT
 GGGGA GG GGGGCAGGGG
 |||| || |||||
 CCCT CC CCTCGTCCCC
 C C__
 GAM3658 ZFP106 5' AGGGGAGGCAGGGCAGGG 82727 A A TG
 AGGGGA GG CA GGGCAGGG
 |||| || || |||||
 TCCCCT CC GT CCCGTCCC
 __ __ __
 GAM3658 LOC115207 3' TAGGTGGGGGTGGGGTGGGGG 82728 _ AA ACA CA
 TAGG GG GG TGGGG GGGG
 |||| || || |||| ||||
 ATCC CC CC ACCCC CCCC
 A C_ __ AC
 GAM3658 LOC124402 3' GGGGAGGGGGCGGCGGGCAGGG 82729 A ACATG_
 G GGGGA GG GGGCAGGGG
 |||| || |||||
 CCCCT CC CCCGTCCCC
 C CCGCCG
 GAM3658 LOC124930 3' GGGTGAGGTGGGGCAGGGG 82730 GA ACA
 GGG AGG TGGGGCAGGGG
 || || |||||

	CCC TCC ACCCCGTCCCC	
	AC ____	
GAM3658 LOC126961 3'	TAGGGGCAGGATATGGGG 82731	A C
	TAGGGG AGGA ATGGGG	
	ATCCCC TCCT TACCCC	
	G A	
GAM3658 LOC137695 5'	TAGGCGGGGGCAGGGGCAGGGG 82732	_ AA A T
	TAGG GG GG CA GGGGCAGGGG	
	ATCC CC CC GT CCCC GTCCCC	
	G C_ _ _	
GAM3658 LOC144110 3'	TAGGGGAAGTGGGTGGGG 82733	GACA GCA
	TAGGGGAAG TGGG GGG	
	ATCCCCTTC ACCC CCC	
	____ AC_	
GAM3658 LOC145082 5'	TAGAGGAAGGTGTGGTCCCTG 82734	ACA GGCAG
G	TAGGGGAAGG TGG GG	
	ATCTCCTTCC ACC CC	
	CAC AGGGA	
GAM3658 LOC146229 3'	TAGGTGGTGTCA GTGGGGCAGG 82735	_ AAGGA _
GG	TAGG GG CA TGGGGCAGGGG	
	ATCC CC GT ACCCCGTCCCC	
	A ACA_ C	
GAM3658 LOC147138 3'	GGGGAGGCAGGGGTAGGGG 82736	A A T C
	GGGGA GG CA GGGG AGGGG	
	CCCCT CC GT CCCC TCCCC	
	_ _ _ A	
GAM3658 LOC147228 3'	GGGGAAGGGACTGAAGCAGGGG 82616	_ A
	GGGGAAGG AC TGGGGCAGGGG	
	CCCCTTCC TG ACTTCGTCCCC	
	C _	
GAM3658 LOC147791 5'	GGGGGCAGGGCTTGAGGCAGGG 82737	A_ ACA
G	GGGG AGG TGGGGCAGGGG	
	CCCC TCC ACTCCGTCCCC	
	CG CGA	
GAM3658 LOC150111 5'	GGGGGGAGCTCGGGCAGGGG 82738	AA CATG
	GGGG GGA GGGCAGGGG	
	CCCC CCT CCCGTCCCC	
	_ CGAG	
GAM3658 LOC150197 3'	CAGGGGAAGGGCAGAAGGG 82739	A T GGC
	TAGGGGAAGG CA GG AGGG	

GTCCCCTTCC GT CT TCCC
 C _ _
 GAM3658 LOC150197 3' TAGGGGGACGGGGCAGGG 82740 AAG AT
 TAGGGG GAC GGGGCAGGG
 ||||| ||| |||||
 ATCCCC CTG CCCC GTCCC

— —
 GAM3658 LOC151176 3' TAGGGGAGGGGCAGGG 82741 AGGACAT
 TAGGGGA GGGGCAGGG
 ||||| |||||
 ATCCCCT CCCC GTCCC

————
 GAM3658 LOC151904 5' CAGGGGATAGAATGGGGCAGGG 82742 A C
 G TAGGGGA GGA ATGGGGCAGGGG
 ||||| ||| |||||
 GTCCCCT TCT TACCCCGTCCCC
 A _

GAM3658 LOC152220 3' GGGGAAGGGGATGGTGGG 82743 AC GGCA
 GGGGAAGG ATGG GGG
 ||||| ||| |||
 CCCCTTCC TACC CCC
 CC A_

GAM3658 LOC152915 3' GGGGGAGGGGTGACAGGGG 82744 A ACAT _
 GGGG AGG GG GGCAGGGG
 ||| ||| || |||||
 CCCC TCC CC CTGTCCCC
 C _ _ A

GAM3658 LOC153232 3' GGGGGGGGGGGGGGCGGGCAGGG 82745 AA ACATG_
 G GGGG GG GGGCAGGGG
 ||| || |||||
 CCCC CC CCGTCCCC
 CC CCCCCG

GAM3658 LOC153525 5' AGGGGGGTGGGGGTGGGG 82707 AA ACA CA
 AGGGG GG TGGGG GGGG
 |||| || |||| |||
 TCCCC CC ACCCC CCCC
 _ _ CA

GAM3658 LOC158062 3' AGGGGAGGGACAGAG 82746 AGGACAT
 AGGGGA GGGGCAGGG
 |||| |||||
 TCCCCT CCCTGTCTC

————
 GAM3658 LOC158067 3' GGGGGGCTGGGGGCAGGG 82747 AA ACAT
 GGGG GG GGGGCAGGG
 ||| || |||||
 CCCC CC CCCC GTCCC
 _ GAC_

GAM3658 LOC158333 3' GGGTGGAGGAATGAGCAGGGG 82748 GA_ CATG
 GGG AGGA GGGCAGGGG
 || ||| |||||

	CCC TCCT CTCGTCCCC		
	ACC TA__		
GAM3658 LOC170393 3'	GGGGCAAGGGTGGGAGGG 78815	_	ACATG C
	GGGG AAGG GGG AGGG		
	CCCC TTCC CCC TCCC		
	G CA__ _		
GAM3658 LOC170393 3'	GGGGCAAGGGTGGGAGGG 78815	_	ACATG C
	GGGG AAGG GGG AGGG		
	CCCC TTCC CCC TCCC		
	G CA__ _		
GAM3658 LOC170393 3'	GGGGCAAGGGTGGGAGGG 78815	_	ACATG C
	GGGG AAGG GGG AGGG		
	CCCC TTCC CCC TCCC		
	G CA__ _		
GAM3658 LOC170393 3'	GGGGCAAGGGTGGGAGGG 78815	_	ACATG C
	GGGG AAGG GGG AGGG		
	CCCC TTCC CCC TCCC		
	G CA__ _		
GAM3658 LOC170393 3'	GGGGCAAGGGTGGGAGGG 78815	_	ACATG C
	GGGG AAGG GGG AGGG		
	CCCC TTCC CCC TCCC		
	G CA__ _		
GAM3658 LOC170393 3'	GGGGCAAGGGTGGGAGGG 78815	_	ACATG C
	GGGG AAGG GGG AGGG		
	CCCC TTCC CCC TCCC		
	G CA__ _		
GAM3658 LOC201501 5'	AGGGAAGGGTGGCGGTGGGGG 82749	ACA _ CA	
	GGGGAAGG TGG GG GGGG		
	TCCCTTCC ACC CC CCCC		
	C__ G AC		
GAM3658 LOC253842 3'	GGGGTAGGGGGAGGCAGGGG 24996	A ACAT	
	GGGG AGG GGGGCAGGGG		
	CCCC TCC CTCCGTCCCC		
	A CC__		
GAM3658 LOC254016 3'	TAGGGGAAGGTTGGGG 82750	ACA	
	TAGGGGAAGG TGGGG		
	ATCCCCTTCC ACCCC		
	A__		
GAM3658 LOC255121 5'	CAGGGGAAGGCGGTGGGG 82751	ACA	
	TAGGGGAAGG TGGGG		

	GTCCCCTTCC ACCCC		
	GCC		
GAM3658 LOC255270 3'	AGGGAGAGGAGGGCAGGGG 82635	GA	CATG
	AGGG AGGA GGGCAGGGG		
	TCCC TCCT CCCGTCCCC		
	TC ____		
GAM3658 LOC257395 3'	TAGGGGCAGGATATGGGG 82731	A	C
	TAGGGG AGGA ATGGGG		
	ATCCCC TCCT TACCCC		
	G A		
GAM3658 LOC257484 5'	GGGGGAACGGGTAGCAAAGG 82752	AA	AT _
	GGGG GGAC GGG GCAGGGG		
	CCCC CTTG CCC CGTTTCC		
	_ _ AT		
GAM3658 LOC85414 3'	TAGGGGAAAGTTGGGGGTAGGG 82753	ACAT	C
G	TAGGGGAAGG GGGG AGGGG		
	ATCCCCTTTC CCCC TCCCC		
	AAC_ A		
GAM3658 LOC85414 3'	GGGGAAAGTTGGGGGTAGGGG 82754	ACAT	C
	GGGGAAGG GGGG AGGGG		
	CCCCTTTC CCCC TCCCC		
	AAC_ A		
GAM3658 LOC90379 3'	GGGGGCGGGCAGGGCAGGGG 82755	AA A	TG
	GGGG GG CA GGGCAGGGG		
	CCCC CC GT CCCGTCCCC		
	CG C _		
GAM3658 LOC90631 3'	GGGGGGCAGGGGGCAGGG 82756	AA A	T
	GGGG GG CA GGGGCAGGG		
	CCCC CC GT CCCC GTCCC		
	_ _ C		
GAM3658 LOC90678 3'	GGGGAAGGGGCCAGGGCAGGG 82757	ACA_	
G	GGGGAAGG TGGGCAGGGG		
	CCCCTTCC GTCCCGTCCCC		
	CCGG		
GAM3658 LOC91097 5'	GGGGAAGGTAGCGGGGTGGGGG 82678	ACA	CA
	GGGGAAGG TGGGG GGGG		
	CCCCTTCC GCCCC CCCC		
	ATC AC		
GAM3658 LOC91517 3'	GGGGGCAGGGGTGGGCTGGGG 82758	A_	ACATG A
	GGGG AGG GGGC GGGG		

CCCC TCC CCGC CCCC
 CG CCA__ A
 GAM3658 LOC92578 3' CAGGGGAATGGGGTGGGG 82759 AGGAC CA
 TAGGGGA ATGGGG GGG
 ||||| ||||| ||
 GTCCCCCT TACCCC CCC
 _____ AC
 GAM3659 PHKA1 3' GAGCCTCCAGGTAAT 82762 TTGTTC A
 GAGCTTCCAG GTAA T
 ||||| |||||
 CTCGGAGGTC CATT A
 _____ C
 GAM3659 DKFZp547I224 5' GAGTTTCCAGTTTTTCTGCTCT 82763 C G GTAAA
 GT GAG TTCCAGTT TTC TGT
 || ||||| || ||
 CTC AAGGTCAA AAG ACA
 A A ACGAG
 GAM3659 EPB41L4 3' AGCCAGGTTGTTGTAGATGT 82764 TCCA C A
 AGCT GTTGTT GTA ATGT
 ||| ||||| || ||||
 TCGG CAACAA CAT TACA
 TC__ A C
 GAM3659 LOC161734 3' GAGTTTCCAGTTTTTCTGCTCT 82763 C G GTAAA
 GT GAG TTCCAGTT TTC TGT
 || ||||| || ||
 CTC AAGGTCAA AAG ACA
 A A ACGAG
 GAM3660 FLJ20689 3' TGGAAGTTCTCAAGGCC 82767 A C GC
 TG AAG TC CAAGGTCT
 || ||| || |||||
 AC TTC AG GTTCCGGG
 C A A_
 GAM3660 FLJ20689 3' TGGAAGTTCTCAAGGCC 82767 A C GC
 TG AAG TC CAAGGTCT
 || ||| || |||||
 AC TTC AG GTTCCGGG
 C A A_
 GAM3660 SEC14L2 3' TGAAAGCTCCTGAGGTCT 82768 GCCA
 TGAAAGCTC AGGTCT
 ||||| |||||
 ACTTTCGAG TCCAGA
 GAC_
 GAM3660 LOC56851 3' TGAAAGCTGGGTTTTCTCGTGT 82769 CGCCAAGG C
 TGAAAGCT TCTCG GT
 ||||| ||||| ||
 ACTTTCGA AGAGC CA
 CCCAAA__ A
 GAM3661 LOC150622 3' ATAATATTAGCATTGCTATAAA 82772 CG TCC
 A ATAATA GGT GCTATAAAA
 ||||| || |||||

			TATTAT TCG CGATATTTT		
			AA TAA		
GAM3662	ASL	3'	CCAGGCTATTTGTTTTATTATT 82775	T	TAA_
			CC GGCTATTT TGTTATT		
			GG CCGATAAA ATAATAA		
			T CAAA		
GAM3662	CUBN	3'	CCTGGCTAATTATTATATT 82776	T	TA_
			CCTGGCTA TT ATGTT		
			GGACCGAT AA TATAA		
			T TAA		
GAM3662	DYRK2	3'	CCTGCCACTGATGTTATTA 82777	G	TTA
			CCTG CTATT ATGTTATTA		
			GGAC GGTGA TACAATAAT		
			_ C_		
GAM3662	DYRK2	3'	CCTGCCACTGATGTTATTA 82777	G	TTA
			CCTG CTATT ATGTTATTA		
			GGAC GGTGA TACAATAAT		
			_ C_		
GAM3662	IL22RA2	5'	TGGTAATTTTAATGCCATT 82778	CT	
			TGG ATTTTAATGTTATT		
			ACC TAAAATTACGGTAA		
			AT		
GAM3662	PLA2G10	5'	GCTCTTTTGATGTTATTACT 82779	A	A
			GCT TTTT ATGTTATTACT		
			CGA AAAA TACAATAATGA		
			G C		
GAM3662	SNCAIP	5'	CTGGTTCTTTTGGTCATCACT 82780	CTA	AAT
			CTGG TTTT GTTATTACT		
			GACC AAAA CAGTAGTGA		
			AAG C_		
GAM3662	SRC	3'	CCTGGCAGTGGGAATGTTATTG 82781	TATTTT	A
	CT		CCTGGC AATGTTATT CT		
			GGACCG TTACAATAA GA		
			TCACCC C		
GAM3662	BC008967	5'	CCTGGCTATGATTGTTATT 82782	TTTAA	
			CCTGGCTAT TGTTATT		
			GGACCGATA ACAATAA		
			CTA_		
GAM3662	BLOV1	3'	CCTGGCTAATTTTGTATTATT 82783	T	AA
			CCTGGCTA TTT TGTTATT		

			GGACCGAT AAA ATAATAA		
			T AC		
GAM3662	FBXO26	3'	CCTGGCTAATTTTTTAAAAATT 82784	___	T_
	ATT		CCTGGCTA TTTTAA GTTATT		
			GGACCGAT AAAATT TAATAA		
			TAA TT		
GAM3662	FLJ11700	3'	CCTGGCTAATTTTTGTATT 82785	_	AA
			CCTGGCTA TTTT TGTT		
			GGACCGAT AAAA ATAA		
			T AC		
GAM3662	FLJ20793	3'	TGGCATTTAAATGTTATT 82786	T	T
			TGGC ATTT AATGTTATT		
			ACCG TAAA TTACAATAA		
			_ T		
GAM3662	KIAA1871	3'	CCTGGCTAATTTTTGTATT 82787	T	AA
			CCTGGCTA TTT TGTTATT		
			GGACCGAT AAA ACAATAA		
			T A_		
GAM3662	POFUT1	3'	CCTGGCTATTATTATTATT 82788		TTAA
			CCTGGCTATT TGTTATT		
			GGACCGATAA ATAATAA		
			TA__		
GAM3662	SPRY4	3'	CCTGGCTATTTTGTAGTT 82789		AAT
			CCTGGCTATTTT GTT		
			GGACCGATAAAA CAA		
			CAT		
GAM3662	TCL6	3'	TGGCTATTTTCATGGTTATT 82790	A	_
			TGGCTATTTT ATG TTATT		
			ACCGATAAAA TAC AATAA		
			G C		
GAM3662	TCL6	3'	TGGCTATTTTCATGGTTATT 82790	A	_
			TGGCTATTTT ATG TTATT		
			ACCGATAAAA TAC AATAA		
			G C		
GAM3662	TRPM3	3'	CTGGCTATTTTATTTTATT 82791		ATG
			CTGGCTATTTTA TTATT		
			GACCGATAAAAT AATAA		
			AA_		
GAM3662	WBSCR23	5'	CCTGGCTATTTATTTTATT 82792		TAATG
			CCTGGCTATTT TTATT		

	GGACCGATAAA AATAA		
	TAA__		
GAM3662 LOC148823 3'	CCTGGCTAATTTTTTAATTATT 82793	_ AAT	
	CCTGGCTA TTTT GTTATT		
	GGACCGAT AAAA TAATAA		
	T AAT		
GAM3662 LOC149113 5'	CCTAGCTAACTGTTGTTATT 82794	TTTTAA	
	CCTGGCTA TGTTATT		
	GGATCGAT ACAATAA		
	TGACA_		
GAM3662 LOC153688 3'	CTGGCAAGGGAATGTTATTGCT 82795	TATTTT A	
	CTGGC AATGTTATT CT		
	GACCG TTACAATAA GA		
	TTCCC_ C		
GAM3662 LOC154403 5'	CCTAGCTAACTGTTGTTATT 82794	TTTTAA	
	CCTGGCTA TGTTATT		
	GGATCGAT ACAATAA		
	TGACA_		
GAM3662 LOC154992 5'	CCTAGCTAATTGTTGTTATT 82796	TTTTAA	
	CCTGGCTA TGTTATT		
	GGATCGAT ACAATAA		
	TAACA_		
GAM3662 LOC158438 3'	TGGCTATTTATAAATGTT 82797	T__	
	TGGCTATTT AATGTT		
	ACCGATAAA TTACAA		
	TAT		
GAM3662 LOC202052 3'	CCTGGCTAATTTTTGTATTATT 82799	_ AA	
	CCTGGCTA TTTT TGTTATT		
	GGACCGAT AAAA ATAATAA		
	T AC		
GAM3662 LOC202052 3'	CTGGCTATTTCTAGAAATGCT 82798	_____	
	CTGGCTATTTT AATGTT		
	GACCGATAAAG TTACGA		
	ATCT		
GAM3662 LOC221641 5'	CCTGGCTATTTTGTTATCA 82800	TAA	
	CCTGGCTATTT TGTTATTA		
	GGACCGATAAA ACAATAGT		

GAM3662 LOC222104 3'	TGGCTATTCCTCATTGTTATT 82801	AA__	
	TGGCTATTTT TGTTATT		

		ACCGATAAGG ACAATAA		
		AGTA		
GAM3662	LOC255196 5'	CCTGGCTAATTTTAGTATT	82802	_ A
		CCTGGCTA TTTTA TGTT		
		GGACCGAT AAAAT ATAA		
		T C		
GAM3662	LOC90786 5'	TGGCATATTTTAGCTAATTTAC	82803	_ AT _
	T	TGGC TATTTTA GTTA TTA		
		ACCG ATAAAAT CGAT AATGA		
		T _ TA		
GAM3662	LOC91069 3'	TGGCCATTTTGATGTGCACT	82804	A TAT
		TGGCTATTTT ATGT TACT		
		ACCGGTAAAA TACA GTGA		
		C C_		
GAM3662	LOC92539 5'	TGGATAACTATGTTATTACT	82805	C TTTTA
		TGG TA ATGTTATTACT		
		ACC AT TACAATAATGA		
		T TGA_		
GAM3663	CEACAM1 3'	AAATTGTGTATTCTTTAAC	82808	C
		AGATTGTGTATTCTT AAC		
		TTTAACACATAAGAA TTG		
		A		
GAM3663	MSL3L1 3'	TAAAGGTATGCCTTCTTCAAC	82809	AT A
		TAAAG TGTGT TTCTTCAAC		
		ATTTC ATACG AAGAAGTTG		
		C_ G		
GAM3663	SCAP2 3'	TATAAAGTTTGAACATTCTT	82810	A TG
		TATAAAG TTG TATTCTT		
		ATATTTC AAC GTAAGAA		
		A TT		
GAM3663	SLC4A4 3'	AAGAAAAATATTCTTCAA	82811	TTGT
		AAGA GTATTCTTCAA		
		TTCT TATAAGAAGTT		
		TTT_		
GAM3663	CSAD 3'	TATAAAGACTTGTATTC	82812	G
		TATAAAGATT TGTATTC		
		ATATTCTGA ACATAAG		
		-		
GAM3663	DKFZP434P0721 3'	TATAAAGATTGTGGTTCCT	82813	TA
		TATAAAGATTGTG TTCT		

		ATATTTCTAACAC AGGA		
		CA		
GAM3663	FLJ11021	3' TACAAAAATTTGTATTTTCAA	82814	G C
		TATAAAGATT TGTATT TTCAA		
		ATGTTTTTAA ACATAA AAGTT		
		_ A		
GAM3663	KIAA1237	3' AGACTGTGTGACCTCAAC	82815	ATT
		AGATTGTGT CTTCAAC		
		TCTGACACA GGAGTTG		
		CT_		
GAM3663	KIAA1829	3' TATGAAGGCTGTGTATTC	82816	A AT
		TAT AAG TGTGTATTC		
		ATA TTC ACACATAAG		
		C CG		
GAM3663	PC326	3' GAAAATTATTCTTCAAC	82817	TT G
		GA GT TATTCTTCAAC		
		CT TA ATAAGAAGTTG		
		TT _		
GAM3663	RPH3A	3' AAGATTGCCTGACTTCAAC	82818	GTATT
		AAGATTGT CTTCAAC		
		TTCTAACG GAAGTTG		
		GACT_		
GAM3663	SENP7	3' TATAAAGATAGTGCCAAAATCA	82819	T ATTCT
	AC	TATAAAGAT GTGT TCAAC		
		ATATTTCTA CACG AGTTG		
		T GTTTT		
GAM3663	UNC5D	3' TATAAAATTTAGTTTCTTCAAC	82820	A T A
		TATAAAG TTG GT TTCTTCAAC		
		ATATTTT AAT CA AAGAAGTTG		
		A _ _		
GAM3664	FGF23	3' CTAGCAGGGCAGATTTTCG	82823	C A_ C
		CT GCG GCAGATT TCG		
		GA CGT CGTCTAA AGC		
		T CC A		
GAM3664	KIAA1266	5' TTGCCACTTGCAAGTCT	82824	CGCGA AT
		TTGCCACT GCAG TCT		
		AACGGTGA CGTC AGA		
		A _ _		
GAM3664	LOC150378	3' TTGCCACTTGCAAGCAGAGTC	82825	C A T
		TTGCCACT GCG GCAGA TC		

			AACGGTGA CGT CGTCT AG		
			A C C		
GAM3665	PMCHL1	3'	AGGGGTTTTAAACCT 82828	A	GTAAAA
			AGG GTTT TAAATCT		
			TCC CAAA ATTTTGGA		
			C _____		
GAM3665	SCN8A	3'	GAAGTTTGTAACAATCT 82829		ATAA
			GGAGTTTGTAAG AATCT		
			CTTCAAACATTT TTAGA		
			G_____		
GAM3665	SYN2	3'	GAAGTTTGATCTTGAAAATCTC 82830		TAAAAT
	T		GGAGTTTG AAAATCTCT		
			CTTCAAAC TTTTAGAGA		
			TAGAAC		
GAM3665	TRPM8	3'	AGGGGTCTGAAAATCT 82831	A	TAAAAT
			AGG GTTTG AAAATCT		
			TCC CAGAC TTTTAGA		
			C _____		
GAM3665	FJX1	3'	AAATTCTGTAAAATAAAAT 82832	G	
			GGA TTTGTAAAATAAAAT		
			TTT AGACATTTTATTTTA		
			A		
GAM3665	FLJ13386	5'	GGAGGTCTGCTAGTGAAATCTC 82833	_	AAAATA
	T		GGAG TTTGT AAATCTCT		
			CCTC AGACG TTTAGAGA		
			C ATCAC_		
GAM3665	GALNT6	3'	AGGAGCTTGTGGGGGCTCTCT 82834		AAAATAAAA
			AGGAGTTTGT TCTCT		
			TCCTCGAACA AGAGA		
			CCCCCG_____		
GAM3665	GIT2	3'	AGGGGTTTGCAAGATAAA 82835	A	A
			AGG GTTTGTAA ATAAA		
			TCC CAAACGTT TATTT		
			C C		
GAM3665	GIT2	3'	AGGGGTTTGCAAGATAAA 82835	A	A
			AGG GTTTGTAA ATAAA		
			TCC CAAACGTT TATTT		
			C C		
GAM3665	GIT2	3'	AGGGGTTTGCAAGATAAA 82835	A	A
			AGG GTTTGTAA ATAAA		

TCC CAAACGTT TATTT
 C C
 GAM3665 KIAA1715 3' GGAGTTTGGGAAGGCATCTCT 82836 TA ATAAA
 GGAGTTTG AA ATCTCT
 ||||| || |||||
 CCTCAAAC TT TAGAGA
 CC CCG__
 GAM3665 KIAA1718 3' AGGAATTTGTAAAATGCTC 82837 AAAAT
 AGGAGTTTGTAAAAT CTC
 ||||| ||||| |||||
 TCCTTAAACATTTTA GAG
 C____
 GAM3665 RBAK 3' AGAAGTTTGTGAATAAAATTTTC 82838 AA C
 T AGGAGTTTGT AATAAAAT TCT
 ||||| ||||| |||||
 TCTTCAAACA TTATTTTA AGA
 C_ A
 GAM3666 ABCC3 3' TGGATCCGTTTCAGAGACA 82841 C AAAGCCC
 TGGA CC TCAGAGACA
 ||| || |||||
 ACCT GG AGTCTCTGT
 A CAA____
 GAM3666 ADORA1 3' GGGGTCCAGAGTCCTCAGAG 82842 T AC A C
 G GG CCA AG CCTCAGAG
 | || ||| |||||
 C CC GGT TC GGAGTCTC
 _ CA C A
 GAM3666 BMP1 3' ATGGACCCGTCAGAGA 82843 AAAGCCC
 GTGGACCC TCAGAGA
 ||||| |||||
 TACCTGGG AGTCTCT
 C____
 GAM3666 CAPON 5' GCGGACCCGCTCCTTCGGAG 82844 AAA _ _ A
 GTGGACCC GC CCT C GAG
 ||||| || ||| |||||
 CGCCTGGG CG GGA G CTC
 _ A A C
 GAM3666 CBFB 3' GTGGACCGAAAGCCCTTAGCTA 82845 C C _
 GACA GTGGACC AAAGCCCT AG AGACA
 ||||| ||||| || |||||
 CACCTGG TTTCGGGA TC TCTGT
 C A GA
 GAM3666 CBFB 3' GTGGACCGAAAGCCCTTAGCTA 82845 C C _
 GACA GTGGACC AAAGCCCT AG AGACA
 ||||| ||||| || |||||
 CACCTGG TTTCGGGA TC TCTGT
 C A GA
 GAM3666 CIT 3' GGACCCAAAGCAACAGA 82846 CCT
 GGACCCAAAGC CAGA
 ||||| ||||| |||||

			CCTGGGTTTCG GTCT		
			TT_		
GAM3666	CTLA4	3'	GGACCCAAGGTGGAAAGACA 82847	AGCCCTC	
			GGACCCAA AGAGACA		
			CCTGGGTT TTTCTGT		
			CCACC_		
GAM3666	CYP46	3'	GTGGGCACAGGGGGCTCAGAGA 82848	ACC AAGCC	
	CA		GTGG CA CTCAGAGACA		
			CACC GT GAGTCTCTGT		
			CGT CCCCC		
GAM3666	DIAPH2	3'	TGGGCCTAAAAGGGACAGAGAC 82849	A C CCCT	
	A		TGG CC AAAG CAGAGACA		
			ACC GG TTTT GTCTCTGT		
			C A CCCT		
GAM3666	EPHB6	5'	GTGGACCCGGGGCTCCTGGAG 82850	AAA _ CA	
			GTGGACCC GC CCT GAG		
			CACCTGGG CG GGA CTC		
			CCC A C_		
GAM3666	FN14	3'	TGGGCCCAGGCCTCAGAG 82851	A AA C	
			TGG CCCA GCC TCAGAG		
			ACC GGGT CGG AGTCTC		
			C C_ _		
GAM3666	GAS7	3'	GGGTCTTCAGCCTCAGAGACA 82852	ACCCAA C	
			GG AGCC TCAGAGACA		
			CC TCGG AGTCTCTGT		
			CAGAAG _		
GAM3666	GAS7	3'	GGGTCTTCAGCCTCAGAGACA 82852	ACCCAA C	
			GG AGCC TCAGAGACA		
			CC TCGG AGTCTCTGT		
			CAGAAG _		
GAM3666	GRIA1	3'	GACTCTACTCTCAGAGACA 82853	CCAAA C	
			GAC GC CTCAGAGACA		
			CTG TG GAGTCTCTGT		
			AGA_ A		
GAM3666	PPP2R4	3'	GTGGACCCAGACACAGGA 82854	AA CCT A	
			GTGGACCCA GC CAG GA		
			CACCTGGGT TG GTC CT		
			C_ T_ _		
GAM3666	RNF26	3'	GTGGCCCCAAAGTCAG 82855	A CCC	
			GTGG CCAAAG TCAG		

CACC GGGTTTC AGTC
 G ____
 GAM3666 USF2 3' GGACCCAGAAACAAGAG 82856 _ CCTC
 GGACCCA AAGC AGAG
 ||||| ||| |||
 CCTGGGT TTTG TCTC
 C T____
 GAM3666 CACH-1 3' GTGGCCCCAAAGCTTGAC 82857 A CCTCAGA
 GTGG CCCAAAGC GAC
 ||| ||||| |||
 CACC GGGTTTCG CTG
 G AA____
 GAM3666 FLJ10482 3' GTGGCCCCAATTTCTCAGAGA 82858 A AGC
 CA GTGG CCAA CCTCAGAGACA
 ||| ||| |||||
 CACC GGGTT GGAGTCTCTGT
 G AAA
 GAM3666 FLJ13291 3' TGGACTCAGAGCCCTCAA 82859 C A
 TGGAC CA AGCCCTCAG
 |||| || |||||
 ACCTG GT TCGGGAGTT
 A C
 GAM3666 FLJ20045 5' TGGACTCAGAGCCCCCAG 82860 C A
 TGGAC CA AGCCCTCAG
 |||| || |||||
 ACCTG GT TCGGGGGTC
 A C
 GAM3666 KIAA0061 3' TGGATCCAAAGACATTCAGAGG 82861 C _CC A
 CA TGGG CCAAAG C TCAGAG CA
 ||| ||||| | ||||| ||
 ACCT GGTTC G AGTCTC GT
 A TTA C
 GAM3666 KIAA0247 3' GGCCTATAGGGCCCTCAGAGA 82862 A CAAA____
 GG CC GCCCTCAGAGA
 || || |||||
 CC GG CGGGAGTCTCT
 _ ATATCC
 GAM3666 KIAA0767 3' GCGGGTGGCCCTCAGAGC 82863 ACCCAAA A
 GTGG GCCCTCAGAG C
 ||| ||||| |
 CGCC CGGGAGTCTC G
 CAC____ C
 GAM3666 KIAA1199 3' GTGGACCCAATAGCTGTTTCTCAGA 82864 _ CC_
 GTGGACCCAA AGC TCAGA
 ||||| ||| |||
 CACCTGGGTT TCG AGTCT
 A ACA
 GAM3666 KIAA1297 3' GTGGACCCACAGCCTTGAG 82865 A CTCA
 GTGGACCCA AGCC GAG
 ||||| ||| |||

CACCTGGGT TCGG CTC
G AA__
GAM3666 KIAA1904 3' GGGTTCAAGGCCCTCAGAG 82866 ACC A
GG CAA GCCCTCAGAG
|| ||| |||||
CC GTT CGGGAGTCTC
CAA C
GAM3666 KREMEN2 3' GGCCCAGAGTCAGAGA 82867 A A CCC
GG CCCA AG TCAGAGA
|| ||| || |||||
CC GGGT TC AGTCTCT
_ C _
GAM3666 LIMR 3' GTGGTCCAAAGCCCCTCCAGGA 82868 AC _ A
GTGG CCAAAGCCCT CAG GA
||| ||||| ||| ||
CACC GGTTCGGGG GTC CT
A_ AG _
GAM3666 MGC3146 3' GTCGACTCCCTCAGAGAC 82869 G CCAAAG
GT GAC CCCTCAGAGAC
|| ||| |||||
CA CTG GGGAGTCTCTG
G A____
GAM3666 PLAGL2 3' GTGGCTCCAAAGCCTTGAC 82870 AC CTCAGA
GTGG CCAAAGCC GAC
||| ||||| |||
CACC GGTTCGG CTG
GA AA____
GAM3666 PP1628 5' TGGACCCAAGGCCTCTGCA 82871 A _ _
TGGACCCA GCC CT CA
||||| ||| |||
ACCTGGGTT CGG GA GT
C A C
GAM3666 PPP1R16B 3' GGACTTAAAGCCCCAAGAA 82872 CC C
GGAC AAAGCCCT AGAG
||| ||||| |||
CCTG TTTCTGGGG TCTT
AA T
GAM3666 SFRS11 3' TGGACTCCCTCAGAGC 82873 CCAAAG A
TGGAC CCCTCAGAG C
||| ||||| |
ACCTG GGGAGTCTC G
A____ C
GAM3666 LOC144596 3' GGACCCAGAAACAAGAG 82856 _ CCTC
GGACCCA AAGC AGAG
||||| ||| |||
CCTGGGT TTTG TCTC
C T____
GAM3666 LOC144698 5' TGGATCCAAAGCCCTGAG 82874 C CA
TGGA CCAAAGCCCT GAG
||| ||||| |||

	ACCT GGTTCGGGA CTC		
	A ____		
GAM3666 LOC152317 3'	GGACCCAAAGCTCTGAC 82875	C CAGA	
	GGACCCAAAGC CT GAC		
	CCTGGGTTTCG GA CTG		
	A ____		
GAM3666 LOC154386 5'	GTAGGCCGTTCTCAGAGGCA 82876	A CAAAGC A	
	GTGG CC CCTCAGAG CA		
	CATC GG GGAGTCTC GT		
	C CAA__ C		
GAM3666 LOC158235 5'	GTGGACCCAGAGCGCCAG 82877	A C T	
	GTGGACCCA AGC C CAG		
	CACCTGGGT TCG G GTC		
	C C_		
GAM3666 LOC160391 5'	GTGGACCCGGGTCCCTTCCTGG 82878	AAAG _A__	
AGAC	GTGGACCC CCCT C GAGAC		
	CACCTGGG GGGA G CTCTG		
	CCCA A GAC		
GAM3666 LOC196759 3'	GTGGCGCCCAGAACTTGGAGA 82879	A_ _ CCTCA	
	GTGG CCCA AAGC GAGA		
	CACC GGGT TTTG CTCT		
	GC C AAC__		
GAM3666 LOC202152 5'	GGATCCACGCTCAGAGAC 82880	C AAGCC	
	GGA CCA CTCAGAGAC		
	CCT GGT GAGTCTCTG		
	A GC__		
GAM3666 LOC253046 5'	TGGGCCCTCTTCCCCTCAGAGG 82881	A AAAG_ A	
CA	TGG CCC CCCTCAGAG CA		
	ACC GGG GGGAGTCTC GT		
	C AGAAG C		
GAM3666 LOC257407 5'	GTGGCTCAGAGAAACCGAGACA 82882	ACC ____ CTCA	
	GTGG CA AAGCC GAGACA		
	CACC GT TTTGG CTCTGT		
	GA_ CTC ____		
GAM3666 LOC90139 3'	GTGGGTTCCGAGTCCTCAAAGA 82883	AC_ AA C	
CA	GTGG CC AG CCTCAGAGACA		
	CACC GG TC GGAGTTTCTGT		
	CAA C_ A		
GAM3666 LOC92997 3'	GTGGCTCAGAGAAACCGAGACA 82882	ACC ____ CTCA	
	GTGG CA AAGCC GAGACA		

			CACC GT TTTGG CTCTGT		
			GA_ CTC ____		
GAM3667	CENPB	3'	TGACGTGGATGGCAGAGGG 82886	AC	TAAA
			TGACGTGGAT TAG AGGG		
			ACTGCACCTA GTC TCCC		
			CC ____		
GAM3667	HUNK	3'	GATGTGGATACATGTGGAGGG 82887	C	TA AAA
			GA GTGGATAC GT AGGG		
			CT CACCTATG CA TCCC		
			A TA CC_		
GAM3667	NBS1	3'	TGACTGGATACTTGTATGGGGG 82888	G	A AAA
	A		TGAC TGGATACT GTA GGGA		
			ACTG ACCTATGA CAT CCCT		
			_ A ACC		
GAM3667	TFF3	3'	TGACGTGGGTGCCAGTCTGGA 82889	ATA	AAAAG
			TGACGTGG CTAGT GGA		
			ACTGCACC GGTCA CCT		
			CAC GA__		
GAM3667	ALS2CR3	3'	TGGCGGGGATGCCTCAAAAGGG 82890	A T	A AG
			TG CG GGAT CT TAAAAGGG		
			AC GC CCTA GG GTTTTCCC		
			C C C A_		
GAM3667	FLJ23590	5'	TGACGTGGGCACTCAGCAGGG 82891	A _	AAA
			TGACGTGG TACT AGT AGGG		
			ACTGCACC GTGA TCG TCCC		
			C G ____		
GAM3667	KIAA1297	3'	TGACGTGGGTACTGGGTAGGG 82892	A	A_ AAA
			TGACGTGG TACT GT AGGG		
			ACTGCACC ATGA CA TCCC		
			C CC ____		
GAM3667	KIAA1937	5'	TGGACACCTTGGTGGAAGGG 82893	A__	AA
			TGGATACT GT AAGGG		
			ACCTGTGG CA TTCCC		
			AAC CC		
GAM3667	PSR	3'	TGACACAAGCTAGTGGGAGGG 82894	TG ATA	AAA
			TGACG G CTAGT AGGG		
			ACTGT T GATCA TCCC		
			GT C__ CCC		
GAM3667	Spir-1	3'	TGACGTGAAGTGTGGAGGG 82895	TACTA	AAA
			TGACGTGGA GT AGGG		

			ACTGCACTT CA TCCC		
			CA__ CC_		
GAM3668	ALS2	3'	TAAAAGTTCCTTTCTCCCCT 82898	_	__
			TAAAA TTCC CTCCCCT		
			ATTTT AAGG GAGGGGA		
			C AAA		
GAM3668	ASGR2	3'	CTTAAACTACCTCCTTTCTCT 82899	A	C CC
			CT AAATT CCTCC TTTCTCT		
			GA TTTGA GGAGG AAAGAGA		
			A T _		
GAM3668	ASGR2	3'	CTTAAACTACCTCCTTTCTCT 82899	A	C CC
			CT AAATT CCTCC TTTCTCT		
			GA TTTGA GGAGG AAAGAGA		
			A T _		
GAM3668	ASGR2	3'	CTTAAACTACCTCCTTTCTCT 82899	A	C CC
			CT AAATT CCTCC TTTCTCT		
			GA TTTGA GGAGG AAAGAGA		
			A T _		
GAM3668	ASGR2	3'	CTTAAACTACCTCCTTTCTCT 82899	A	C CC
			CT AAATT CCTCC TTTCTCT		
			GA TTTGA GGAGG AAAGAGA		
			A T _		
GAM3668	CALCRL	3'	CTAGGAATTCCCTCCCCT 82900	A_	_
			CTA AATTCCCTCCC CT		
			GAT TTAAGGGAGGG GA		
			CC T		
GAM3668	CDH12	5'	CCCAGGATTCCCTCCTGTCATC 82901	AA	CCTT _
	T		CCTA ATTCCCTCC TC TCT		
			GGGT TAAGGGAGG AG AGA		
			CC AC_ T		
GAM3668	CNTNAP2	3'	CCTAGTAATTCCCTCCTCCCT 82902	A_	_
			CCTA AATTCCCTCC CCTT		
			GGAT TTAAGGGAGG GGGA		
			CA A		
GAM3668	DDX6	3'	AAATTCCCTCTCCCACCCCT 82903	_	TT
			AAATTCCCTC CCC TCTCT		
			TTTAAGGGAG GGG GGGA		
			A T_		
GAM3668	ELK3	5'	TTCCCCCTTTTTTCTTTCTCT 82904	CC_	__
			TTCCCTC CTTTCTCT		

AAGGGGG GAAAGAGA
 AAAAAA
 GAM3668 ENPP3 3' CTAAACTCTCCTTTCTCT 82905 CCTCC
 CTAAAATTC CCTTTCTCT
 ||||| |||||
 GATTTTGAG GGAAAGAGA
 A____
 GAM3668 ETS1 5' CTCAAATTCCTGCTGCTTTCT 82906 A TCC_
 CTAAATTCCC CCTTTCT
 || ||||| |||||
 GA TTTAAGGG GGAAAGA
 G CGAC
 GAM3668 FHIT 5' CCTAGGATACCTTCTTTCTCTT 82907 AA T C CC_
 TCTCT CCTA AT CC TC CTTTCTCT
 ||| || || |||||
 GGAT TA GG AG GAAAGAGA
 CC T A AAAGA
 GAM3668 FOXO1A 3' AAATTCCTCCTTCCACT 82908 CC T
 AAATTCCTCC TTTC CT
 ||||| ||| ||
 TTTAAGGGAGG AAGG GA
 _ T
 GAM3668 GALNT7 3' CCAAATCTCTTTTCCTTC 82909 C CC_
 CTAAAATTC CT CCTTT
 ||||| || |||||
 GGTTTTAAG GA GGAAG
 A AAA
 GAM3668 HPCA 3' CCTAGAATCCTTCTCTCCCCT 82910 A C_
 CCTA AATTC CTCCCCT
 ||| |||| |||||
 GGAT TTAGG GAGGGGA
 C AAGA
 GAM3668 IFNGR2 5' CCCGCCCCCTCCCCTTT 82911 AAAA
 CCT TTCCCTCCCCTTT
 ||| |||||
 GGG GGGGGAGGGGAAA
 CG_
 GAM3668 KCNJ5 5' CCTTGGGTCACTCCCTTTCTCT 82912 AAAAT C C
 CCT TC CTCCC TTTCTCT
 ||| || |||| |||||
 GGA AG GAGGG AAAGAGA
 ACCC_ T _
 GAM3668 KCNK6 3' CCTTCCATCTTTCCCTTTCT 82913 AAAAT C _
 CCT TCC TC CCCTTTCT
 ||| ||| || |||||
 GGA AGG AG GGGAAAGA
 _ T AAA
 GAM3668 MEF2C 5' TTCCTTCCTTTTCTTTCTCT 82914 C C_
 TTCC TCC CTTTCTCT
 ||| ||| |||||

		AAGG AGG GAAAGAGA	
		A AAAA	
GAM3668	NFIX	3' CAAAATTTCTTCTCCCCCT	82915 _ C_
		TAAAATT C CTCCCCTTT	
		I	
		GTTTTAA G GAGGGGGGA	
		A AA	
GAM3668	NR5A2	3' CCTCATCCTTTCCTTTCTCT	82916 AAAATTC CC
		CCT CCT CTTTCTCT	
		GGA GGA GGAAAGAGA	
		GTA___ AA	
GAM3668	PLXNA2	3' TTCTTCTCCTCTTTCTCT	82917 C_ C
		TTC CTCC CTTTCTCT	
		AAG GAGG GAAAGAGA	
		AA A	
GAM3668	PTP4A2	3' AATTCCTTTTCTCTTTCTCT	82918 C__ CC
		AATTCC TC CTTTCTCT	
		TTAAGG AG GAAAGAGA	
		AAA A_	
GAM3668	PTP4A2	3' AATTCCTTTTCTCTTTCTCT	82918 C__ CC
		AATTCC TC CTTTCTCT	
		TTAAGG AG GAAAGAGA	
		AAA A_	
GAM3668	RPS6KA5	3' AAAACAGACCCCTTTCTCT	82919 TCCCT
		AAAAT CCCCTTTCTCT	
		TTTTG GGGGAAAGAGA	
		TCT__	
GAM3668	SCA1	5' CTGAAATCCACTCTTTCTCT	82920 A C CCC
		CT AAATTC CTC TTTCTCT	
		GA TTTAGG GAG AAAGAGA	
		C T _	
GAM3668	SCD	3' CCTTAAATCCTTCCCTTT	82921 A TC C
		CCT AAAT CCT CCCTTT	
		GGA TTTA GGA GGGAAA	
		A _ A	
GAM3668	SLC7A6	3' CCTAGCATTCCCTCTTCCCC	82922 AA _
		CCTA ATTCCCTC CCCT	
		GGAT TAAGGGAG GGGG	
		CG AA	
GAM3668	SNCA	3' CTAAAATTCCTCCTTCT	82923 C CCT
		CTAAAATTCC TCC TTCT	

GATTTTAAGG AGG AAGA

GAM3668 SNCA 3' CTAAAATTCCTCCTTCT 82923 C CCT
CTAAAATTCC TCC TTCT
||||||| ||| |||
GATTTTAAGG AGG AAGA

GAM3668 TARDBP 3' TAAAATTCCTTTAGCTCTTCCT 82924 C_ C III
TTTTCTA TTCC CTC CCTTT TCT A
||| ||| ||||| ||| I
AAGG GAG GGAAA AGA T

GAM3668 VASP 3' AAATTCCCTCCTTCC 82925 CCT
AAATTCCCTCC TTCT
||||||| |||
TTTAAGGGAGG AAGG

GAM3668 AKAP7 3' CCCAAAGTTCCTTTCCCT 82926 A C_
CCTAAA TTCCCT CCCT
||||| ||||| |||
GGGTTT AAGGGA GGGA
C AA

GAM3668 AKAP7 3' CCCAAAGTTCCTTTCCCT 82926 A C_
CCTAAA TTCCCT CCCT
||||| ||||| |||
GGGTTT AAGGGA GGGA
C AA

GAM3668 AKAP7 3' CCCAAAGTTCCTTTCCCT 82926 A C_
CCTAAA TTCCCT CCCT
||||| ||||| |||
GGGTTT AAGGGA GGGA
C AA

GAM3668 ATP10D 3' CCTAGAATCCCTCTTTCCCCTT 82927 A _ _
T CCTA AATTCC C TCCCCTTT
||| ||||| I |||||
GGAT TTAGGG G AGGGGAAA
C A AA

GAM3668 C17orf26 3' AATTTCCTTCCCTTTTCTA 82928 C C C III
AATT CCT CCCTTT TCT A
||| ||| ||||| ||| I
TTAA GGA GGGAAA AGA T
A A A III

GAM3668 C20orf82 3' CCAAATTCCTTTCTC 82929 CCCCT
CTAAAATTCCT TTCTC
||||||| |||
GGTTTAAAGGGA AAGAG

GAM3668 C21orf7 3' TAAAATATCCCTTCTC 82930 _ CCCCTT
TAAAAT TCCCT TCTC
||||| ||||| |||

ATTTTA AGGGA AGAG
 T _____
 GAM3668 dA141H5.1 3' CCTACTAAGCAATTCCCTTCTC 82931 A_____ CCC
 TTTCT CCTA AATTCCCT CTTTCT
 ||| ||||| |||||
 GGAT TTAAGGGA GAAAGA
 GATTCT AGA
 GAM3668 DD5 3' AAATTCCCTATTCCCTCT 82932 C____
 AAATTCCCT CCCTTT
 ||||| |||||
 TTTAAGGGA GGGAGA
 TAA
 GAM3668 DKFZP434N161 3' CCTAAGATTCCCACCCCT 82933 A T
 CCTAA ATTCCC CCCCTT
 ||| ||||| |||||
 GGATT TAAGGG GGGGGA
 C T
 GAM3668 DKFZP761F241 3' CTAAAATGTTCTCTCCCC 82934 ____ C
 CTAAAAT TC CTCCCC
 ||||| || |||||
 GATTTTA AG GAGGGG
 CA A
 GAM3668 ESPL1 5' CCTGAGGTCCTTCTCCCGAC 82935 AAAA ____ TT
 CT CCT TTC CCTCCCC TCT
 ||| ||| ||||| |||
 GGA AGG GGAGGGG GGA
 CTCC AA CT
 GAM3668 FADS2 3' CCTGAGACTCCCTCCCGCTCT 82936 AAA CTTT
 CCT ATTCCCTCCC CTCT
 ||| ||||| ||||| |||
 GGA TGAGGGAGGG GAGA
 CTC C____
 GAM3668 FLJ10057 3' CTGAATTCCTTGGCCTTCT 82937 AA CCC
 CT AATTCCT CTTTCT
 || ||||| |||||
 GA TTAAGGGA GGAAGA
 C_ ACC
 GAM3668 FLJ10300 5' CTGGAATTCCTTTTCC 82938 AA CCCC
 CT AATTCCT TTTCT
 || ||||| |||||
 GA TTAAGGGA AAAGG
 CC _____
 GAM3668 FLJ10803 3' CTACAGTTCCTTCCTCCTCT 82939 AAA C _
 CTA TTCC TCC CCTTT
 ||| ||| ||| |||||
 GAT AAGG AGG GGAGA
 GTC A A
 GAM3668 FLJ11164 3' CCCGAATTCTCTCCCTTTCTC 82940 AA C |||
 TA CT AATTC CTCCCTTTCTCT A
 || ||||| ||||| ||||| |||

GG TTAAG GAGGGGAAAGAGA T
C_ A III
GAM3668 FLJ13188 3' CTAAAACTTTGCTTTCTC 82941 CCCTCCC
CTAAAATT CTTTCTC
||||| |||||
GATTTTGA GAAAGAG
AAC____
GAM3668 FLJ13910 3' CCTGGAATTCTCTACCTTCTCT 82942 AA CC CC
CCT AATTC TC CTTTCTCT
||| ||||| || |||||
GGA TTAAG AG GGAAGAGA
CC _ AT
GAM3668 FLJ14442 3' CTAAAGTTCCTTCCTCCT 82943 A C _
CTAAA TTCC TCC CCT
||||| ||||| ||| |||
GATTT AAGG AGG GGA
C A A
GAM3668 FLJ22390 3' CCCACCCACTCTTCCTCTTTCT 82944 AA_ CC C
CT CCTA ATTC TCC CTTTCTCT
||||| ||||| ||| |||||
GGGT TGAG AGG GAAAGAGA
GGG A_ A
GAM3668 FLJ22800 3' CCTCCTTCCTTCTCCTTTCTC 82945 AAAA _C
T CCT TTCCCT C CTTTCTCT
||| ||||| ||| |||||
GGA AAGGGA G GGAAAGAGA
GG_ A A
GAM3668 FLJ22938 3' CTGCAATTTCTCTCCCCCTT 82946 A_ A _
CT AA TTCC CTCCCCTTT
|| || ||||| |||||
GA TT AAGG GAGGGGGAA
CG A A
GAM3668 FLJ23516 3' CCTGGAATTCTCCCCCCTTCT 82947 AA C
CCT AATTC CTCCCCTTTCT
||| ||||| |||||
GGA TTAAG GGGGGGGAAGA
CC A
GAM3668 FLJ32884 5' CCTATAATTCCTTCTCCCC 82948 A _
CCTA AATTCC CTCCCC
||||| ||||| |||||
GGAT TTAAGG GAGGGG
A AA
GAM3668 KIAA0438 3' CCTAAAACCTCAATTTTCT 82949 TTC CCC
CCTAAAA CCTC TTTCT
||||| ||||| |||||
GGATTTT GGAG AAAGA
_ TTA
GAM3668 KIAA0644 3' CTATAATTTCTTCCCCTCT 82950 A CCC
CTA AATT TCCCCTTT
||| ||||| |||||

		GAT TTAA AGGGGAGA		
		A AGA		
GAM3668 KIAA0847	3'	CCTAAAATTCCATTCTATCT	82951	CTCCC T
		CCTAAAATTCC CT TCT		
		GGATTTTAAGG GA AGA		
		TAA__ T		
GAM3668 KIAA0972	5'	CCTGGGGCTCCCTCCTTCC	82952	AAAA CCT
		CCT TTCCCTCC TTCT		
		GGA GAGGGAGG AAGG		
		CCCC ____		
GAM3668 KIAA1016	3'	CCTGGAATTCTCCTCCCCTCT	82953	AA _
		CCT AATTC CCTCCCCTTT		
		GGA TTAAG GGAGGGGAGA		
		CC A		
GAM3668 KIAA1228	3'	TAAAATTCCCTTTTCT	82954	CCCC
		TAAAATTCCCT TTTCT		
		ATTTTAAGGGA AAAGA		

GAM3668 KIAA1462	3'	CCTTGGGGATCCTTCTCTTTCT	82955	AAAAT_ C CC
	CT	CCT TCC TC CTTTCTCT		
		GGA AGG AG GAAAGAGA		
		ACCCCT A A_		
GAM3668 KIAA1918	3'	CTAAAATTCTCCCTTT	82956	CCTC
		CTAAAATTC CCCTTT		
		GATTTTAAG GGGAAA		
		A__		
GAM3668 LPAAT-delta	3'	CCTAAAATACCCTTTTCT	82957	TCCCTC
		CCTAAAAT CCCTTTCT		
		GGATTTTA GGGAAAGA		
		T_____		
GAM3668 MGC11082	5'	CCTTAAGCCCTTTTCTTTCTC	82958	A ATT CC_
	T	CCT AA CCCT CTTTCTCT		
		GGA TT GGGA GGAAAGAGA		
		A C__ AAA		
GAM3668 NINJ2	3'	CCTGGAATGCCCTTCCTATTCT	82959	AA T C CT
		CCT AAT CCCT CC TTCT		
		GGA TTA GGGA GG AAGA		
		CC C A AT		
GAM3668 P2RXL1	3'	TAGAATTCCCTGCCCCGCCCT	82960	A _ TTT
		TA AATCCCT CCCC CTCT		

		AT TTAAGGGA GGGG GGA		
		C C C_		
GAM3668	PEPP3	3' CTGAGGATCTCTCTCTCTCTCT 82961	AAAAT C CC	
		CT TC CTC CTTTCTCT		
		GA AG GAG GAGAGAGA		
		CTCCT A A_		
GAM3668	PNMA5	3' AATTCTCCTCCTCTTTCTCT 82962	_ C	
		AATTC CCTCC CTTTCTCT		
		TTAAG GGAGG GAAAGAGA		
		A A		
GAM3668	Rab11-FIP3	3' CCTGGGACTTCCCTTTCTCCCT 82963	AAAA_ CCC TT	
	CT	CCT TTCCCT CT CTCT		
		GGA AAGGGA GA GAGA		
		CCCTG AA_ GG		
GAM3668	RoXaN	3' CCTGAACACCCTCCCCTTTTTC 82964	A ATT C	
	T	CCT AA CCCTCCCCTTT TCT		
		GGA TT GGGAGGGGAAA AGA		
		C GT_ A		
GAM3668	SEC22C	3' CCAAAATATTTCTTTCTC 82965	TCCCTCC	
		CTAAAAT CCTTTCTC		
		GGTTTTA GGAAAGAG		
		TAAA_		
GAM3668	SPA17	5' CCTATGGAACCTCCTTTCTCT 82966	AAATTC CC	
		CCTA CCTCC TTTCTCT		
		GGAT GGAGG AAAGAGA		
		ACCTT_ _		
GAM3668	SPTLC2	3' CCTAACAATTTTTTTTCCCCCT 82967	_ CCC_	
	C	CCTAA AATT TCCCCTTT		
		GGATT TTAA AGGGGGAG		
		G AAAAA		
GAM3668	SYT12	5' CCCAAAATTCTTTCTCCACTTT 82968	C_ C	
		CCTAAAATTC CTCC CTTT		
		GGGTTTAAAG GAGG GAAA		
		AAA T		
GAM3668	THTPA	3' CCCAGAGTTCCCTTCCCCTTC 82969	AAA _	
		CCTA TTCCCT CCCCTTT		
		GGGT AAGGGA GGGAAG		
		CTC A		
GAM3668	URB	5' CCACTTTTTCTCCTCTTTTTC 82970	AAATTC C C	
	T	CTA CCTCC CTTT TCT		

GGT GGAGG GAAA AGA
GAAAAA A A
GAM3668 ZAK 3' CCTTAAGACCACCTCTTTCTCT 82971 AAAATTC T C
CCT CC CC CTTTCTCT
||| || |||||
GGA GG GG GAAAGAGA
ATTCT__ T A
GAM3668 ZFP95 3' CCTAAGGTCCCTCTCCCT 82972 AAT _
CCTAA TCCCTC CCCT
|||| ||||| |||
GGATT AGGGAG GGGA
CC_ A
GAM3668 ZFP95 3' CCTAAGGTCCCTCTCCCT 82972 AAT _
CCTAA TCCCTC CCCT
|||| ||||| |||
GGATT AGGGAG GGGA
CC_ A
GAM3668 LOC116068 3' AAATCACTTTCCCCTTTCTCT 82973 CCC_
AAATT TCCCCTTTCTCT
|||| |||||
TTTAG AGGGGAAAGAGA
TGAA
GAM3668 LOC123036 3' CCTAAAATATCACCATCTTTCT 82974 _ _ TCCC
CT CCTAAAAT TC CC CTTTCTCT
||||| || |||||
GGATTTTA AG GG GAAAGAGA
T T TA__
GAM3668 LOC123316 5' CCTGGACTTTCCTGGCCTTTCT 82975 AAAA C CC
CT CCT TT CCT CTTTCTCT
||| || |||||
GGA AA GGA GGAAAGAGA
CCTG A CC
GAM3668 LOC124460 3' CCTAAAATTCTCCCCTCTCT 82976 CC
CCTAAAATTC TCCCCTTTCT
||||||| |||||
GGATTTTAAG AGGGGAGAGA

GAM3668 LOC126133 3' CCTCGGGGGTCCCCTTTCTCT 82977 AAAATTCCC
CCT TCCCCTTTCTCT
||| |||||
GGA AGGGGAAAGAGA
GCCCCC____
GAM3668 LOC127703 5' CTAGCATTCTCTTCCCCTC 82978 AA C _
CTA ATTC CT CCCCTT
||| |||| |||||
GAT TAAG GA GGGGGAG
CG A A
GAM3668 LOC129676 3' CCTTCCCTTTTCTCTTTCTCT 82979 AAAAT ____ C
CCT TCCC TCC CTTTCTCT
||| |||| |||||

	GGA AGGG AGG GAAAGAGA		
	_____ AAA A		
GAM3668 LOC142955 5'	TAAAATTCCCCTCTTGTCT 82980	_	CCC
	TAAAATTCCC TC TTTCT		
	ATTTTAAGGG AG AAAGA		
	G AAC		
GAM3668 LOC142955 5'	CCTAAACCCCCCTTTCTC 82981	ATTCC	
	CCTAAA CTCCCCTTTCTC		
	GGATTG GGGGGGAAAGAG		

GAM3668 LOC143279 5'	CCCCCTCCTTTTCCTTTTCT 82982	_____	C
	TTCCCTCC CCTT TCT		
	GGGGGAGG GAAA AGA		
	AAAA A		
GAM3668 LOC143308 5'	CCTCCCTCCCTCCCTTTTTTCT 82983	AAAA	C C
	CCT TTCCCTCCC TTT TCT		
	GGA GAGGGAGGG AAA AGA		
	GG_ A A		
GAM3668 LOC143915 3'	CCTAAGGCTCCCTCCTACCT 82984	AA	_
	CCTAA TTCCCTCC CCT		
	GGATT GAGGGAGG GGA		
	CC AT		
GAM3668 LOC145694 5'	CCTGGGACTCCCTCCCCATCT 82985	AAA	TT
	CCT ATTCCCTCCCC TCT		
	GGA TGAGGGAGGGG AGA		
	CCC T_		
GAM3668 LOC145945 5'	CCTAAAATGTCTACTTTCT 82986	TCCC	CC
	CCTAAAAT TC CTTTCT		
	GGATTTTA AG GAAAGA		
	C_ AT		
GAM3668 LOC146520 5'	TAAATATTCCTCTCTTC 82987	_	CC
	TAAA ATTCCTC CTTT		
	ATTT TAAGGGAG GAAG		
	A A_		
GAM3668 LOC147057 3'	CCTGGAATGCCTTTCCCCCT 82988	AA T C_	
	CCT AAT CC TCCCCTT		
	GGA TTA GG AGGGGGA		
	CC C AA		
GAM3668 LOC147515 3'	CCTAAGGTTCCACTTTCCCC 82990	AA	_ _
	CCTAA TTCC C TCCCC		

GGATT AAGG G AGGGG
CC T AA
GAM3668 LOC147515 3' CTAAAATTCCCTTTTCCCC 82989 ____
CTAAAATTCCC TCCCCT
||||||| |||||
GATTTTAAGGG AGGGGG
AAA
GAM3668 LOC149995 3' CTAAAATTCCCTTTTCCCC 82989 ____
CTAAAATTCCC TCCCCT
||||||| |||||
GATTTTAAGGG AGGGGG
AAA
GAM3668 LOC150213 3' CCTGTTCCCCCCTTT 82991 AAAA T
CCT TTCCC CCCCTTT
||| |||| |||||
GGA AAGGG GGGGAAA
C_____
GAM3668 LOC150372 3' CCTGGGGCTTCCCTTCCCCACC 82992 AAAA_ _ TTT
CT CCT TTCCCT CCCC CTCT
||| |||| ||| |||
GGA AAGGGA GGGG GGGA
CCCCG A T____
GAM3668 LOC150481 3' CCTGAAAATCCCTCATTCT 82993 A T CCCT
CCT AAA TCCCTC TTCT
||| ||| ||||| |||
GGA TTT AGGGAG AAGA
C T T____
GAM3668 LOC158431 3' AAATCCTTTCTCTTTCTCT 82994 CC CC
AAATTC TC CTTTCTCT
||||| || |||||
TTTAGG AG GAAAGAGA
AA A_
GAM3668 LOC161734 3' CTAAACTTCCCTTCTC 82995 A CCCCTT
CTAAA TTCCCT TCTC
||||| ||||| |||
GATTT AAGGGA AGAG
G _____
GAM3668 LOC170372 5' CCATGATTCTTTTCCCTTTCT 82996 AA CCTC
CTA ATTC CCCTTTCT
||| ||| |||||
GGT TAAG GGGAAAGA
AC AAAA
GAM3668 LOC219513 5' CCTAAATTTCTTTCCCGCCCC 82997 A C_ C TT
TCT CCTAAA TTCC TCCC T CTCT
||||| ||| ||| | |||
GGATTT AAGG AGGG G GAGA
A AA C GG
GAM3668 LOC222933 5' CTGCAAACCCTTCCTTTCT 82998 AA TT CC
CT AA CCCT CCTTTCT
|| || ||| |||||

		GA TT GGGG GGAAAGA		
		CG T_ A_		
GAM3668	LOC254428 3'	CTAAAATTCCTTCCAATTCT	82999	C CCT
		CTAAAATTCC TCC TTCT		
		GATTTTAAGG AGG AAGA		
		A TT_		
GAM3668	LOC255520 3'	TAAAATTTTCCCCTTC	83000	CCC
		TAAAATT TCCCCTTT		
		ATTTTAA AGGGGAAG		
		A_		
GAM3668	LOC256337 3'	TCCTCCTCTTCTTTCTCT	83001	_ CC
		TTC CCTC CTTTCTCT		
		AGG GGAG GAAAGAGA		
		A AA		
GAM3668	LOC257364 3'	CCTGAAAGTCCTTCTCCCCC	83002	A T _
		CCT AAA TCC CTCCCCT		
		GGA TTT AGG GAGGGGG		
		C C AA		
GAM3668	LOC63904 3'	CCAACCCCCTCCCTTTTTTCT	83003	TAA C C
		CC AATTCCCTCCC TTT TCT		
		GG TTGGGGGAGGG AAA AGA		
		_ A A		
GAM3668	LOC91344 5'	TTCCTTCTTTCCCTTTTTTCT	83004	C _ C
		TTCC TC CCCTTT TCT		
		AAGG AG GGGAAA AGA		
		A AAA A		
GAM3668	LOC91516 5'	CCTGGAGTCCTTCCCTGGAGCC	83005	AAAAT C CTT_
	TCT	CCT TCC TCCC TCTCT		
		GGA AGG AGGG GGAGA		
		CCTC_ A ACCTC		
GAM3669	ARHGEF5 3'	CATACGGCTATCACTGAAA	83008	A ATTT
		TATAC GCTATCACT GAAA		
		GTATG CGATAGTGA CTTT		
		C _		
GAM3669	GDF8 3'	TATACAGCCATCATGAA	83009	CTATT
		TATACAGCTATCA TGAA		
		ATATGTCGGTAGT ACTT		
		_		
GAM3669	MTM1 3'	TATACAGCTATTTCTCCTTAA	83010	CA A
		TATACAGCTAT CT TTTGA		

			ATATGTCGATA GA GAATT		
			AA G		
GAM3669	MXI1	3'	ACAGTTATCAAAAATCTGAAA 83011	C	CT
			ACAG TATCA ATTTGAAA		
			TGTC ATAGT TAGACTTT		
			A TT		
GAM3669	MXI1	3'	ACAGTTATCAAAAATCTGAAA 83011	C	CT
			ACAG TATCA ATTTGAAA		
			TGTC ATAGT TAGACTTT		
			A TT		
GAM3669	SLC20A1	3'	TACACAGCTAATTTTGA 83012		TCACTA
			TATACAGCTA TTTGA		
			ATGTGTCGAT AACT		
			TA_____		
GAM3669	TRPS1	3'	CAGGCACCATTATTTGAAA 83013	C	C
			CAG TATCA TATTTGAAA		
			GTC GTGGT ATAACTTT		
			C A		
GAM3669	USH2A	3'	TACAGCTATATTGAAA 83014		CACTAT
			TACAGCTAT TTGAAA		
			ATGTCGATA AACTTT		
			T_____		
GAM3669	C21orf42	5'	CATACAGCTACAAGTTTGA 83015		T CTA
			TATACAGCTA CA TTTGA		
			GTATGTCGAT GT AACT		
			_ TC_		
GAM3669	CHSY1	3'	CAAGTCTATCACTGTTTGAAA 83016	C _	A
			A AG CTATCACT TTTGAAA		
			G TC GATAGTGA AACTTT		
			T A C		
GAM3669	GALNAC4ST-2	3'	CATACACTCATGCTATTTGA 83017		G ATCA
			TATACA CT CTATTTGA		
			GTATGT GA GATAAACT		
			_ GTAC		
GAM3669	KIAA0547	3'	TACAGCCCTATTTGAAA 83018		ATCA
			TACAGCT CTATTTGAAA		
			ATGTCGG GATAAACTTT		

GAM3669	KIAA0972	3'	TATACAGCTGACATACTGTG 83019	AT C _	
			TATACAGCT CA TATT TG		

		ATATGTCGA GT ATGA AC		
		CT _ C		
GAM3669	KIAA1320	5' TATACAACCATATTTGGAA	83020	TCAC A
		TATACAGCTA TATTTG AA		
		ATATGTTGGT ATAAAC TT		
		_____ C		
GAM3669	KIAA1718	3' ACAGTCACTTATTTGAAAC	83021	CTA _
		ACAG TCACT ATTTGAAAC		
		TGTC AGTGA TAAACTTTG		
		_____ A		
GAM3669	STX12	3' AACATCACTATTTGAAAC	83022	T
		AGC ATCACTATTTGAAAC		
		TTG TAGTGATAAACTTTG		

GAM3669	LOC151521	3' TACATGGAACCCCTATTTGAAA	83023	GCT_ A
	C	TACA ATC CTATTTGAAAC		
		ATGT TGG GATAAACTTTG		
		ACCT G		
GAM3669	LOC221547	3' AGCAGTCTATATTTGAAAC	83024	TA AC
		AGC TC TATTTGAAAC		
		TCG AG ATAAACTTTG		
		TC AT		
GAM3669	LOC257577	3' AGCAGTCTATATTTGAAAC	83024	TA AC
		AGC TC TATTTGAAAC		
		TCG AG ATAAACTTTG		
		TC AT		
GAM3669	LOC91948	3' TACAGCTATCATAGCTGA	83025	C T
		TACAGCTATCA TA TTGA		
		ATGTCGATAGT AT GACT		
		_____ C		
GAM3670	ADAM22	3' CGATGTATCACATGTAAA	83028	GGTAT
		TGATGTA TATGTAAA		
		GCTACAT GTACATTT		
		AGT__		
GAM3670	ADAM22	3' CGATGTATCACATGTAAA	83028	GGTAT
		TGATGTA TATGTAAA		
		GCTACAT GTACATTT		
		AGT__		
GAM3670	CNTN3	3' TGAAGTATGTAATATGTAAA	83029	T G T
		TGA GTA GTA TATGTAAA		

		ACT CAT CAT ATACATTT		
		T A T		
GAM3670	GBP1	3' TGTGTATTTGGCATTATGT	83030	A ____
		TG TGTA GGTATTATGT		
		AC ACAT CCGTAATACA		
		_ AAA		
GAM3670	HTR2C	3' TAATGTAGGCATGATTGTAAA	83031	TA_
		TGATGTAGGTAT TGTA		
		ATTACATCCGTA ACATTT		
		CTA		
GAM3670	PMP22	3' ATGTACATATATGTAAA	83032	G T
		ATGTA GTAT ATGTA		
		TACAT TATA TACATTT		
		G _		
GAM3670	ZNF18	3' TAATGTAGAACATGTAA	83033	TAT
		TGATGTAGG TATGTAA		
		ATTACATCT GTACATT		
		T__		
GAM3670	ATIP1	3' ATGTAGTGACATGTAAA	83034	_ T
		ATGTAG GTAT ATGTA		
		TACATC CATG TACATTT		
		A _		
GAM3670	C21orf93	3' GATGTAGAAGTATGTAAA	83035	TAT
		GATGTAGG TATGTAA		
		CTACATCT ATACATTT		
		TC_		
GAM3670	CDC14A	3' ATGTAGGCACATGTGTAAA	83036	TA_
		ATGTAGGTAT TGTA		
		TACATCCGTG ACATTT		
		TAC		
GAM3670	CHL1	3' TGTGTAGGAATTTCTATGTAAA	83037	A TA__
		TG TGTAGG TTATGTAA		
		AC ACATCC GATACATTT		
		_ TAAA		
GAM3670	DKFZp434O0515	5' TGATGTAGATTCCCTTTGTAAA	83038	A_ A
		TGATGTAGGT TT TGTA		
		ACTACATCTA GA ACATTT		
		AG A		
GAM3670	DNM1L	3' TAATGTAGGAATTAATGTA	83039	T _
		TGATGTAGG ATTA TGTA		

			ATTACATCC TAAT ACAT		
			T T		
GAM3670	FLJ10493	3'	TGATGTAGGTATTAATAAA 83040	T	
			TGATGTAGGTATTA GTAAA		
			ACTACATCCATAAT TATTT		
GAM3670	FLJ13340	3'	TGTTGTAGGTTTCTCTGTAAA 83041	A	A A_
			TG TGTAGGT TT TGTA		
			AC ACATCCA AG ACATTT		
			A A AG		
GAM3670	FLJ20126	3'	TGCTGTAGGTATACCTA 83042	A	T G
			TG TGTAGGTAT AT TA		
			AC ACATCCATA TG AT		
			G _ G		
GAM3670	FLJ20445	3'	GATGTCAACATTATGTAAA 83043	AG	
			GATGT GTATTATGTAAA		
			CTACA TGTAATACATTT		
			GT		
GAM3670	HSPC055	3'	TGATTAGGTATCATACA 83044	G	
			TGAT TAGGTATTATGTA		
			ACTA ATCCATAGTATGT		
GAM3670	KIAA1915	5'	ATGTAAATCCATGTAAA 83045	A	
			ATGTAGGT TTATGTAAA		
			TACATTTA GGTACATTT		
GAM3670	KLHL4	3'	TGATATAGGAAATGTAAA 83046	TATT	
			TGATGTAGG ATGTAAA		
			ACTATATCC TACATTT		
			TT_		
GAM3670	PRO0097	5'	TGATAAATATTATGTAA 83047	TA	
			TGATG GGTATTATGTAA		
			ACTAT TTATAATACATT		
GAM3670	PSIP2	3'	TAATGTAGCACAATGTA 83048	G T	
			TGATGTAG TAT ATGTA		
			ATTACATC GTG TACAT		
			_ T		
GAM3670	TBDN100	3'	TGTTGTAGGTTTCTCTGTAAA 83041	A	A A_
			TG TGTAGGT TT TGTA		

		AC ACATCCA AG ACATTT		
		A A AG		
GAM3670	LOC120892 3'	TGATGTAGGATCTGCA	83049	T A
		TGATGTAGG ATT TGTA		
		ACTACATCC TAG ACGT		
		- -		
GAM3670	LOC144571 3'	TGAGTAGGCTTCATGTAA	83050	T A
		TGA GTAGGT TTATGTAA		
		ACT CATCCG AGTACATT		
		- A		
GAM3670	LOC56959 5'	TGCATGGTTATTATGTAAA	83051	- -
		TGTA GGT ATTATGTAAA		
		ACGT CCA TAATACATTT		
		A A		
GAM3670	LOC91963 5'	TGAGTGGGATCATGTAA	83052	T A T
		TGA GT GG ATTATGTAA		
		ACT CA CC TAGTACATT		
		- C -		
GAM3671	APXL 3'	TAAGTAAGTTATAAATTATAA	83055	CT
		TAAG AGTTATAAGTTATAA		
		ATTC TCAATATTTAATATT		
		AT		
GAM3671	CR1 3'	TAAGCTAGTACTTTTATAATAA	83056	TATAAG
		TAAGCTAGT TTATAATAA		
		ATTCGATCA AATATTATT		
		TGAA__		
GAM3671	SHANK2 3'	AGCTAGTTCTGAAATAATAA	83057	ATAAGTT
		AGCTAGTT ATAATAA		
		TCGATCAA TATTATT		
		GACTT__		
GAM3671	FLJ20420 3'	ACCATAATAAGTTATAAT	83058	GTT
		GCTA ATAAGTTATAAT		
		TGGT TATTCAATATTA		
		AT__		
GAM3671	GRID1 3'	GCTAGTTATCACCTCATAA	83059	AAG__
		GCTAGTTAT TTATAA		
		CGATCAATA AGTATT		
		GTGGG		
GAM3671	LOC150279 3'	TGACTAGTTACTCAGATATAAT	83060	A A_ T
	A	A GCTAGTTAT AG TATAATA		

A TGATCAATG TC ATATTAT
 C AG T
 GAM3671 LOC222068 3' AGCTAGTTACAGGCAGTAA 83061 A TA
 AGCTAGTTATA GT TAA
 ||||| || |||
 TCGATCAATGT CG ATT
 C TC
 GAM3672 ATP11A 3' GTGCATGTGTGTATTACGCCT 83064 A C__ C
 GCAG GTGCA GTGTGTG CGCC GCAG
 |||| |||| ||| ||||
 CACGT CACACAT GCGG CGTC
 A AAGT A
 GAM3672 CREBBP 3' GTGTACGTGTGTGCACGCC 83065 CAA _
 GTG GTGTGTGC CGCC
 || ||||| ||||
 CAC CACACACG GCGG
 ATG T
 GAM3672 EN2 5' GTGCGTGTGTGTGCGTGTGCAG 83066 AA CGCCC
 GTGC GTGTGTGC GCAG
 ||| ||||| |||
 CACG CACACACG CGTC
 CA CACA_
 GAM3672 IMMP2L 5' CGGGCCAGGTGTGCCGCC 83067 T A T
 CG GC AG GTGTGCCGCC
 || || ||||| ||||
 GC CG TC CACACGGCGG
 C G _
 GAM3672 KCNS2 5' GTGCGAGTGTGTGCGCCCG 83068 A C
 GTGC AGTGTGTGC GCCCG
 |||| ||||| ||||
 CACG TCACACACG CGGGC
 C _
 GAM3672 MAB21L1 5' GTGCTGAGTGTGTGTCCG 83069 A_ _
 GTGC AGTGTGTG CCG
 |||| ||||| |||
 CACG TCACACAC GGC
 AC A
 GAM3672 NDRG1 3' GTGAAGTGTGTGCTGCTAC 83070 C C CC
 GTG AAGTGTGTGC GC GC
 || ||||| || ||
 CAC TTCACACACG CG TG
 _ A A_
 GAM3672 PTPN18 5' CGGCGAGTGTGGACGCCGC 83071 T A _
 CG GC AGTGTG TGCCGC
 || || |||| ||||
 GC CG TCACAC GCGGCG
 _ C CT
 GAM3672 CBX6 3' CGTGCAAGTGTGTGGGAGGC 83072 CC_
 CGTGCAAGTGTGTG GC
 ||||| || ||

		GCACGTTACACAC	CG		
		CCTC			
GAM3672	DKFZP564D172	3'	CGTGCGGGTGGGTGCGCC	83073	AA T C
			CGTGC GTG GTGC GCC		
			GCACG CAC CACG CGG		
			CC C _		
GAM3672	FHOD2	5'	CGGCGGTCTGGCTGCCGCCCGCA	83074	T AAG TG
	G		CG GC TG TGCCGCCCGCAG		
			GC CG GC ACGCGGGCGTC		
			_ CCA CG		
GAM3672	HRH3	3'	GTGCAGGTGTGTGCACGTGCAG	83075	A _ CCC
			GTGCA GTGTGTGC CG GCAG		
			CACGT CACACACG GC CGTC		
			C T A__		
GAM3672	KIAA1243	3'	GTGCAAGTGGAGTGGCTTGCAG	83076	T_ CC CC
			GTGCAAGTG GTG GC GCAG		
			CACGTTAC CAC CG CGTC		
			CT _ AA		
GAM3672	KIAA1536	3'	GTGTGAGTGTGTGTGTGCAG	83077	CA CCGCCC
			GTG AGTGTGTG GCAG		
			CAC TCACACAC CGTC		
			AC ACA__		
GAM3672	MGC23427	5'	TGCGGCGCGCCGCCCGC	83078	AAGT
			TGC GTGTGCCGCCCGC		
			ACG CGCGCGGCGGGCG		
			C__		
GAM3672	RAB3D	5'	CGCGTAGGGGGCGCCGCTGCA	83079	CA TGT C
	G		CGTG AG GTGCCGCC GCAG		
			GCGC TC CGCGGCGG CGTC		
			A_ CCC A		
GAM3672	STARD7	3'	GTGCATGTGTGTGCGCTCGCAG	83080	A C C
			GTGCA GTGTGTGC GC CGCAG		
			CACGT CACACACG CG GCGTC		
			A _ A		
GAM3672	STARD7	3'	GTGCATGTGTGTGCGCTCGCAG	83080	A C C
			GTGCA GTGTGTGC GC CGCAG		
			CACGT CACACACG CG GCGTC		
			A _ A		
GAM3672	URG4	3'	CGTGAAGTGTGTGGC	83081	C CCGCCC
			CGTG AAGTGTGTG GC		

GCAC TTCACACAC CG

GAM3672 LOC115110 3' CGTGCAGTGTGTGTCCAC 83082 A _
CGTGCA GTGTGTG CCGC
||||| ||||| |||
GCACGT CACACAC GGTG

GAM3672 LOC145258 3' CGGGCAAGTGTCCCGC 83083 T GTGCCG
CG GCAAGTGT CCCGC
|| ||||| |||
GC CGTTCACA GGGCG

GAM3672 LOC149576 3' CGTTAGCCCGCCGCCCGC 83084 GCAAGT G
CGT GT TGCCGCCCGC
||| || |||||
GCA CG GCGGCGGGCG
AT__ G

GAM3672 LOC149711 3' GTGCATGTGTGTGTGTGCAG 83085 A CCGCCC
GTGCA GTGTGTG GCAG
||||| ||||| |||
CACGT CACACAC CGTC
A ACA__

GAM3672 LOC153711 5' GTGTATGTGCGGAGCTCGCAG 83086 CAA C_ C
GTG GTGTGTGC GC CGCAG
||| ||||| || |||||
CAC TACACGCG CG GCGTC
A__ CT A

GAM3672 LOC155179 5' CGGGCAGCCCTGGCCGCCCGCA 83087 T A G_ T
G CG GCA GT TG GCCGCCCGCAG
|| ||| || || |||||
GC CGT CG AC CGGCGGGCGTC
C _ GG _

GAM3672 LOC196993 5' CGTGGGAGTGTGTGTGTGACC 83088 CA CC__
CGTG AGTGTGTG GCC
||||| ||||| |||
GCAC TCACACAC TGG
CC ACAC

GAM3672 LOC257054 3' CGTGCCGGGGCCCTCGCCCGCA 83089 AAGT GTGC
G CGTGC GT CGCCCGCAG
||||| || |||||
GCACG CG GCGGGCGTC
GCCC GGA_

GAM3673 SLK 3' ACAAATCACTGAAATAATTTTT 83092 ATA_
ACAGA TGAAATAATTTTT
||||| |||||
TGTTT ACTTTATTAATAA
AGTG

GAM3673 LOC200132 3' ACTAGAATATGAAAAAATT 83093 _ T
AC AGAATATGAAA AATT
|| ||||| |||

TG TCTTATACTTT TTAA
 A T
 GAM3673 LOC257482 3' CAGGATGTGAAATAATTTTT 83094 A A
 CAG AT TGAAATAATTTTT
 ||| || |||||
 GTC TA ACTTTATTAAAAA
 C C
 GAM3674 ARHGDIA 3' GGGCTGGAGGACGGCCCGG 83097 CA A CA
 GGGCTGG GGGACGGC CC G
 ||||| ||||| || I
 CCCGACC TCCTGCCG GG C
 — — C—
 GAM3674 BAI2 5' GGCGCTGGCGGGGGCGGCCACG 83098 — A A — CCA
 GGGC GG GCTGGC GGG CGGC AC GC
 || ||||| ||| ||| || ||
 CC CGACCG CCC GCCG TG CG
 G C C G CCC
 GAM3674 CD9 5' GGA CTGGCGGGACCTGGC 83099 A —
 GGGCTGGC GGGAC GGC
 ||||| ||||| |||
 CCTGACCG CCCTG CCG
 — GA
 GAM3674 CELSR2 3' GGGCTGCTGGGAACACCCAGC 83100 G A CG
 GGGCTG C GGGA GCACCCAGC
 ||||| I |||| |||||
 CCCGAC G CCCT TGTGGGTCG
 — A —
 GAM3674 CRYBA2 5' GGGTGGCACCACGCGCTCAGC 83101 C GGG — ACC
 GGG TGGCA ACG GC CAGC
 ||| ||||| ||| || ||||
 CCC ACCGT TGC CG GTCG
 — GG_ G A—
 GAM3674 DNMT3B 5' GGGCTGGCTGGGGCGCGGC 83102 A_ A_
 GGGCTGGC GGG CGGC
 ||||| ||| ||||
 CCCGACCG CCC GCCG
 AC GC
 GAM3674 EGLN2 5' GGGTGGCAGGGAAGGGGTCCAG 83103 C C CAC
 GGG TGGCAGGGA GG CCAG
 ||| ||||| || ||||
 CCC ACCGTCCCT CC GGTC
 — T CCA
 GAM3674 EPHA8 3' GGGCTGGCAGGGGGCAC 83104 AC
 GGGCTGGCAGGG GGCAC
 ||||| ||||| ||||
 CCCGACCGTCCC CCGTG
 —
 GAM3674 EPHB2 3' GGGCTGGCGGGAGTGGGC 83105 A C—
 GGGCTGGC GGGA GGC
 ||||| ||||| |||

			CCCGACCG CCCT CCG		
			— CAC		
GAM3674	EPHB2	3'	GGGCTGGCGGGAGTGGGC 83105	A	C__
			GGGCTGGC GGGA GGC		
			CCCGACCG CCCT CCG		
			— CAC		
GAM3674	FSTL3	3'	GGGCTGGCAGGGAATGGTGGCA 83106		C_ CACC
	GC		GGGCTGGCAGGGA GG CAGC		
			CCCGACCGTCCCT CC GTCG		
			TA ACC_		
GAM3674	GAS7	3'	GGGCTGGCAGGGTGGGGGC 83107	AC__	
			GGGCTGGCAGGG GGC		
			CCCGACCGTCCC CCG		
			ACCC		
GAM3674	GAS7	3'	GGGCTGGCAGGGTGGGGGC 83107	AC__	
			GGGCTGGCAGGG GGC		
			CCCGACCGTCCC CCG		
			ACCC		
GAM3674	ICAM2	5'	GGGCTCGCAGGGACCAGC 83108	G	_
			GGGCT GCAGGGAC GGC		
			CCCGA CGTCCCTG TCG		
			G G		
GAM3674	IL6R	5'	GGGCGGCAGGGGTGGCA 83109	T	AC
			GGGC GGCAGGG GGCA		
			CCCG CCGTCCC CCGT		
			— CA		
GAM3674	JTB	5'	GGGCCGCGCGGGGGCTCGCGGC 83110	A	A_____
			GGGCTGGC GGG CGGC		
			CCCGGCCG CCC GCCG		
			C CGAGC		
GAM3674	JUNB	5'	GGGCTGGCGCGGGCGGGTAGC 83111	A_	A CACCC
			GGGCTGGC GGG CGG AGC		
			CCCGACCG CCC GCC TCG		
			CG _ CA__		
GAM3674	LDB1	5'	GGGCTGACGGGGGGACAACCTTC 83112	A__	ACC
	AGC		GGGCTGGC GGGACGGC CAGC		
			CCCGACTG CCCTGTTG GTCG		
			CCC AA_		
GAM3674	LY64	3'	GGGCCGCGCAGTCCCTGCCAG 83113		GGACGGCA
			GGGCTGGCAG CCCAG		

		CCCGGCCGTC	GGGTC		
		AGGGAC__			
GAM3674	MMP11	3' GGCCTGGCAGGGGTCAGC	83114	G	A_
		GG CTGGCAGGG CGGC			
		CC GACCGTCCC GTCG			
		G CA			
GAM3674	NAV2	5' GGA CTGGCCACGGCGCTCAGC	83115		AGGG ACC
		GGGCTGGC ACGGC CAGC			
		CCTGACCG TGCCG GTCG			
		G__ CGA			
GAM3674	NEU1	3' GGGTGGTGGGGCCACACTTAGC	83116	C CA ACG CC	
		GGG TGG GGG GCAC AGC			
		CCC ACC CCC TGTG TCG			
		_ AC GG_ AA			
GAM3674	NFATC2	5' GGGCTGGCGGAGGCGGCTCGAG	83117		A A ACCC
	C	GGGCTGGC GGG CGGC AGC			
		CCCGACCG CTC GCCG TCG			
		C C AGC_			
GAM3674	PDCD2	5' GGGCTGGCGTGGGGCGCAG	83118		AG AC ACC
		GGGCTGGC GG GGC CAG			
		CCCGACCG CC CCG GTC			
		CA _ C_			
GAM3674	PLA2G4B	3' GGGTGGCAGGGGCCCCG	83119	C	ACG A A
		GGG TGGCAGGG GC CCC G			
		CCC ACCGTCCC CG GGG C			
		_ _ _ C			
GAM3674	PML	3' GGGCTGGCGAGGACTGTGGC	83120	AG	_
		GGGCTGGC GGAC GGC			
		CCCGACCG CCTG CCG			
		CT ACA			
GAM3674	PML	3' GGGCTGGCGAGGACTGTGGC	83120	AG	_
		GGGCTGGC GGAC GGC			
		CCCGACCG CCTG CCG			
		CT ACA			
GAM3674	RCN2	5' AGGCTGGCGGGGGCCCGGGC	83121		A AC A CA
		GGGCTGGC GGG GGC CC GC			
		TCCGACCG CCC CCG GG CG			
		_ _ _ CC			
GAM3674	SH3BP2	3' GGGTGGCAGGGAGCCTGGC	83122	C	C_
		GGG TGGCAGGGA GGC			

CCC ACCGTCCCT CCG
 _ CGGA
 GAM3674 SLC39A4 5' GGGCCGGCAGGGGGAGTTGGC 83123 AC____
 GGGCTGGCAGGG GGC
 ||||| |||
 CCCGGCCGTCCC CCG
 CCTCAA
 GAM3674 SLC8A2 5' GGGCTGGCAGTGGTGGGC 83124 _ AC
 GGGCTGGCAG GG GGC
 ||||| || |||
 CCCGACCGTC CC CCG
 A AC
 GAM3674 SNL 3' GGGTTAGCAGGGAGGGTTGGC 83125 C C____
 GGG TGGCAGGGA GGC
 || ||||| |||
 CCC ATCGTCCCT CCG
 A CCAA
 GAM3674 TRPV3 3' GGGCTGACGGGGGAAGCTGGC 83126 A_ C____
 GGGCTGGC GGGGA GGC
 ||||| ||| |||
 CCCGACTG CCCT CCG
 CC TCGA
 GAM3674 ARHGAP8 3' GGGCTGGCGGGACGGGACGCAG 83127 A C C
 GGGCTGGC GGGACGG AC CAG
 ||||| ||||| || |||
 CCCGACCG CCCTGCC TG GTC
 _ C C
 GAM3674 ARHU 5' GGGCTAGCAGGGCCCGGC 83128 A_
 GGGCTGGCAGGG CGGC
 ||||| |||
 CCCGATCGTCCC GCCG
 GG
 GAM3674 C20orf110 3' GGGTTGGAGGGAGATTCAGC 83129 C C ____
 GGG TGG AGGGA CGGC
 || || ||| |||
 CCC ACC TCCCT GTCG
 A _ CTAA
 GAM3674 CLPTM1 3' GGGCTGGCAGGGCGAGATGGC 83130 AC____
 GGGCTGGCAGGG GGC
 ||||| |||
 CCCGACCGTCCC CCG
 GCTCTA
 GAM3674 COTL1 5' GGGCTGGCGGCGGTGGCGACGG 83131 A____ _
 C GGGCTGGC GG GACGGC
 ||||| || |||||
 CCCGACCG CC CTGCCG
 CCGCCA G
 GAM3674 CTNNBIP1 5' GGGCCGGCAGGGGCAGCGGGTC 83132 A AC__ A
 CGGC GGGCTGGCAGGG CGGC CC GC
 ||||| ||| || ||

CCCGGCCGTCCC GTCG GG CG
 C CCCA C
 GAM3674 CXYorf1 3' GGGTGGGCAGAAAGCACCCAG 83133 CT AC
 GGG GGCAGGG GGCACCCAG
 ||| ||||| |||||
 CCC CCGTCTT TCGTGGGTC
 AC _
 GAM3674 DD96 3' GGGCTGGAGGGAGTCAGC 83134 C _
 GGGCTGG AGGGA CGGC
 ||||| |||| |||
 CCCGACC TCCCT GTCG
 _ CA
 GAM3674 DKFZp434N035 3' GGGCGGCAGGGAGCGCCTAGC 83135 T CG A C
 GGGC GGCAGGGA GC CC AGC
 ||| ||||| || |||
 CCCG CCGTCCCT CG GG TCG
 _ _ C A
 GAM3674 DKFZp547M072 3' AGGTTGGCAGGGAGGACCGACC 83136 C C _ CA
 TGGC GGG TGGCAGGGA GGC ACC GC
 ||| ||||| || ||| ||
 TCC ACCGTCCCT CTG TGG CG
 A C GC AC
 GAM3674 EPN2 3' GGGCTGGCAGGTGGTCAGC 83137 GA_
 GGGCTGGCAGG CGGC
 ||||| |||
 CCCGACCGTCC GTCG
 ACCA
 GAM3674 FAF1 5' GGGCTGGCGGGCGAGCCGGC 83138 A _ _
 GGGCTGGC GG GA CGGC
 ||||| || |||
 CCCGACCG CC CT GCCG
 C G CG
 GAM3674 FLJ00001 3' GGGCTGGCGGAGGCGGCA 83139 A A
 GGGCTGGC GGG CGGCA
 ||||| || |||
 CCCGACCG CTC GCCGT
 C C
 GAM3674 FLJ10815 3' GGGCTGGCAGGGGAGGAGGC 83140 AC_
 GGGCTGGCAGGG GGC
 ||||| |||
 CCCGACCGTCCC CCG
 CTCCT
 GAM3674 FLJ12089 5' GGGCTGGGGACGGCGCGCCTAG 83141 CAG A_ C
 C GGGCTGG GGACGGC CC AGC
 ||||| ||||| || |||
 CCCGACC CCTGCCG GG TCG
 _ CGC A
 GAM3674 FLJ12122 5' GGGCTGGCAGGGATGAGC 83143 C_
 GGGCTGGCAGGGA G GC
 ||||| ||| ||

CCCGACCGTCCCT C CG
 A T
 GAM3674 FLJ12122 5' GGGCTGCAGGGACCTGGGC 83142 G ____
 GGGCTG CAGGGAC GGC
 ||||| ||||| ||
 CCCGAC GTCCCTG CCG
 _ GAC
 GAM3674 FLJ20186 5' GGGCTCGCAGGGACAGGATGGC 83144 G ____
 GGGCT GCAGGGAC GGC
 ||||| ||||| ||
 CCCGA CGTCCCTG CCG
 G TCCTA
 GAM3674 FLJ20359 3' GGGCTGGCAGGGACTGAGC 83145 ____
 GGGCTGGCAGGGAC GGC
 ||||| ||||| ||
 CCCGACCGTCCCTG TCG
 AC
 GAM3674 FLJ21817 3' GCTGGCAGGGACAGGACAGC 83146 CACC
 GCTGGCAGGGACGG CAGC
 ||||| ||||| ||
 CGACCGTCCCTGTC GTCG
 CT__
 GAM3674 FLJ22341 3' GGCATGGTGGGCACCCAG 83147 _ GAC
 GGCA GG GGCACCCAG
 ||| || |||||
 CCGT CC CCGTGGGTC
 A AC_
 GAM3674 FLJ23119 3' GGGATGGCAGGAAGGCCCGGC 83148 C C A CA
 GGG TGGCAGGGA GGC CC GC
 ||| ||||| ||| ||
 CCC ACCGTCCTT CCG GG CG
 T _ _ C_
 GAM3674 FLJ23191 5' GGGCTGGCGCGGGCTTCGCCGG 83149 A_ A____
 C GGGCTGGC GGG CGGC
 ||||| ||| |||
 CCCGACCG CCC GCCG
 CG GAAGCG
 GAM3674 FLJ25416 3' GGGCTGGCAGGAAGACAACCAG 83150 C C
 C GGGCTGGCAGGGA GGCA CCAGC
 ||||| ||| |||
 CCCGACCGTCCCTT CTGT GGTCG
 _ T
 GAM3674 FLJ32356 3' GGCCTGGCAGGGGACTTTTGGC 83151 G _ ____
 GG CTGGCAGGG AC GGC
 || ||||| || ||
 CC GACCGTCCC TG CCG
 G C AAAA
 GAM3674 FXYD5 3' GGGCTTGGTCTTCGGGTGCCCA 83152 _ CAGGGA CA_
 GC GGGCT GG CGG CCCAGC
 ||||| || ||| |||||

CCCGA CC GCC GGGTCG
 A AGAA__ CAC
 GAM3674 GIT1 3' GGGCACCAGGGCACCTGGC 83153 T G _ _
 GGGC G CAGGG AC GGC
 |||| | |||| | ||
 CCCG T GTCCC TG CCG
 _ G G GA
 GAM3674 GOLPH2 3' AGGCTGGCACCAGCAC 83154 GGGA
 GGGCTGGCA CGGCAC
 |||| ||||
 TCCGACCGT GTCGTG
 G__
 GAM3674 GPS1 3' AGGCTGGGTGGCAGCCAG 83155 CAGGGAC
 GGGCTGG GGCAGCCAG
 |||| | ||||
 TCCGACC CCGTGGGTC
 CA____
 GAM3674 HEMK 3' GGGTGGCAGGGGGCA 83156 C AC
 GGG TGGCAGGG GGCA
 || |||| ||||
 CCC ACCGTCCC CCGT
 _ _
 GAM3674 jdp2 3' GGGCTGGCGAGGGTGCGCCCGG 83157 _ ACG A A
 C GGGCTGGC AGGG GC CCC GC
 |||| || || || ||
 CCCGACCG TCCC CG GGG CG
 C A__ C C
 GAM3674 KIAA0205 5' GGGCTGGCCGGGCCCCAG 83158 AGGGAC A
 GGGCTGGC GGC CCCAG
 |||| | || ||||
 CCCGACCG CCG GGGTC
 GC____ _
 GAM3674 KIAA0476 5' GGGCGGCGGGGGCTACCCG 83159 T A ACG _ A
 GGGC GGC GGC GC ACCC G
 || || || || || || ||
 CCCG CCG CCC CG TGGG C
 _ _ _ A C
 GAM3674 KIAA0544 3' GGGCTGGCAGGTAGATGTCAGC 83160 GA____
 GGGCTGGCAGG CGGC
 |||| || || ||
 CCCGACCGTCC GTCG
 ATCTACA
 GAM3674 KIAA0854 3' GGGCTGGCTGGGCACAGC 83161 A _
 GGGCTGGC GGC ACGGC
 |||| || || || ||
 CCCGACCG CCC TGTCG
 A G
 GAM3674 KIAA0964 3' GGGCTGGCGGGGCACCTCCCAG 83162 A A G A_
 GGGCTGGC GGC CG C CCCAG
 |||| || || || || ||

CCGACCG CCC GT G GGGTC
 C _ _ GA
 GAM3674 KIAA1037 3' GGGCCGGCACTGCACCTG 83163 GGGACG CA
 GGGCTGGCA GCACC G
 ||||| ||| |
 CCGGCCGT CGTGG C
 GA _ _ AC
 GAM3674 KIAA1199 3' GGGCTGGGGGACCCA 83164 CA CGGCA
 GGGCTGG GGGA CCA
 ||||| ||| |||
 CCGACC CCCT GGGT
 _ _
 GAM3674 KIAA1677 5' GGGCGCCGGGACGGCACTCGGC 83165 TG A CCA
 GGGC GC GGGACGGCAC GC
 ||| || ||||| ||
 CCG CG CCCTGCCGTG CG
 _ G AGC
 GAM3674 KIAA1754 3' GGGCTGCTGAGCTGGCACCCAG 83166 G A AC
 GGGCTG C GGG GGCACCCAG
 ||||| | ||| |||||
 CCGAC G CTC CCGTGGGTC
 _ A GA
 GAM3674 KIAA1872 5' GGGCTGGCAGAGGCTCGGC 83167 _ A_
 GGGCTGGCAG GG CGGC
 ||||| || |||
 CCGACCGTC CC GCCG
 T GA
 GAM3674 MAPKAPK2 3' GGGCGGCAGGGGTGGGAG 83168 T AC CACCC
 GGGC GGCAGGG GG AG
 ||| ||||| || ||
 CCG CCGTCCC CC TC
 _ CA C _
 GAM3674 MGC11335 5' AGGCTGGCGGGGATGCGCGGGC 83169 A C_
 GGGCTGGC GGGA GGC
 ||||| ||| |||
 TCGACCG CCCT CCG
 C ACGCGC
 GAM3674 MGC12921 3' GGGCTGTGGCGTGTGCACCCGG 83170 GCAG ACG_ A
 C GGGCTG GG GCACCC GC
 ||||| || ||||| ||
 CCGAC CC CGTGGG CG
 A _ GCACA C
 GAM3674 MGC2306 3' GGGCTGGCAGGAGTGGTGTCGG 83171 A_
 C GGGCTGGCAGGG CGGC
 ||||| ||| |||
 CCGACCGTCCT GCCG
 CACCACA
 GAM3674 MGC2752 5' GGGCTGGCGGGGCTTCGGC 83172 A A_
 GGGCTGGC GGG CGGC
 ||||| ||| |||

		CCCGACCG CCC GCCG		
		C GAA		
GAM3674 MGC4504	3'	GGGCTGGCCGGGGCCTCAG	83173	A ACG ACC
		GGGCTGGC GGG GC CAG		
		CCCGACCG CCC CG GTC		
		G ____ GA_		
GAM3674 moblak	3'	GGGTGGCAGGGGTTTCAGC	83174	C A__
		GGG TGGCAGGG CGGC		
		CCC ACCGTCCC GTCG		
		____ CAA		
GAM3674 MSRA	5'	GGGCGGCAGGGGCGCGGGC	83175	T A ____
		GGGC GGCAGGG C GGC		
		CCCG CCGTCCC G CCG		
		____ C CGC		
GAM3674 NIFU	5'	GGGCAGGCGGGGGCTCCGCAGC	83176	T A AC A _
		GGGC GGC GGG GGC CC CAGC		
		CCCG CCG CCC CCG GG GTCG		
		T _ _ A C		
GAM3674 OBSCN	3'	GGGCTGGCCAGCACCTG	83177	AGGGA CA
		GGGCTGGC CGGCACC G		
		CCCGACCG GTCGTGG C		
		____ AC		
GAM3674 P5CR2	3'	GGGTGGCAGGGGCGGCA	83178	C A
		GGG TGGCAGGG CGGCA		
		CCC ACCGTCCC GCCGT		
		____ C		
GAM3674 PRO0149	3'	GGGCTGTTGTTGGGCACCCAG	83179	GCAGGGAC
		GGGCTG GGCACCCAG		
		CCCGAC CCGTGGGTC		
		AACAAC__		
GAM3674 RAB11B	3'	GGGCTGGCTGGGCCACCC	83180	A ACGG
		GGGCTGGC GGG CACCC		
		CCCGACCG CCC GTGGG		
		A G__		
GAM3674 RAI1	3'	GGA CTGGCAGGGACTGGC	83181	_
		GGGCTGGCAGGGAC GGC		
		CCTGACCGTCCCTG CCG		
		A		
GAM3674 RNF10	5'	GGGCCGGCGGGGGTCGGC	83182	A_ A
		GGGCTGGC GGG CGGC		

		CCCGGCCG CCC GCCG	
		CC A	
GAM3674 SH3BGL2	5'	GGGCTGGCGTGGACGCAGAGC 83183	AG G CCC
		GGGCTGGC GGACG CA AGC	
		CCCGACCG CCTGC GT TCG	
		CA _ C__	
GAM3674 TMPIT	3'	GGGCCGGCAGGGGAAGGCCAG 83184	AC_ AC
C		GGGCTGGCAGGG GGC CCAGC	
		CCCGGCCGTCCC CCG GGTCG	
		CTT _	
GAM3674 TREX2	5'	GCTGGCAGCACTCGCCCAGC 83185	G G GGCA
		GCTGGCA G AC CCCAGC	
		CGACCGT C TG GGGTCG	
		_ G AGC_	
GAM3674 TREX2	5'	GCTGGCAGCACTCGCCCAGC 83185	G G GGCA
		GCTGGCA G AC CCCAGC	
		CGACCGT C TG GGGTCG	
		_ G AGC_	
GAM3674 WBSCR20A	5'	GGCGCTGGAGATCACGGCATCC 83186	_ C G_ C
AGC		GG GCTGG AGG ACGGCA CCAGC	
		CC CGACC TCT TGCCGT GGTCG	
		G _ AG A	
GAM3674 ZFP36L2	5'	GGGCCGGCGGGAGGGTCCGGC 83187	___ A_
		GGGCTGGC AGGG CGGC	
		CCCGGCCG TCCC GCCG	
		CCC AG	
GAM3674 LOC112868	5'	GGGCTGGGAGGACCCGGC 83188	C A_
		GGGCTGG AGGG CGGC	
		CCCGACC TCCT GCCG	
		C GG	
GAM3674 LOC115073	5'	GGA CTGGCATGGGCGCCTGGC 83189	_ AC__
		GGGCTGGCA GGG GGC	
		CCTGACCGT CCC CCG	
		A GCGGA	
GAM3674 LOC123591	5'	GGGCCGGCGGGGGCCTCCAGC 83190	A AC AC
		GGGCTGGC GGG GGC CCAGC	
		CCCGGCCG CCC CCG GGTCG	
		_ _ GA	
GAM3674 LOC126528	3'	GGTTGGCAGGGCGTGCCAGC 83191	C A GCA
		GG TGGCAGGG CG CCCAGC	

	CC ACCGTCCC GC GGGTCG	
	A _ AC_	
GAM3674 LOC143677 5'	GAGCTGGCAGGGGACTCCCAG 83192	AC A
	GGGCTGGCAGGG GGC CCCAG	
	CTCGACCGTCCC CTG GGGTC	
	_ A	
GAM3674 LOC144455 5'	GGGCTGGCGGGGACCCCGC 83193	A GGCA A
	GGGCTGGC GGGAC CCC GC	
	CCCGACCG CCCTG GGG CG	
	C _ _	
GAM3674 LOC146378 3'	GGCAGGCGAGGGCGCCCAG 83194	_ C A
	GGCAGG GA GGC CCCAG	
	CCGTCC CT CCG GGGTC	
	G C C	
GAM3674 LOC147645 5'	GGGTGGGCGGGGACGGCCGCCA 83195	CT A AC
GC	GGG GGC GGGACGGC CCAGC	
	CCC CCG CCCTGCCG GGTGC	
	AC C GC	
GAM3674 LOC149373 3'	GGGTTGCTGGATAAACACCCAG 83196	CTG A AC
C	GGG GC GGG GGCACCCAGC	
	CCC CG CCT TTGTGGGTCG	
	AA_ A AT	
GAM3674 LOC152065 5'	AGGCTGGCAGGGCCCTGGC 83197	AC_
	GGGCTGGCAGGG GGC	
	TCCGACCGTCCC CCG	
	GGGA	
GAM3674 LOC161344 5'	GGGCTAGCAGGGGGCTGAGCAC 83198	AC_
CCAGC	GGGCTGGCAGGG GGCACCCAGC	
	CCCGATCGTCCC TCGTGGGTCG	
	CCGAC	
GAM3674 LOC162137 3'	GGGCGGGCGGGCTGGCTGTCCA 83199	T A AC AC_
GC	GGGC GGC GGC GGC CCAGC	
	CCCG CCG CCC CCG GGTGC	
	C _ GA ACA	
GAM3674 LOC163682 3'	GGGTTGCTGCCTGGCACCCAGC 83200	CTG AGGGAC
	GGG GC GGCACCCAGC	
	CCC CG CCGTGGGTCG	
	AA_ ACGGA_	
GAM3674 LOC196410 3'	GGCTTGGCAGGGATGCAGGC 83201	_ C_
	GGCT GGCAGGGA GGC	

		CCGA CCGTCCCT CCG			
		A ACGT			
GAM3674	LOC200093 3'	GGGTGGGCAGAAAGCACCC	83202	CT	AC
		GGG GGCAGGG GGCACCC			
		CCC CCGTCTT TCGTGGG			
		AC _			
GAM3674	LOC201689 3'	GGGTCTGGCAGGCACCCAG	83203	_	GGGAC
		GGG CTGGCA GGCACCCAG			
		CCC GACCGT CCGTGGGTC			
		A _			
GAM3674	LOC202284 5'	GGGCTGGTAGGGGACTCAG	83204	C	AC ACC
		GGGCTGG AGGG GGC CAG			
		CCCGACC TCCC CTG GTC			
		A _ A_			
GAM3674	LOC206836 5'	GGGTTGGCAGGAGCAGCA	83205	C	GA
		GGG TGGCAGG CGGCA			
		CCC ACCGTCC GTCGT			
		A TC			
GAM3674	LOC219920 5'	AGGCTGGCATAGTGCCCAG	83206	G	ACGGCA
		GGGCTGGCA GG CCCAG			
		TCCGACCGT TC GGGTC			
		A AC_			
GAM3674	LOC245727 3'	GGGCGGCAGGACCCA	83208	T	GACGGC
		GGGC GGCAGG ACCCA			
		CCCG CCGTCC TGGGT			
		_ _			
GAM3674	LOC245727 3'	GGGTGGCAGGGCCCCA	83207	C	ACGGCA
		GGG TGGCAGGG CCCA			
		CCC ACCGTCCC GGGT			
		_ _			
GAM3674	LOC253128 3'	AGGCTGGCAGGGGCCCA	83209		ACG A
		GGGCTGGCAGGG GC CCA			
		TCCGACCGTCCC CG GGT			
		_ _			
GAM3674	LOC255057 5'	GGGCTGGCGGCGGGCGGC	83210	A_ A	
		GGGCTGGC GGG CGGC			
		CCCGACCG CCC GCCG			
		CCG _			
GAM3674	LOC255826 5'	GGGCTGGCAGGGAGCAAGAGC	83211		CG CCC
		GGGCTGGCAGGGA GCA AGC			

CCGGACCGTCCCT CGT TCG
 _ TC_
 GAM3674 LOC51112 5' GGGCTGGCGGGGGCCGGGAGC 83212 A A_ CACCC
 GGGCTGGC GGG CGG AGC
 ||||| ||| ||| |||
 CCGGACCG CCC GCC TCG
 C CG CC_
 GAM3674 LOC91040 3' GGGTTGGGCAGAAAGCACCC 83213 CT_ AC
 GGG GGCAGGG GGCACCC
 ||| ||||| |||||
 CCC CCGTCTT TCGTGGG
 AAC _
 GAM3674 LOC92148 5' GGGCGGCAGGGCGAGACTCAG 83214 T A C C
 GGGC GGCAGGG CGG AC CAG
 ||| ||||| ||| |||
 CCGG CCGTCCC GCT TG GTC
 _ _ C A
 GAM3675 MTCP1 5' AGGGTTCTATGGCAATT 83217 TATCAT
 AGGGTTCTAT CAATT
 ||||| |||||
 TCCAAGATA GTTAA
 CC_
 GAM3675 MYBL1 5' TAGAGTCCAATCATCAGTTCC 83218 TATT A
 TAGGGTTC ATCATCA TTCC
 ||||| ||||| |||||
 ATCTCAGG TAGTAGT AAGG
 T_ C
 GAM3675 TIAM1 3' GGATTCTGATCAATTC 83219 ATTATC
 GGGTTCT ATCAATTC
 ||||| |||||
 CCTAAGA TAGTTAAG
 C_
 GAM3675 FHX 3' TAGGATTTTATTGTCAACCCTCC 83220 C A AA
 TAGGGTT TATT TCATC TTCC
 ||||| ||| ||||| |||||
 ATCCTAA ATAA AGTGG GAGG
 A C _
 GAM3675 KIAA1582 5' GAGGTACCATCATCAATT 83221 TTC
 GGG TATTATCATCAATT
 ||| |||||
 CTC ATGGTAGTAGTTAA
 C_
 GAM3675 LOC202460 5' TAGAGTTGGTTCATCAATT 83222 CTATTA
 TAGGGTT TCATCAATT
 ||||| |||||
 ATCTCAA AGTAGTTAA
 CCA_
 GAM3675 LOC222444 3' TAGGGATTCAGTCTCATCGATT 83223 _ TATTA A
 TAGGG TTC TCATC ATT
 ||||| ||| ||||| |||

			ATCCC AAG AGTAG TAA		
			T TCAG_ C		
GAM3676	CHRN2	3'	TTGGCAGGAATCGCTGACCACT	83226	AA TTGCG C
		GT	TTG AG GCTGACCAC GT		
			AAC TC CGACTGGTG CA		
			CG CTTAG A		
GAM3676	DKFZp761F2014	3'	CTGGGAGTTGCAGATCACTGT	83227	AA CTGAC C
			TTG AGTTGCGG CAC GT		
			GAC TCAACGTC GTG CA		
			CC TA__ A		
GAM3676	OPRL1	5'	TTGGGAGCTGGGACCACCG	83228	AA C CTG
			TTG AGTTG GG ACCACCG		
			AAC TCGAC CC TGGTGGC		
			CC _ _		
GAM3676	LOC196746	5'	TTGGAGGTGTGGCTGGTCAC	83229	AA T C AC
			TTG AG TG GGCTG CAC		
			AAC TC AC CCGAC GTG		
			C_ C A CA		
GAM3676	LOC200226	3'	TGGGAGTTGCGGGCAGGCCGT	83230	AA _ TGACCA
			TG AGTTGCGG C CCGT		
			AC TCAACGCC G GGCA		
			CC C TCC__		
GAM3677	CLCN3	3'	TTGCATGTGAGCAAACAG	83233	A CTT
			TTGCATGT AGC ATAG		
			AACGTACA TCG TGTC		
			C TT_		
GAM3677	DIO3	3'	TTGCACGTGGGCTTCGAAGG	83234	AA C ATA
			TTGCATGT GC TT GAGG		
			AACGTGCA CG AA TTCC		
			CC _ GC_		
GAM3677	GYPA	3'	ATGTAATAACGCCTTATAGAGG	83235	_____
			ATGTAA GCCTTATAGAGG		
			TACATT CGGAATATCTCC		
			ATTG		
GAM3677	SCML2	3'	TTGTGTGTAAACCTACAG	83236	CA T
			TTG TGTAAGCCT ATAG		
			AAC ACATTTGGA TGTC		
			AC _		
GAM3677	STAC	3'	TTGCATGTGGCATCAGAGAGG	83237	AA C T
			TTGCATGT GC TTA AGAGG		

		AACGTACA CG AGT TCTCC		
		C_ T C		
GAM3677	ALDH9	5' TTGCATGTAAGCATCCTAG	83238	C A
		TTGCATGTAAGC TT TAG		
		AACGTACATTCTG AG ATC		
		T G		
GAM3677	FLJ12661	5' TTGCATGTGGTCGGCATGGAGG	83239	AAGCCT A
		TTGCATGT TAT GAGG		
		AACGTACA GTA CTCC		
		CCAGCC C		
GAM3677	FLJ22569	3' TTGCATGTAACCTTTTTTATTGA	83240	GCC__ A
	GG	TTGCATGTAA TTAT GAGG		
		AACGTACATT AATA CTCC		
		GAAAA A		
GAM3677	FLJ32865	3' TTACATGCACATTTTTTATAGG	83241	AGCC__ A
	G	TTGCATGTA TTATAG GG		
		AATGTACGT AATATC CC		
		GTA AAA _		
GAM3677	KIAA0469	3' TTGATGTAAGCCCCTGGCAGGG	83242	C A__ A
		TTG ATGTAAGCCTT TAG GG		
		AAC TACATTCGGGG GTC CC		
		_ ACC _		
GAM3677	KIAA1553	3' TTGCATGTGGTCGTAAAGG	83243	AAGCC TA
		TTGCATGT T TAGAGG		
		AACGTACA A ATTTCC		
		CC__ GC		
GAM3677	KIAA1775	3' TTGCATGCAAGCTGTAAGG	83244	CTTATA
		TTGCATGTAAGC GAGG		
		AACGTACGTTCTG TTCC		
		ACA__		
GAM3677	KIAA1948	5' TTACATGTAGGCCAGAG	83245	A TTAT
		TTGCATGTA GCC AGAG		
		AATGTACAT CGG TCTC		
		C ____		
GAM3677	LOC113230	3' ACTGTAAGTTTTATAGAGG	83246	A CC
		GC TGTAAG TTATAGAGG		
		TG ACATTC AATATCTCC		
		_ AA		
GAM3677	LOC120939	3' GCGTGTGTCACTATAGAGG	83247	A AA_ CT
		GC TGT GC TATAGAGG		

		CG ACA TG ATATCTCC	
		C CAG _	
GAM3677	LOC158038 5'	TTGCATGTGGCCAAAAG 83248	AA TTAT
		TTGCATGT GCC AGAG	
		AACGTACA CGG TTTC	
		C_ T__	
GAM3677	LOC169545 5'	TGTAATGCTTATTATAGAGG 83249	_ C__
		TGTAA GC TTATAGAGG	
		ACATT CG AATATCTCC	
		A AAT	
GAM3677	LOC170063 3'	TTACATATTTATAGAG 83250	AAGCC
		TTGCATGT TTATAGAG	
		AATGTATA AATATCTC	

GAM3677	LOC170409 3'	TTGCATATAAGTCTGGAGG 83251	C TATA
		TTGCATGTAAG CT GAGG	
		AACGTATATTC GA CTCC	
		A C__	
GAM3677	LOC89932 3'	TTGCATGTTGGCCTCAGGAGG 83252	AA TA
		TTGCATGT GCCTTA GAGG	
		AACGTACA CGGAGT CTCC	
		AC C_	
GAM3678	MGC24976 5'	TATCTTGTCAAAATTGGT 83255	TAGTC
		TATTTTGTCAAA ATTGGT	
		ATAGAACAGTTT TAACCA	

GAM3678	PA26 3'	TATTTTGTCTACCATTGGT 83256	AAA G
		TATTTTGTCT TA TCATTGGT	
		ATAAAACAG AT GGTAACCA	

GAM3678	SLC26A7 3'	TTTGTCAATTATCCTGTTGGT 83257	A GT A_
		TTTGTCAA TA C TTGGT	
		AAACAGTT AT G AACCA	
		A AG AC	
GAM3678	TRPC3 3'	TATTTTGTGTTGGCAGTTCAGTTG 83258	CAAA _ _
	GT	TATTTTGT TAGT CA TTGGT	
		ATAAAACA GTCA GT AACCA	
		ACC_ A C	
GAM3679	OPCML 3'	CAAATGAACTTACGTTTT 83261	TTT _
		CAAATGGA ACT ACGTTTT	

		GTTTACTT TGA TGCAAAA	
		___ A	
GAM3679	LOC154428 3'	ACACGTGACATTTATTACGTTT 83262	AA _ C
	T	GCA TGG ATTTA TACGTTTT	
		TGT ACT TAAAT ATGCAAAA	
		GC G A	
GAM3680	IFNAR2 3'	TATTTACAGAAATATCACAGG 83265	_ A G GAA
	GC	TATTTAC GAAA AT AT GGC	
		ATAAAGTG CTTT TA TG CCG	
		T A G TC_	
GAM3680	FLJ20972 3'	TATTTCACTGAAAATTCCTGTA 83266	GA GA_ A
	GG	TATTTAC AAAAT TG AGG	
		ATAAAGTG TTTTA AC TCC	
		AC AGG A	
GAM3680	NUDT5 3'	TATTTTACGAAAAAGCTAATGG 83267	C TGA A
	C	TATTT ACGAAAAA TGA GGC	
		ATAAA TGCTTTTT ATT CCG	
		A CG_ A	
GAM3680	LOC170395 3'	TATTTACAGAAAGTGTTAAGG 83268	A A ATG
	C	TATTTACG AAA TG AAGGC	
		ATAAAGTGT TTT AC TTCCG	
		C C AA_	
GAM3680	LOC256239 3'	TATTTCACTGGGGAATGATGAA 83269	GAAA_
	GA	TATTTAC AATGATGAAGG	
		ATAAAGTG TTACTACTTCT	
		ACCCC	
GAM3680	LOC90462 3'	TTCAAAAAAATGATGGGGG 83270	C AA
		TTCA GAAAAATGATG GG	
		AAGT TTTTTTACTAC CC	
		_ CC	
GAM3681	ACCN1 3'	TAGCAGAGAGTCCCATGG 83273	TAC G
		TAGCAGAG GTTC CATGG	
		ATCGTCTC CAGG GTACC	
		T_ _	
GAM3681	CD5 3'	CAGCAGAGTGTGAGCTGG 83274	AC TC A
		TAGCAGAGT GT GC TGG	
		GTCGTCTCA CA CG ACC	
		_ CT _	
GAM3681	MTMR3 3'	CAGCAGAGTCAAGCATGG 83275	A TTC
		TAGCAGAGT CG GCATGG	

			GTCGTCTCA GT CGTACC		
			_ T_		
GAM3681	STARD5	3'	GCCAGAGTGCATCGCATGG 83276	_ A T	
			GC AGAGT CGT CGCATGG		
			CG TCTCA GTA GCGTACC		
			G C _		
GAM3681	C1orf24	3'	GCAGAGTAAATACATGG 83277	C TC	
			GCAGAGTA GT GCATGG		
			CGTCTCAT TA TGTACC		
			T _		
GAM3681	CENTA2	3'	TAGCAGAATGCCCCTAATG 83278	AC GC_	
			TAGCAGAGT GTTC ATG		
			ATCGTCTTA CGGG TAC		
			_ GAT		
GAM3681	DEPP	3'	CAGCAGAGTGCCCCAGTGG 83279	AC G _	
			TAGCAGAGT GTTC CA TGG		
			GTCGTCTCA CGGG GT ACC		
			_ _ C		
GAM3681	EBNA1BP2	5'	TAGCAGAGGGCGGCCCTGG 83280	TA TTC A_	
			TAGCAGAG CG GC TGG		
			ATCGTCTC GC CG ACC		
			CC _ GG		
GAM3681	EFA6R	3'	GCAGAGCAGTGGCATGG 83281	C TC	
			GCAGAGTA GT GCATGG		
			CGTCTCGT CA CGTACC		
			_ C_		
GAM3681	KIAA1243	3'	AGCAAAGTGTTTGCATGG 83282	AC C	
			AGCAGAGT GTT GCATGG		
			TCGTTTCA CAA CGTACC		
			_ A		
GAM3681	KIAA1462	3'	TAGCAGAGTTGTCAGTGG 83283	AC CGCA	
			TAGCAGAGT GTT TGG		
			ATCGTCTCA CAG ACC		
			A_ TC_		
GAM3681	NUDEL	3'	CAGCAGAGTGGGGGCTATGG 83284	ACGTTC _	
			TAGCAGAGT GC ATGG		
			GTCGTCTCA CG TACC		
			CCCC_ A		
GAM3681	OBTP	3'	TAGTGGAAGCTTCGCATGG 83285	C_ ACG	
			TAG AGAGT TTCGCATGG		

		ATC TTTCG AAGCGTACC		
		ACC ____		
GAM3681	PDGFC	3' TAGTGAATACGTACATGG	83286	CA TC
		TAG GAGTACGT GCATGG		
		ATC CTTATGCA TGTACC		
		AC ____		
GAM3681	REPRIMO	3' TAGCAAAGTGGGCAGGCGTGG	83287	AC TC A
		TAGCAGAGT GT GC TGG		
		ATCGTTTCA CG CG ACC		
		CC TC C		
GAM3681	SFXN5	3' CAGCAGAGTGGGGCATGG	83288	ACGTTC
		TAGCAGAGT GCATGG		
		GTCGTCTCA CGTACC		
		CCC____		
GAM3681	SIMRP7	3' GCAGAGCAGCCGTGTGG	83289	C T CA
		GCAGAGTA GT CG TGG		
		CGTCTCGT CG GC ACC		
		__ _ AC		
GAM3681	ZNF361	5' TAGCAGGTACCACATG	83290	A GTT
		TAGCAG GTAC CGCATG		
		ATCGTC CATG GTGTAC		
		__ _		
GAM3681	LOC145978	5' GCAGGGCAATCGCATGG	83291	A CGT
		GCAG GTA TCGCATGG		
		CGTC CGT AGCGTACC		
		C T__		
GAM3681	LOC153328	3' TAGCAGAGTGGGCATTGG	83292	ACGTTC _
		TAGCAGAGT GCAT GG		
		ATCGTCTCA CGTA CC		
		CC____ A		
GAM3681	LOC220070	3' TAGCAGAGCATCCAGTGG	83293	CGT G _
		TAGCAGAGTA TC CA TGG		
		ATCGTCTCGT AG GT ACC		
		__ G C		
GAM3681	LOC254778	3' TAGCAGAGGTGCGTGTGG	83294	TAC T CA
		TAGCAGAG GT CG TGG		
		ATCGTCTC CA GC ACC		
		__ C AC		
GAM3681	LOC90355	3' ACAGAGTACAGCAGTGG	83295	TTC _
		GCAGAGTACG GCA TGG		

			TGTCTCATGT CGT ACC		
			___ C		
GAM3682	DUSP4	5'	TGTCATGGGCATTGTATTAC 83298	AC C GC	
			TGTCATGG CAT GTG TAC		
			ACAGTACC GTA CAT ATG		
			C_ A A_		
GAM3682	DYRK1A	3'	TGTCATGGAGTGGTGA CT 83299	CCATC	
			TGTCATGGA GTGGCT		
			ACAGTACCT CACTGA		
			CAC__		
GAM3682	HNRPD	3'	TGTATGGACCAATACTCTAC 83300	C TCGTGG	
			TGT ATGGACCA CTAC		
			ACA TACCTGGT GATG		
			_ TATGA_		
GAM3682	IL5RA	5'	TGTCTATGCTCGTGGCT 83301	_ GACCA	
			TGTC ATG TCGTGGCT		
			ACAG TAC AGCACCGA		
			A G__		
GAM3682	OPHN1	3'	TGTCATGGAATTGTGCATAC 83302	CCATCG _ _	
			TGTCATGGA TG GC TAC		
			ACAGTACCT AC CG ATG		
			TA__ A T		
GAM3682	PML	3'	TGCCATGGGCTGCCAGGGCT 83303	ACCA T	
			TGTCATGG TCG GGCT		
			ACGGTACC GGT CCGA		
			CGAC C		
GAM3682	DJ473B4	3'	TGTCTGGACCACAACC 83304	A CGT	
			TGTC TGGACCAT GGCT		
			ACAG ACCTGGTG TTGG		
			_ _		
GAM3682	FLJ12484	3'	TGTCTGGGCCACAGCTGC 83305	A A C G	
			TGTC TGG CCAT GT GC		
			ACAG ACC GGTG CG CG		
			_ C T A		
GAM3682	FLJ12899	3'	TGCCATGGATCATATGC 83306	CCA _	
			TGTCATGGA TCGTG GC		
			ACGGTACCT AGTAT CG		
			_ A		
GAM3682	FLJ22477	3'	TGTGTGGACCACTCACTGC 83307	CA _ TG	
			TGT TGGACCA TCG GC		

		ACA ACCTGGT AGT CG	
		C_ G GA	
GAM3682 HT002	3'	TGTCATGATCATAGCC 83308	GACC
		TGTCATG ATCGTGGCT	
		ACAGTAC TAGTATCGG	

GAM3682 KIAA0323	3'	TGCCATGGGCCACATGCT 83309	A T G
		TGTCATGG CCA CGTG CT	
		ACGGTACC GGT GTAC GA	
		C _ _	
GAM3682 KIAA0820	3'	TGTCATGGGACACCCCTAC 83310	AC GTGG
		TGTCATGG CATC CTAC	
		ACAGTACC GTGG GATG	
		CT G_	
GAM3682 KIAA1322	3'	TGTCAGGAAATGGCTA 83311	T CCATC
		TGTCA GGA GTGGCTA	
		ACAGT CCT TACCGAT	
		_ T_	
GAM3682 KIAA1671	3'	TGTCATGGATTTTCAAAGGC 83312	CCA T_
		TGTCATGGA TCG GGC	
		ACAGTACCT AGT CCG	
		AAA TT	
GAM3682 PDE8B	3'	TGTAGTGCCTCGTGGCT 83313	CA GA A
		TGT TG CC TCGTGGCT	
		ACA AC GG AGCACCGA	
		TC _ _	
GAM3682 TACTILE	5'	TGTCATGGAGCAGTTGC 83314	C TC G
		TGTCATGGA CA GT GC	
		ACAGTACCT GT CA CG	
		C _ A	
GAM3682 TU3A	3'	TGTCATGGTAGCAAAGTGGCT 83315	AC_ TC
		TGTCATGG CA GTGGCT	
		ACAGTACC GT CACCGA	
		ATC TT	
GAM3682 LOC114987	3'	TGTCATGGTCTATGACT 83316	ACCA _
		TGTCATGG TC GTGGCT	
		ACAGTACC AG TACTGA	
		_ A	
GAM3682 LOC115442	3'	TGTCTGGACCATCCCTGAC 83317	A _ G
		TGTC TGGACCAT C TGGC	

	ACAG ACCTGGTA G ACTG	
	— G G	
GAM3682 LOC120196 3'	TGTCATGGAACATGTGACT 83318	C C
	TGTCATGGA CAT GTGGCT	
	ACAGTACCT GTA CACTGA	
	T —	
GAM3682 LOC146138 3'	TGTCATGATTGGTCCAGCTA 83319	ACCA G
	TGTCATGG TC TGGCTA	
	ACAGTACT AG GTCGAT	
	AACC —	
GAM3682 LOC150299 3'	TGTCATGGATCTGGATA 83320	CCA G C
	TGTCATGGA TC TGG TA	
	ACAGTACCT AG ACC AT	
	— — T	
GAM3682 LOC152179 5'	TGTCATGGACTACAATGATTA 83321	C C GC
	TGTCATGGAC AT GTG TA	
	ACAGTACCTG TG TAC AT	
	A T TA	
GAM3682 LOC152582 5'	TGCCATGGGCCAGGCC 83322	A TCGT
	TGTCATGG CCA GGCT	
	ACGGTACC GGT CCGG	
	C —	
GAM3682 LOC160954 5'	GCCGCCGCCGTCGTGGCTAC 83323	A_ GA A
	GTC TG CC TCGTGGCTAC	
	CGG GC GG AGCACCGATG	
	CG — C	
GAM3682 LOC162048 5'	TGTCTGCCCTCGTGGCT 83324	A GA A
	TGTC TG CC TCGTGGCT	
	ACAG AC GG AGCACCGA	
	— GG —	
GAM3682 LOC196214 5'	TGCCATGGGCCGTCAGGGC 83325	A A T
	TGTCATGG CC TCG GGC	
	ACGGTACC GG AGT CCG	
	C C C	
GAM3682 LOC201252 3'	TGTCATGACCGTGTGC 83326	GACC —
	TGTCATG ATCGTG GC	
	ACAGTAC TGGCAC CG	
	— A	
GAM3682 LOC205888 5'	TGTGATGAAATTGTGGCTAC 83327	C CC C
	TGT ATGGA AT GTGGCTAC	

		ACA TACTT TA CACCGATG	
		C _ A	
GAM3682	LOC221814 5'	TGACATGGATCAAAACTA 83328	T C TCGT
		TG CATGGA CA GGCTA	
		AC GTACCT GT TTGAT	
		T A TT__	
GAM3682	LOC221922 5'	TGTCATGGTGCCATTCAT 83329	A_ _
		TGTCATGG CCAT CGT	
		ACAGTACC GGTA GTA	
		AC A	
GAM3682	LOC222166 3'	TGCCATGGACACCACAGGCTAC 83330	C GT_
		TGTCATGGAC ATC GGCTAC	
		ACGGTACCTG TGG CCGATG	
		_ TGT	
GAM3682	LOC255328 3'	TGTCATGGCACTGTCCAAC 83331	_ CA G
		TGTCATGG AC TC TGGC	
		ACAGTACC TG AG GTTG	
		G AC _	
GAM3682	LOC93444 3'	TGCCATGGGTTTCGAAAGCT 83332	ACCA T_
		TGTCATGG TCG GGCT	
		ACGGTACC AGC TCGA	
		CAA_ TT	
GAM3683	CRYZL1 3'	TATCAAGAGTAGTGACTTTT 83335	TAC TCT
	GC	TATCAAG AGT ACTTTTGC	
		ATAGTTC TCA TGAAAACG	
		TCA CAC	
GAM3683	DLX4 3'	GTCCACTTCTGCTTTTGC 83336	A G A
		GT CA TTCT CTTTGC	
		CA GT AAGA GAAAACG	
		G G C	
GAM3683	DLX4 3'	GTCCACTTCTGCTTTTGC 83336	A G A
		GT CA TTCT CTTTGC	
		CA GT AAGA GAAAACG	
		G G C	
GAM3683	EHD3 3'	CATTGAGTACAGTGGGGATTG 83337	CA TCTACT
	C	TAT AGTACAGT TTTGC	
		GTA TCATGTCA AAACG	
		AC CCCCT_	
GAM3683	HIP2 3'	CATCAAGTATTTACTATTTTGC 83338	CAGTT C
	C	TATCAAGTA CTA TTTTGC	

			GTAGTTCAT	GAT AAAACG		
			AAAT_	A		
GAM3683	MNAT1	3'	AAGTCTGCTTTACTTTTGC	83339	ACA	C
			AAGT GTT TACTTTTGC			
			TTCA CGA ATGAAAACG			
			GA_	A		
GAM3683	PIGN	3'	TACCAAGCACTTTCTACTTTTG	83340	AG	
			TATCAAGTAC TTCTACTTTTG			
			ATGGTTCGTG AAGATGAAAAC			
			A_			
GAM3683	KIAA1026	3'	GCTGAGTTCCTACTTTTG	83341	AC	_
			GT AGTTC TACTTTTG			
			CG TCAAG ATGAAAAC			
			AC G			
GAM3683	VIT1	3'	TCAAGTACAGTAAGATTTTGC	83342	TCTAC	
			TCAAGTACAGT TTTTGC			
			AGTTCATGTCA AAAACG			
			TTCT_			
GAM3684	KIR2DL3	3'	TGAGGGAAGGTGGAACA	83345	CG	A
			TGAGGGAAGG TG GAGCG			
			ACTCCCTTCC AC CTTGT			
			_ _			
GAM3684	KIR2DL5	3'	TGAGGGAAGGTGGAACA	83345	CG	A
			TGAGGGAAGG TG GAGCG			
			ACTCCCTTCC AC CTTGT			
			_ _			
GAM3684	KIR3DL2	3'	TGAGGGAAGGTGGAACA	83345	CG	A
			TGAGGGAAGG TG GAGCG			
			ACTCCCTTCC AC CTTGT			
			_ _			
GAM3684	LENG4	5'	TGGGGGAAGGCTGACTGCA	83346	A	G GA
			TG GGGAAGGC TGA GCG			
			AC CCCTTCCG ACT CGT			
			C _ GA			
GAM3684	MYOD1	3'	TGGGGGAGGGCGCGAGAA	83347	A	A
			TG GGGA GGCGTGAGAG			
			AC CCCT CCGCGCTCTT			
			C C			
GAM3684	NUP98	5'	TGGGGAAGGGGAAGTGTCA	83348	A	CGTGA C
			TG GGGAAGG GAG GTCA			

		AC CCCTTCC	TTC CAGT	
		— CC— A		
GAM3684	FLJ10342	5'	TGAGGGAAGGGGTGAAGAGCG	83349 C _
			TGAGGGAAGG GTGA GAGCG	
			ACTCCCTTCC CACT CTCGC	
			C T	
GAM3684	FLJ20886	3'	TGAGGGAAGGCGGGGACAG	83350 T_ G
			TGAGGGAAGGCG GA AG	
			ACTCCCTTCCGC CT TC	
			CC G	
GAM3684	JM11	3'	TGAGAGAAGAAGCAGGGTGTCA	83351 C G AGC
	G		TGAGGGAAGG GT AG GTCAG	
			ACTCTCTTCT CG TC CAGTC	
			T _ CCA	
GAM3684	KIR3DS1	3'	TGAGGGAAGGTGGAACA	83345 CG A
			TGAGGGAAGG TG GAGCG	
			ACTCCCTTCC AC CTTGT	
			— —	
GAM3684	MGC12904	3'	TGGGGGAAGGGTGAGAGCTCAG	83352 A C G
			TG GGAAGG GTGAGAGC TCAG	
			AC CCCTTCC CACTCTCG AGTC	
			C _ —	
GAM3684	LOC219920	3'	TGAGGGAAGGCTGGGAG	83353 G A
			TGAGGGAAGGC TG GAG	
			ACTCCCTTCCG AC CTC	
			— C	
GAM3684	LOC90317	3'	TGGTGAAGGCAAAGCG	83354 AG TGA
			TG GGAAGGCG GAGCG	
			AC CCTTCCGT TTCGC	
			CA —	
GAM3685	PTMA	3'	TATAAAATGTAAATAAAAAA	83357 T
			TATAAAAT GTAAATAAAAAA	
			ATATTTTA CATTTATTTTTT	
			—	
GAM3685	LOC145123	3'	TATAAAATGTAAATAAAAAA	83357 T
			TATAAAAT GTAAATAAAAAA	
			ATATTTTA CATTTATTTTTT	
			—	
GAM3685	LOC150928	3'	TATAAAATGTAAATAAAAAA	83357 T
			TATAAAAT GTAAATAAAAAA	

ATATTTTA CATTTATTTTTT

GAM3685 LOC151277 5' AAAACTGCCATAAAAAACA 83358 AA
—
AAAATTGT ATAAAAAACA
||||| |||||||
TTTTGACG TATTTTTTTGT

G_

GAM3685 LOC151507 3' TAAAATTGCAAACAAGAAA 83359 A
TAAAATTGTAAATAA AAA
||||||| |||
ATTTTAACGTTTGTT TTT

C

GAM3686 CD4 3' CTTGACTGGCTTGGCTGTGTGA 83362 A AAAACT_
T CTTGACTG CTT TGAT
||||| ||| |||
GAACTGAC GAA ACTA

C CCGACAC

GAM3686 MAD2L1 3' CACTTTCACCTTAAACTTTGAT 83363 GACTG
TACTT ACTTAAACTTTGAT
||||| |||||||||
GTGAA TGAATTTGAACTA

AG_

GAM3686 MTR 3' CTTGACAATAAACTTG 83364 TGACT
CTTGAC TAAAACTTG
||||| |||||||
GAACTG ATTTTGAAC

TT_

GAM3686 FLJ20457 3' TACTTGGCTACTTAAACT 83365 A A
TACTTG CTG CTTAAACT
||||| ||| |||||||
ATGAAC GAT GAATTTTGA

C _

GAM3686 LOC146446 3' TGCTGACTGGGGAACCTTGA 83366 A TAA_
TG CTGACT AACTTGA
|| ||||| |||||||
AC GACTGA TTGAACT

_ CCCC

GAM3687 GATA1 3' TATTTTACAAAAGCTTTGAAG 83369 CA_ A
TATTT AAAAGCTTT GAAG
||||| ||||||| |||
ATAAA TTTTCGAAA CTTC

ATG _

GAM3687 IFI16 3' TTTCAAATTATAGAAGTTG 83370 AAGCTT
TTTCAA TAGAAGTTG
||||| |||||||
AAAGTTT ATCTTCAAC

AAT_

GAM3687 LBR 3' TTTCAATGTAGTTT TAGAAGTT 83371 AA_ C
G TTTCAA AG TTTAGAAGTTG
||||| || |||||||||

AAAGTT TC AAATCTTCAAC
 ACA A
 GAM3687 FLJ21162 3' CATTTCAGGAAACTGGAAGTT 83372 A_ TTA
 G TATTTCAA AAGCT GAAGTTG
 ||||| ||| |||||
 GTAAAGTT TTTGA CTTCAAC
 CC C_

GAM3687 KIAA0354 3' TATTTCAAAAATCTCAAGTTG 83373 G TAG
 TATTTCAAAA CTT AAGTTG
 ||||| ||| |||||
 ATAAAGTTTTT GAG TTCAAC
 A _

GAM3687 TUCAN 5' TATTTCAAAAAGAAGT 83374 AAGCTTT
 TATTTCAA AGAAGT
 ||||| |||
 ATAAAGTTT TCTCA

GAM3687 LOC221935 3' CATTTCAGAAACAGATGAAGTT 83375 AA TTTA
 G TATTTCA AAGC GAAGTTG
 ||||| ||| |||||
 GTAAAGT TTTG CTTCAAC
 C_ TCTA

GAM3687 LOC93550 3' TATTTCAAAAGGTAAAAAGTTG 83376 AGCTTT
 TATTTCAAAA AGAAGTTG
 ||||| |||||
 ATAAAGTTTT TTTTCAAC
 CCAT_

GAM3688 ChGn 3' AGATTGTTTGGTTCAC 83379 AGCTA A
 GGATTGTTT GG TTCAC
 ||||| || |||||
 TCTAACAAA CC AAGTG

GAM3688 KIAA0660 3' AGAATTGTTTAAAGATTCA 83380 CTA
 AGGATTGTTTAG GGATTCA
 ||||| |||||
 TCTTAACAAATT TCTAAGT

GAM3688 KIAA0769 3' AGGGTCCGCTAGGATT 83381 ATT A
 AGG GTTT GCTAGGATT
 || ||| |||||
 TCC CAGG CGATCCTAA

GAM3688 KIAA1046 3' AGAATTGTTTGAGCCCAG 83382 _ A
 AGGATTGTTT AGCT GG
 ||||| ||| ||
 TCTTAACAAA TCGG TC
 C G

GAM3688 KIAA1655 3' GGGTTGTAGAATTAGGATT 83383 A TT C
 GG TTGT AG TAGGATT
 || ||| || |||||

CC AACA TT ATCCTAA
 C TC A
 GAM3688 LGI3 3' GGGTGAGCTGGGATTCACG 83384 AT TTT A
 GG TG AGCT GGATTCACG
 || || ||| |||||
 CC AC TCGA CCTAAGTGC
 C_ _ _ C
 GAM3689 KIAA0352 3' TAAATATTAATGTCCAAAA 83387 T A
 A AATATTAATGT CTAAAA
 | ||||| |||||
 A TTATAATTACA GGTTTT
 T _
 GAM3689 KIAA1586 5' TATAATATCAATGCCATAAAA 83388 AC
 TATAATATTAATGT TAAAA
 ||||| |||||
 ATATTATAGTTACG ATTTT
 GT
 GAM3690 GAK 3' ATGAATCAGCTGTTCTTC 83391 TGAAA C
 ATGAGTCA TGT CCTTC
 ||||| ||| |||||
 TACTTAGT ACA GGAAG
 CG_ _ A
 GAM3690 GBA 3' TGAGCTGACTCTGTCCCTT 83392 CA AA_
 TGAGT TGA TGTCCCTT
 |||| ||| |||||
 ACTCG ACT ACAGGGAA
 _ GAG
 GAM3690 GPR17 3' TGGCCTGTGTCTCTTCAA 83393 A A AAA C
 TG GTC TG TGTC CTTCAA
 || ||| ||| |||||
 AC CGG AC ACAG GAAGTT
 _ _ _ A
 GAM3690 IHPK3 3' ATGAGCTCATGAAC TCACTCTT 83394 _ ATGTCC
 CAA ATGAG TCATGAA CTTCAA
 |||| ||||| |||||
 TACTC AGTACTT GAAGTT
 G GAGTGA
 GAM3690 PIWIL1 3' GAGTCTTAAAATGTTTCTT 83395 A CC
 GAGTC TGAAATGT CTT
 |||| ||||| |||
 CTCAG ATTTTACA GAA
 A AA
 GAM3690 RNF18 3' ATGATCATGAATAATGATTTTT 83396 G _ TCCC
 CAA ATGA TCATGAA ATG TTCAA
 |||| ||||| ||| |||||
 TACT AGTACTT TAC AAGTT
 _ AT TAAA
 GAM3690 C21orf59 3' CATGAAAATGTCTTTTCA 83397 _ CC
 CATGAAA TGTC TTCA
 ||||| ||| |||||

GTACTTT ACAG AAGT
 T AA
 GAM3690 DKFZp547C176 3' AGTCATGAAACATTTCA 83398 CCC
 AGTCATGAAATGT TTCA
 ||||| ||||
 TCAGTACTTTGTA AAGT

 GAM3690 FLJ10876 3' ATGAGTCAATGACCTT 83399 _ AATGTC
 ATGAGTCA TGA CCTT
 ||||| || ||||
 TACTCAGT ACT GGAA
 T _____
 GAM3690 FLJ12998 3' ATGAGAAAATGTCCTTTCAA 83400 TCAT C
 ATGAG GAAATGTCC TTCAA
 |||| ||||| ||||
 TACTC TTTTACAGG AAGTT
 _____ A
 GAM3690 KIAA0125 3' ATGGGTTAGAAATGCCTTCAA 83401 A CAT TC
 ATG GT GAAATG CCTTCAA
 || || ||||| |||||
 TAC CA CTTTAC GGAAGTT
 C AT_ _
 GAM3690 KIAA0367 3' ATGTGTCATGAAATATTCA 83402 A CCCT
 ATG GTCATGAAATGT TCA
 || ||||| ||||| ||||
 TAC CAGTACTTTATA AGT
 A _____
 GAM3690 KIAA0892 3' TGGTCATGAAAAGCACTT 83403 A T CC
 TG GTCATGAAA GT CTT
 || ||||| || ||||
 AC CAGTACTTT CG GAA
 _ T T_
 GAM3690 LOC144144 3' ATGATCATGAATAATGATTTTT 83396 G _ TCCC
 CAA ATGA TCATGAA ATG TTCAA
 |||| ||||| || ||||
 TACT AGTACTT TAC AAGTT
 _ AT TAAA
 GAM3690 LOC144453 3' ATAAGTCATGTATGTTTTTCA 83404 AA CCC
 ATGAGTCATG ATGT TTCA
 ||||| |||| ||||
 TATTCAGTAC TACA AAGT
 A_ AA_
 GAM3690 LOC145035 3' ATGAGTCAGAAGTTCCTCA 83405 T ATG CT
 ATGAGTCA GAA TCC TCA
 ||||| || || ||||
 TACTCAGT CTT AGG AGT
 _ CA_ _
 GAM3690 LOC155060 3' TGAGCACCTTGGATGTCCCTTC 83406 T GAA_
 AA TGAG CAT ATGTCCCTTCAA
 |||| || ||||| |||||

ACTC GTG TACAGGGAAGTT
 _ GAACC
 GAM3690 LOC159089 3' ATGGCCAAGTGTCCCTT 83407 A TGAAA
 ATG GTCA TGTCCCTT
 ||| ||| |||||
 TAC CGGT ACAGGGAA
 _ TC__
 GAM3690 LOC197201 3' ATGAGTCAGGACATGGCTTCA 83408 T A TCC
 ATGAGTCA GA ATG CTTCA
 ||||| || ||| ||||
 TACTCAGT CT TAC GAAGT
 C G C__
 GAM3690 LOC199678 3' TAAGTCATGTCTTTTCA 83409 TGAAA CC
 TGAGTCA TGTC TTCA
 ||||| ||| |||
 ATTCAGT ACAG AAGT
 ____ AA
 GAM3690 LOC220486 3' ATGATCATGAATAATGATTTTT 83396 G ____ TCCC
 CAA ATGA TCATGAA ATG TTCAA
 ||| ||||| ||| ||||
 TACT AGTACTT TAC AAGTT
 _ AT TAAA
 GAM3690 LOC221395 3' AGTGAAAATGTCTCTTC 83410 CAT C
 AGT GAAATGTC CTTC
 ||| ||||| |||
 TCA TTTTACAG GAAG
 C__ A
 GAM3690 LOC253461 3' GTCATGAAAGTTTCA 83411 T CCC
 GTCATGAAA GT TTCA
 ||||| || |||
 CAGTACTTT CA AAGT
 _ _
 GAM3690 LOC255326 3' ATGAAGTCCTGTCCCTT 83412 _ ATGAAA
 ATGA GTC TGTCCCTT
 ||| ||| |||||
 TACT CAG ACAGGGAA
 T G__
 GAM3691 ATP11A 3' GTGTGTGCATGTGTGTAT 83415 TAC _
 GTGT TGT TGTGTGTAT
 ||| ||| |||||
 CACA ACG ACACACATA
 C__ T
 GAM3691 CCND1 3' GTGTGTGTGTGTGTGTATC 83416 TAC _
 GTGT TGT TGTGTGTATC
 ||| ||| |||||
 CACA ACA ACACACATAG
 CAC C
 GAM3691 CDKN1B 3' AGTGTTATTGTGTTGT 83417 TAC _
 AGTGT TGTTGTGT GT
 |||| ||||| ||

			TCACA ATAACACA CA		
			_____ A		
GAM3691	CSF2RB	3'	TACGTGTGTGTGTGTGTGT 83418	A	TAC _
			TAC GTGT TGT TGTGTGT		
			ATG CACA ACA ACACACA		
			_ C_ C		
GAM3691	DISC1	3'	TACACTGTTACTGAGTAT 83419	G	TT
			TACA TGTTACTG GTGT		
			ATGT ACAATGAC CATA		
			G T_		
GAM3691	FGFRL1	3'	GTGTGTCTGTGTGTGTGT 83420	TA	_
			GTGT CTGT TGTGTGT		
			CACA GACA ACACACA		
			CA C		
GAM3691	FMR2	3'	AGTGTGTGTGTGTGTGTAT 83421	TAC	_
			AGTGT TGT TGTGTGTAT		
			TCACA ACA ACACACATA		
			C_ C		
GAM3691	GLP1R	3'	CAGTGCTGCTGTGTGT 83422	TTA	
			CAGTG CTGTTGTGTGT		
			GTCAC GACGACACACA		

GAM3691	LAMP2	3'	ATGTCTGTGTGTGTGTAT 83423	TA	_
			GTGT CTGT TGTGTGTAT		
			TACA GACA ACACACATA		
			_ C		
GAM3691	MBNL	3'	TACAGTGTGCTGTTTGGT 83424	TA	G T
			TACAGTGT CTGTT TG GT		
			ATGTCACA GACAA AC CA		
			C_ _ _		
GAM3691	MGMT	3'	CAGTGTTACACGTGTGTGT 83425	_	T
			CAGTGTTAC TGT GTGTGT		
			GTCACAATG GCA CACACA		
			T _		
GAM3691	PLAG1	3'	GTGTGTGTGTGTGTGTAT 83426	TAC	_
			GTGT TGT TGTGTGTAT		
			CACA ACA ACACACATA		
			C_ C		
GAM3691	TIMP3	3'	AGTGTATGGTGTGTGTAT 83427	TAC	T
			AGTGT TG TGTGTGTAT		

		TCACA AC ACACACATA		
		T__ C		
GAM3691	XYLB	3' TACAGTTTACTGTTTCATGGT	83428	G __ T
		TACAGT TTA	CTG GT	
		ATGTCA AATGACAA	TAC CA	
		_ AG _		
GAM3691	DSCR1L1	3' GTGTTATTGTTCTTGTGTGT	83429	C ____
		GTGTTA TGT	TGTGTGT	
		CACAAT ACA	ACACACA	
		A AGA		
GAM3691	FLJ20048	3' GTGTTACTTGTGTGAGTGTGTG	83430	_ _____
	T	GTGTTACT GT	TGTGTGT	
		CACAATGA CA	ACACACA	
		A CACTC		
GAM3691	HH114	3' GTGTGTGTGTGTGTGTGTATC	83416	TAC _
		GTGT TGT	TGTGTGTATC	
		CACA ACA	ACACACATAG	
		CAC C		
GAM3691	HRASLS2	5' GTGTTGCTGACTCTGTGT	83431	A _ G
		GTGTT CTG TT	TGTGT	
		CACAA GAC GA	ACACA	
		C T G		
GAM3691	HRIHFB2122	3' GTGTGTGTGTGTGTGTGTATC	83416	TAC _
		GTGT TGT	TGTGTGTATC	
		CACA ACA	ACACACATAG	
		CAC C		
GAM3691	HSPC039	3' TACAGTGTAATTGTGATTGT	83432	TACT ____
		TACAGTGT GTTGTG	TGT	
		ATGTCACA TAACAC	ACA	
		T__ TA		
GAM3691	KIAA0222	3' GTGTTTGTGTGTGTGTGT	83433	AC _
		GTGTT TGT	TGTGTGT	
		CACAA ACA	ACACACA	
		AC C		
GAM3691	KIAA0337	3' CAGTGTGCGTACGTGTGTGT	83434	__ T T
		CAGTGT TAC GT	GTGTGT	
		GTCACA ATG CA	CACACA	
		CGC _ _		
GAM3691	KIAA0544	3' GTGTGTGTGTGTGTGTAT	83435	TAC _
		GTGT TGT	TGTGTGTAT	

CACA ACA ACACACATA
 CAC C
 GAM3691 MGC27434 3' CAGTCTTGCTGCACGTAT 83436 G TAC TG
 CAGT T TGTTG TGTAT
 |||| | |||| ||||
 GTCA A ACGAC GCATA
 G__ GT
 GAM3691 OSBPL11 3' TGAGTTCTCATTGTTGTGTGTA 83437 C G_ C
 TC A AGT TTA TGTTGTGTGTATC
 | || | |||| |||| ||||
 A TCA AGT ACAACACACATAG
 C AG A
 GAM3691 OSBPL9 3' GTGTGTGTGTGTGTGTATC 83438 TAC _
 GTGT TGT TGTGTGTATC
 |||| | |||| ||||
 CACA ACA ACACACATAG
 C__ C
 GAM3691 P66 3' CAGTTCATGTGTGTGT 83439 G C T
 CAGT TTA TGT GTGTGT
 |||| ||| || ||||
 GTCA AGT ACA CACACA
 _ _ _
 GAM3691 RPH3A 3' GTGTGTACATGTGTGTGT 83440 _ _ T
 GTGT TAC TGT GTGTGT
 |||| ||| || ||||
 CACA ATG ACA CACACA
 C T _
 GAM3691 LOC112868 3' TACAGTGTTATTTTTTGCTAT 83441 C____
 TACAGTGTTA TGTTGT
 |||| |||| ||||
 ATGTCACAAT ACGATA
 AAAAA
 GAM3691 LOC126917 3' GTGTGTGTGTGTGTGTGTAT 83435 TAC _
 GTGT TGT TGTGTGTAT
 |||| | |||| ||||
 CACA ACA ACACACATA
 CAC C
 GAM3691 LOC130535 3' TACAGTGTTTTGTTTTGT 83442 AC G
 TACAGTGTT TGTT TGT
 |||| |||| ||| |||
 ATGTCACAA ACAA ACA
 A_ A
 GAM3691 LOC132321 3' TACAGGTTGTTGCATGTAT 83443 T TAC
 TACAG GT TGTTGTGTGTAT
 |||| || |||| |||| ||||
 ATGTC CA ACAACGTACATA
 _ _ _
 GAM3691 LOC148394 3' TACAGTGTGGCTGTGGCCAGTA 83444 TA T GT
 T TACAGTGT CTGT GT GTAT
 |||| |||| ||| |||

ATGTCACA GACA CG CATA
 CC C GT
 GAM3691 LOC150112 3' AGTGTGCGTGTGTGTGTGT 83445 TAC _
 AGTGT TGT TGTGTGT
 |||| ||| |||||
 TCACA ACA ACACACA
 CGC C
 GAM3691 LOC151196 3' GTGTGTGTGTGTGTGTATC 83416 TAC _
 GTGT TGT TGTGTGTATC
 |||| ||| |||||
 CACA ACA ACACACATAG
 CAC C
 GAM3691 LOC163479 5' TACAGTGATACTGTTGCTGAGT 83446 T GT_
 TACAGTG TACTGTTGT GT
 ||||| ||||| ||
 ATGTCAC ATGACAACG CA
 T ACT
 GAM3691 LOC219988 3' GTGTGTGTGTGTGTATC 83447 TAC T
 GTGT TGT GTGTGTATC
 |||| ||| |||||
 CACA ACA CACACATAG
 C_ _
 GAM3691 LOC222008 3' GTGTGTGTGTGTGTGTAT 83435 TAC _
 GTGT TGT TGTGTGTAT
 |||| ||| |||||
 CACA ACA ACACACATA
 CAC C
 GAM3691 LOC253982 3' GTGTGTGTGTGTGTAT 83448 TAC T
 GTGT TGT GTGTGTAT
 |||| ||| |||||
 CACA ACA CACACATA
 C_ _
 GAM3691 LOC254196 3' TACAGTGTGGCTGTGGCCAGTA 83444 TA T GT
 T TACAGTGT CTGT GT GTAT
 ||||| |||| || ||||
 ATGTCACA GACA CG CATA
 CC C GT
 GAM3691 LOC92148 5' GTGTTGCTGACTCTGTGT 83431 A _ G
 GTGTT CTG TT TGTGT
 |||| ||| || ||||
 CACAA GAC GA ACACA
 C T G
 GAM3692 AHCY 3' AGCTGTTCCAAGACCACT 83451 CG G C
 AGC GTTC AGG GCCACT
 || |||| ||| |||||
 TCG CAAG TTC TGGTGA
 A_ G _
 GAM3692 KIAA1493 3' TGAGCTGAGATCGCGCCACT 83452 C C _
 C GGTG GAG GCGCCACT
 | |||| ||| |||||

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      A TCGA CTC  CGCGGTGA
      C _ TAG
GAM3693 CIT    3' TGGGGGGTGGGGAAGGAAAGC 83455  A AA A  T
      TG GG TG GGAA GAGAGT
      || || || ||| |||||
      AC CC AC CCTT CTTTCG
      C CC C  C
GAM3693 RASGRP2 5' TGGGGAGCGAGGAATGAAA 83456  A  A
      TG GGA TGAGGAATGAGA
      || ||| ||||| |||||
      AC CCT GCTCCTTACTTT
      C  C
GAM3693 SLC6A1  3' AGGTCGGGGGGGTGAGAGTGTC 83457  AA A AA
      AGG TG GG TGAGAGTGTC
      ||| || || ||||| |||||
      TCC GC CC ACTCTCACAG
      A_ C CC
GAM3693 SLC6A6  3' TGGGGAGTGGGGAGATGAG 83458  A  A A _
      TG GGA TG GGA ATGAG
      || ||| || ||| |||||
      AC CCT AC CCT TACTC
      C  C C C
GAM3693 ABLIM  5' TGAGAAATGGGGAGTG 83459  A AATGA
      TGAGGAATG GG  GAGTG
      ||||| ||  |||||
      ACTCTTTAC CC  CTCAC
      _ _ _ _ _
GAM3693 DOK4   3' TGGGGAGGAGGAATGGGAAGGT 83460  A AT  A T
      C          TG GGA GAGGAATG GAG GTC
      || ||| ||||| || |||
      AC CCT CTCCTTAC CTT CAG
      C C_  C C
GAM3693 FLJ10846 3' TGAGGAATAGGGATATAACTGT 83461  A  A A G
      TGAGGAATG GGA TG GA TGT
      ||||| ||| || || |||
      ACTCCTTAT CCT AT TT ACA
      C _ A G
GAM3693 FLJ13188 3' GAGGAATGGGGAATGGGA 83462  A  A
      GAGGAATG GGAATG GA
      ||||| ||||| ||
      CTCCTTAC CCTTAC CT
      C  C
GAM3693 GAPCENA 3' TGAGGAGTGATTTCTAGAGTGT 83463  A GGAATG
      C          TGAGGA TGA  AGAGTGTC
      ||||| |||  |||||
      ACTCCT ACT  TCTCACAG
      C AAAGA_
GAM3693 KIAA0090 3' AGGAATCTCTGAGAGTGTC 83464  GAGGAA
      AGGAAT  TGAGAGTGTC
      |||||  ||||| |||||

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		TCCTTA ACTCTCACAG		
		GAG__		
GAM3693	KIAA1321	3' GAGGAGTGGGGGGAAAATGT 83465	A A AAT	
		GAGGA TG GG GAGAGTGT		
		CTCCT AC CC CTTTACA		
		C _ CC_		
GAM3693	KIAA1464	3' GAGGAATGGGGGAGATGT 83466	A AAT G	
		GAGGAATG GG GAGA TGT		
		CTCCTTAC CC CTCT ACA		
		_ C_ _		
GAM3693	MGC3178	3' GAGGTGGGTGAAGAGTGT 83467	AA A AAT	
		GAGG TG GG GAGAGTGT		
		CTCC AC CC TTCTCACA		
		_ _ AC_		
GAM3693	RBBP4	3' TGGGGAAAGAGGAACGTGT 83468	A T GAGA	
		TG GGAA GAGGAAT GTGT		
		AC CCTT CTCCTTG CACA		
		C T _		
GAM3693	LOC144512	5' AGGAATGAGGTATGGGTGT 83469	A AGA	
		AGGAATGAGG ATG GTGT		
		TCCTTACTCC TAC CACA		
		A C_		
GAM3693	LOC149863	5' TGGGGGAGAGGAACATGT 83470	A AAT GAGA	
		TG GG GAGGAAT GTGT		
		AC CC CTCCTTG TACA		
		_ CCT _		
GAM3693	LOC150350	5' TGAGGGAGAGAGACAGAGTGT 83471	AAT GA G	
		TGAGG GAG AT AGAGTGT		
		ACTCC CTC TG TCTCACA		
		CT_ TC _		
GAM3693	LOC222182	3' TGAGAGTGGGATGGGAGTGT 83472	AA A A A	
		TGAGG TG GGA TG GAGTGT		
		ACTCT AC CCT AC CTCACA		
		C_ _ _ C		
GAM3693	LOC254143	5' AGGAATGAGGTATGGGTGT 83469	A AGA	
		AGGAATGAGG ATG GTGT		
		TCCTTACTCC TAC CACA		
		A C_		
GAM3693	LOC254428	3' GAGGGATGGGGAAAATGT 83473	A A AAT	
		GAGG ATG GG GAGAGTGT		

			CTCC TAC CC CTTTACAC	
			C _ _ _	
GAM3693	LOC91397	5'	TGAGGAAGGGGAGAAAATGTC 83474	TGA AT
			TGAGGAA GGA GAGAGTGTC	
			ACTCCTT CCT CTTTACAG	
			CC_ _	
GAM3694	ACLY	3'	TAAAAAAAAAAAAAGAGAGACA 83477	AAA
	TT		TAAAAAAGAAAAA AGGCATT	
			ATTTTTTTTTTTTT TCTGTAA	
			CTC	
GAM3694	AK3	3'	AAAAAAGAAAAAAAAAAAA 83478	
			AAAAAAGAAAAAAAAAAG	
			TTTTTTCTTTTTTTTT	
GAM3694	BCL11A	3'	AAAAAGAAAAAAACAGG 83479	_
			AAAAAGAAAAAAA AGG	
			TTTTCTTTTTTT TCC	
			G	
GAM3694	CANX	3'	AAAAAAGAACCAAGAAAAGGC 83480	AAA_
			AAAAAAGAA AAAAGGC	
			TTTTTTCTT TTTCCG	
			GGTTC	
GAM3694	CARPX	3'	AAACAAGAAAAGAAAGGCATT 83481	A AA
			AAA AAGAAAA AAAGGCATT	
			TTT TTCTTTT TTTCCGTAA	
			G C_	
GAM3694	CENTD1	3'	TAAAAAAGAAAAAAAAAAAA 83482	
			TAAAAAAGAAAAAAAAAAAA	
			ATTTTTTTCTTTTTTTTT	
GAM3694	CENTD1	3'	TAAAAAAGAAAAAAAAAAAA 83482	
			TAAAAAAGAAAAAAAAAAAA	
			ATTTTTTTCTTTTTTTTT	
GAM3694	CNP	3'	TAAAAAAAAAAAAAAAAAAAAA 83483	
			TAAAAAAGAAAAAAAAAAGG	
			ATTTTTTTTTTTTTTTTTTT	
GAM3694	CTNNB1	3'	TAAAAAAAAAAAAAAAAAAAAA 83483	
			TAAAAAAGAAAAAAAAAAGG	

ATTTTTTTTTTTTTTTTTT

GAM3694	DAPK1	3'	TAAAAAAGAAAAAACAAACA	83484	A
			TAAAAAAGAAAAAAAGGCA		
			ATTTTTTCTTTTTT TTTGT		
			G		
GAM3694	DPYSL2	3'	AAAAAGAAAAGAAAAGGCA	83485	—
			AAAAAGAAAAGAAAAGGCA		
			TTTTTCTTT TTTTCCGT		
			C		
GAM3694	ERBB2IP	5'	AAAAAAGAAAAAAAAAAAA	83478	
			AAAAAAGAAAAAAAAAAG		
			TTTTTTCTTTTTTTTT		
GAM3694	EWSR1	3'	AAAAAAAAAAAAAAAAACAT	83486	
			AAAAGAAAAAAAAAAGGCAT		
			TTTTTTTTTTTTTTTTGTA		
GAM3694	G6PC	3'	CAAAAAAGAAAAAAAAAAG	83487	
			TAAAAAAGAAAAAAAAAAG		
			GTTTTTTCTTTTTTTTT		
GAM3694	GFRA1	5'	AAAAAAGAAAAAAAAAAAA	83478	
			AAAAAAGAAAAAAAAAAG		
			TTTTTTCTTTTTTTTT		
GAM3694	GLS	3'	AAAAAGAAAAAAAAAAGGAATT	83488	C
			AAAAAGAAAAAAAAAAGG ATT		
			TTTTTCTTTTTTTTCC TAA		
			T		
GAM3694	GLUD1	3'	AAAAAAAAAAAAAAAAAAGC	83489	
			AAAAAGAAAAAAAAAAGGC		
			TTTTTTTTTTTTTTTTCG		
GAM3694	GNAO1	3'	TGAAAAAAAAAAAAAAAAAGG	83490	A
			A AAAAGAAAAAAAAAAGG		
			A TTTTTTTTTTTTTTCC		
			C		
GAM3694	HIS1	5'	AAAAAGAAAAAAAAAACA	83491	G
			AAAAAGAAAAAAAAAAG CA		

TTTTCTTTTTTTTT GT

GAM3694 IFNGR2 3' AAGAAAAAAAAAAAAAGC 83492 A
AA AAAGAAAAAAAAAAGGC
|| |||||
TT TTTTTTTTTTTTTTCG
C

GAM3694 JAM3 3' AAAAAAAAAAATAGCAT 83493 A
AAAGAAAAAAAA GGCAT
||||||| ||||
TTTTTTTTTTTT TCGTA
A

GAM3694 JRKL 3' AAAAAAAAAAAAAAAC 83494
AAAAAGAAAAAAAAAAGGC
|||||||
TTTTTTTTTTTTTTTTTG

GAM3694 LY95 5' TAAAAAAAAAAAAAAAAAAG 83495
TAAAAAGAAAAAAAAAAGG
|||||||
ATTTTTTTTTTTTTTTTC

GAM3694 MAK 3' AAAAAAAAAAAAAAGC 83496
AAAAAGAAAAAAAAAAGGC
|||||||
TTTTTTTTTTTTTTTTTCG

GAM3694 MTP 3' CAAAAAAGAGAAAAAATGG 83497 A _
TAAAAAGA AAAAAA GG
||||||| ||||| ||
GTTTTTTTCT TTTTTT CC
C A

GAM3694 NFRKB 5' AAAAGAAAAAGAAGGCAT 83498 AA
AAAAGAAAAA AAGGCAT
||||||| |||||
TTTTCTTTT TTCCGTA
C_

GAM3694 NPEPPS 3' AAAAAAGAAAAAAAAAGG 83499 A
AAAAAGAAAAAAAAA GG
||||||| ||
TTTTTTCTTTTTTT CC

GAM3694 NRXN3 5' TAAAGAAAGAAAAAAAAAAG 83500 A
TAAA AAAGAAAAAAAAAAGG
||| |||||
ATTT TTTCTTTTTTTTTTC
C

GAM3694 OPHN1 3' AAAAAAGAAAAAAAAA 83478
AAAAAGAAAAAAAAAAG
|||||||

TTTTTTCTTTTTTTTT

GAM3694 OPHN1 3' AAAAAAAGAAAAAAAAAAGG 83501
AAAAAAAGAAAAAAAAAAGG
|||||||
TTTTTTCTTTTTTTTTCC

GAM3694 OSR1 3' CAAAAAAGAAAAAGAAAAGC 83502 A
TAAAAAAGAAAAA AAAGGC
|||||||
GTTTTTTCTTTTT TTTTCG
C

GAM3694 PCDH15 3' TAAAAACGAGAAAAAAACTGC 83503 A_ AG
ATT TAAAA AGAAAAAAA GCATT
|||||
ATTTTT TCTTTTTTTT CGTAA
GC GA

GAM3694 PIAS1 3' TAAAAAAGGAAAAAAACAC 83504 A G
TAAAAAAG AAAAAAA GC
|||||
ATTTTTTC TTTTTTTT TG
C G

GAM3694 PIGR 3' AAAAAAAGAAAAAGAAAAAC 83505 A
AAAAAAAGAAAAA AAAGGC
|||||||
TTTTTTCTTTTT TTTTGT
C

GAM3694 PKP2 3' AAAAAAGTCCAGGAAAGGCATT 83506 AAAAAA
AAAAAAG AAAGGCATT
|||||
TTTTTTC TTTCCGTAA
AGGTCC

GAM3694 PKP4 3' AAAAAGGAAAAAAAAACACACT 83507 A G
AAAAA GAAAAAAAAA GCATT
|||||
TTTTT CTTTTTTTTT TGTGA
C G

GAM3694 PPARGC1 3' AAAAAAGAAAAAATCCACATT 83508 AAG
AAAAAAGAAAAAAA GCATT
|||||||
TTTTTTCTTTTTTT TGTAA
AGG

GAM3694 PRKR 5' AAAAGAGAAAAAAGAAGGC 83509 A A
AAAA AGAAAAAA AAGGC
|||
TTTT TCTTTTTT TTCCG
C C

GAM3694 PTMA 3' CAAAAAAGGAAAAAAAAG 83510 A
TAAAAA GAAAAAAAAG
|||||

			GTTTTTT CTTTTTTTTTC		
			C		
GAM3694	PTP4A2	5'	AAAAAAAAAAAAAGCCA	83511	G
			AAAAGAAAAAAAAAAG CA		
			TTTTTTTTTTTTTTC GT		
			G		
GAM3694	PTP4A2	5'	AAAAAAAAAAAAAGCCA	83511	G
			AAAAGAAAAAAAAAAG CA		
			TTTTTTTTTTTTTTC GT		
			G		
GAM3694	RAD21	3'	TGAAGAAGGAAAAAGGCA	83512	A AA
			A AAGAA AAAAAGGCA		
			A TTCTT TTTTCCGT		
			C CC		
GAM3694	SCAMP1	3'	AAAAAAGAAAAGAAAAAGA	83513	—
			AAAAAAGAAAA AAAAAGG		
			TTTTTTCTTTT TTTTCT		
			C		
GAM3694	SDC1	3'	AAAAAAAAAAAAAAAAAAG	83514	
			AAAAAAGAAAAAAAAAAGG		
			TTTTTTTTTTTTTTTTTTC		
GAM3694	SDC4	3'	TAAAAAAAAAAAAAAAAAAAA	83483	
			TAAAAAAGAAAAAAAAAAGG		
			ATTTTTTTTTTTTTTTTTT		
GAM3694	SEPP1	3'	AAAAAGAAAAAAAAAAGACAT	83515	
			AAAAAGAAAAAAAAAAGGCAT		
			TTTTCTTTTTTTTCTGTA		
GAM3694	SEPP1	3'	AAAAAGAAAAAAAAAAGACAT	83515	
			AAAAAGAAAAAAAAAAGGCAT		
			TTTTCTTTTTTTTCTGTA		
GAM3694	SGCB	3'	AAAAAAAAAAAAAAAAAGGAATT	83516	C
			AAAAAGAAAAAAAAAAGG ATT		
			TTTTTTTTTTTTTTTCC TAA		
			T		
GAM3694	SLC15A1	3'	AAAAAGAAAAAAGAAAATAGCA	83517	— —
	TT		AAAAAGAAAAA AAA GGCATT		

		TTTTTCTTTTTT TTT TCGTAA	
		C TA	
GAM3694	SLC19A1	3' AAAAAAAAAAAAAAGCATC 83518	
		AAGAAAAAAAAAAGGCATT	
		TTTTTTTTTTTTTCGTAG	
GAM3694	SOX12	3' TAAAAAAAAAAAAAAAAAAAAA 83483	
		TAAAAAAGAAAAAAAAAAGG	
		ATTTTTTTTTTTTTTTTTTTT	
GAM3694	SOX9	3' AAAAAAGGGATGGACAAAAAGG 83519	AAAA__
	CATT	AAAAAAG AAAAAGGCATT	
		TTTTTTC TTTTCCGTAA	
		CCTACCTG	
GAM3694	SRC	3' AAAAAAAAAAAAAAGGACA 83520	-
		AAAGAAAAAAAAAAGG CA	
		TTTTTTTTTTTTTCC GT	
		T	
GAM3694	SVIL	3' AAAAAAAAAAAAAAGGCATT 83521	
		AAAAAGAAAAAAAAAAGGCATT	
		TTTTTTTTTTTTTTTCCGTAA	
GAM3694	SVIL	3' AAAAAAAAAAAAAAGGCATT 83521	
		AAAAAGAAAAAAAAAAGGCATT	
		TTTTTTTTTTTTTTTCCGTAA	
GAM3694	TAPBP	3' AAAGAAAAAAAAAAAAAGGCATT 83522	A
		AAA AAGAAAAAAAAAAGGCATT	
		TTT TTTTTTTTTTTTCCGTAA	
		C	
GAM3694	TBX3	5' AAAAAAGAAAAGGAGGC 83523	AAAA
		AAAAAAGAAAA AGGC	
		TTTTTCTTTT TCCG	
		CC__	
GAM3694	TBX3	5' AAAAAAGAAAAGGAGGC 83523	AAAA
		AAAAAAGAAAA AGGC	
		TTTTTCTTTT TCCG	
		CC__	
GAM3694	TGFBR2	5' TGAAAAAAAAAAAAAGCACT 83524	A
		A AAAGAAAAAAAAAAGGCATT	

A TTTTTTTTTTTTTTCGTGA
 C
 GAM3694 TNFRSF11A 3' CAAAAAAGAAAAAAAAA 83525
 TAAAAAAGAAAAAAAAAG
 |||||
 GTTTTTTCTTTTTTTT

GAM3694 TNFSF9 3' AAAGAAAGAAAGAAAAAGC 83526 A A
 AAA AAAGAAA AAAAAGGC
 ||| ||||| |||||
 TTT TTTCTTT TTTTTTCG
 C C

GAM3694 TOMM22 3' AAAAAAAAAAAAAAAAAACA 83527
 AAAAAGAAAAAAAAAAGGCA
 |||||
 TTTTTTTTTTTTTTTTGT

GAM3694 TPI1 5' TAAAAAAAAAAAAAAAAAAC 83528
 TAAAAAAGAAAAAAAAAAGGC
 |||||
 ATTTTTTTTTTTTTTTTTTG

GAM3694 UBL3 3' AAAAGAAAAAGTGGCAT 83529 AAAA
 AAAAGAAAAA GGCAT
 ||||| |||||
 TTTTCTTTT CCGTA
 CA__

GAM3694 UMPK 3' AAAAAGAAAAAAAAAATCAAAG 83530 _____ |||
 GCATTA AGAAAAAAA AGGCATT A
 ||||| ||||| |
 TCTTTTTTT TCCGTAA T
 TTAGTT |||

GAM3694 XKRY 5' AAAGAAAGAAAAAAAAAGA 83531 A
 AAA AAAGAAAAAAAAAAGG
 ||| |||||
 TTT TTTCTTTTTTTTTCT
 C

GAM3694 XKRY 5' AAAGAAAGAAAAAAAAAGA 83531 A
 AAA AAAGAAAAAAAAAAGG
 ||| |||||
 TTT TTTCTTTTTTTTTCT
 C

GAM3694 ZHX1 3' AAAAGAAAAAAAAAAAGC 83532 _
 AAAAGAAAAAAAAAAG GC
 ||||| ||
 TTTTCTTTTTTTTTT CG
 T

GAM3694 ZIC1 5' AAAAAAAAAAAAAAAAAAAG 83514
 AAAAAAAGAAAAAAAAAAGG
 |||||

TTTTTTTTTTTTTTTTTTC

GAM3694 ZNF74 5' AAAAAAAAAAAAAAAAAAGA 83533
AAAAAAGAAAAAAAAAAGG
||||||||||||||
TTTTTTTTTTTTTTTTTCT

GAM3694 ACTR2 3' AAAGGAAAAAAGAAAGCATT 83534 A A
AAA GAAAAAA AAGGCATT
||| ||||| |||||
TTT CTTTTTT TTTCGTAA
C C

GAM3694 ADAMDEC1 3' AAAAAAGAAAAAAAAAAG 83535
AAAAAAGAAAAAAAAAAGG
||||||||||||||
TTTTTCTTTTTTTTTTC

GAM3694 ALY 3' AAAAAAAGAAAAAAAAAAAA 83536
AAAAAAAGAAAAAAAAAAGG
||||||||||||||
TTTTTTCTTTTTTTTTT

GAM3694 AP1S2 3' AAAAAAAAAAAAAAAAAAAGG 83537
AAAAAAGAAAAAAAAAAGG
||||||||||||||
TTTTTTTTTTTTTTTTTCC

GAM3694 APMCF1 3' TAAAAAAAAAAAAAAAAAAAAA 83483
TAAAAAAAGAAAAAAAAAAGG
||||||||||||||
ATTTTTTTTTTTTTTTTTT

GAM3694 ATP9B 3' CAAAAAAAGAAAGAAAAGC 83538 AAA
TAAAAAAAGAAA AAAGGC
||||||||| |||||
GTTTTTTTCTTT TTTCG
C__

GAM3694 B3GALT1 3' AAAAAAAGAAAAAAAAAAAA 83478
AAAAAAAGAAAAAAAAAAG
||||||||||||||
TTTTTTCTTTTTTTTTT

GAM3694 BRD4 3' AAAAAAAGAAAAAAAAAAAA 83478
AAAAAAAGAAAAAAAAAAG
||||||||||||||
TTTTTTCTTTTTTTTTT

GAM3694 C1orf34 3' TAAAAAAAGAAAAAAGG 83539 AAA
TAAAAAAAGAAAAA AGG
||||||||||| |||

ATTTTTTCTTTTT TCC

GAM3694 C20orf177 3' AAAAAAGAAAAAAAAAACCAT 83540 G
AAAAAAGAAAAAAAAAAG CAT
|||||
TTTTTCTTTTTTTTTT GTA

G

GAM3694 C6orf5 3' AAAAAAGAAAAAAAAA 83478
AAAAAAGAAAAAAAAAAG
|||||
TTTTTCTTTTTTTTTT

GAM3694 CCR6 5' AAGAAAAAGAGAGGCATT 83541 AAA
AAGAAAA AGGCATT
|||||
TTCTTTT TCCGTAA
CTC

GAM3694 CDW92 3' AAAAGAAACCAAGGCAT 83542 AAAA
AAAAGAAA AAGGCAT
|||||
TTTTCTT TTCCGTA
GG__

GAM3694 CUL2 3' AAAAAAAAAAAAAAGACAC 83543
AAAAAGAAAAAAAAAAGGCAT
|||||
TTTTTTTTTTTTTTCTGTG

GAM3694 Cyt19 3' AAAAAAGAAAAAGAAAAAA 83544
CATT AAAAAAGAAAAA AAAGGCATT
|||||
TTTTTTCTTTTT TTTTGTA
CTT

GAM3694 DCOHM 3' AAAAAAGAAAGGAGGCA 83545 AAAAA
AAAAAAGAAA AGGCA
|||||
TTTTTTCTT TCCGT
CC__

GAM3694 DKFZP434D146 3' TAAAAAAGAAAAAAAAAGGCA 83546
TAAAAAAGAAAAAAAAAGGCA
|||||
ATTTTTCTTTTTTTTCCGT

GAM3694 DKFZP564D166 3' AAAAAAAAAAAAAAAGG 83547
AAAAAAGAAAAAAAAAAGG
|||||
TTTTTTTTTTTTTTTCC

GAM3694 DKFZP564I122 3' AAAAAAAAAAAAAAACTCATT 83548 GG
AAAAAAGAAAAAAAAA CATT
|||||

		TTTTTTTTTTTTTTTT GTAA		
		GA		
GAM3694	EDIL3	3' TGAAAAAAAAAAAAACCATT 83549	A	G
		A AAAAGAAAAAAAAAAG CATT		
		I		
		A TTTTTTTTTTTTTTT GTAA		
		C G		
GAM3694	ESDN	3' TAAAAAAAAAAAAAAAAAAAA 83483		
		TAAAAAAGAAAAAAAAAAGG		
		ATTTTTTTTTTTTTTTTTT		
GAM3694	FKBP5	3' AAAAAGACAAAAAAGC 83550	AA	
		AAAAAGA AAAAAGGC		
		TTTTTCT TTTTTTCG		
		G_		
GAM3694	FKBP9	3' AAAAAAAGAAAGGAAAAGC 83551	AAA	
		AAAAAAAGAAA AAAGGC		
		TTTTTTCTTT TTTTCG		
		CC_		
GAM3694	FLJ10535	3' AAAAAAAGAAAAAAAAAAAA 83536		
		AAAAAAAGAAAAAAAAAAGG		
		TTTTTTCTTTTTTTTTT		
GAM3694	FLJ10546	3' AAAAAAAGAAAAAAAAAAGC 83552	AA	
		AAAAAAAGAAAAAAAAA GGC		
		TTTTTTCTTTTTTT TCG		
GAM3694	FLJ10697	3' AAAAAAAAAAAAAAAAAAAGG 83547		
		AAAAAAAGAAAAAAAAAAGG		
		TTTTTTTTTTTTTTTTTCC		
GAM3694	FLJ10697	3' TAAAAACACTAAAAAAGGCATT 83553	AAGAAA	
		TAAAAA AAAAAGGCATT		
		ATTTT TTTTTCCGTAA		
		GTGA_		
GAM3694	FLJ12331	3' AAAAAAAGAAAAAAAAAAGAAT 83554	C	
		AAAAAAAGAAAAAAAAAAGG AT		
		TTTTTTCTTTTTTTTTTC TA		
		T		
GAM3694	FLJ12619	3' TAAAAGGAGAAAAAAAAAAAC 83555	AA	
		TAAAA AGAAAAAAAAAAGGC		

		ATTTT TCTTTTTTTTTTG		
		CC		
GAM3694	FLJ12649	3' AAAAAGAAAAAGAAAAAGCATT 83556	—	
		AAAAAGAAAAA AAAAGGCATT		
		TTTTTCTTTT TTTTCGTAA		
		C		
GAM3694	FLJ13385	3' TAAAAACAAGAAAAAAAAAAG 83557	—	—
	C	TAAAAA AAGAAAAAAAAAAG GC		
		ATTTT TTCTTTTTTTTTT CG		
		G T		
GAM3694	FLJ14146	3' AAAAAAGAAAAAAAAAAG 83558		
		AAAAAAGAAAAAAAAAAG		
		TTTTTTCTTTTTTTTC		
GAM3694	FLJ14431	5' AAAAAAGAAAAAAAAAAG 83558		
		AAAAAAGAAAAAAAAAAG		
		TTTTTTCTTTTTTTTC		
GAM3694	FLJ14564	3' TAAAAAAAAAAAAAAAAA 83483		
		TAAAAAAGAAAAAAAAAGG		
		ATTTTTTTTTTTTTTTTTT		
GAM3694	FLJ14621	3' AAAAAAGAAAAACACTGCATT 83559	AAAAG	
		AAAAAAGAAAAA GCATT		
		TTTTTTCTTTT CGTAA		
		GTGA_		
GAM3694	FLJ20060	3' AAAGAAGGCTAAAAGGCATT 83560	AAA_	
		AAAGAA AAAAGGCATT		
		TTTCTT TTTCCGTAA		
		CCGA		
GAM3694	FLJ20527	3' AAAAAAGAAAAAAAAAACCA 83561	G	
		AAAAAAGAAAAAAAAAAG CA		
		TTTTTTCTTTTTTTTTT GT		
		G		
GAM3694	FLJ20984	3' TAAAAAAGAAAAAGAAAG 83562	A	
		TAAAAAAGAAAAA AAAG		
		ATTTTTTTCTTTT TTTC		
		C		
GAM3694	FLJ21032	3' AAAAAAGACAAAGAAGGGCATT 83563	A A A	
		AAAAAGA AAA AA GGCATT		

		TTTTTTCT TTT TT CCGTAA		
		G C C		
GAM3694	FLJ21324	5' AAAAAAAGAAAAAGAAAAGC	83564	A
		AAAAAAAGAAAAA AAAGGC		
		TTTTTTCTTTTT TTTTCG		
		C		
GAM3694	FLJ21657	3' TGAAAGAAAAAGGAAAAAGCA	83565	A
		A AAAGAAAAA AAAAGGCA		—
		A TTTCTTTTT TTTTTCGT		
		C CC		
GAM3694	FLJ22313	3' AAAAAAAAAAAAAAAAAAAC	83494	
		AAAAAAGAAAAAAAAAAGGC		
		TTTTTTTTTTTTTTTTTTG		
GAM3694	FLJ22944	3' AAAAAAGAAATGAGGCATT	83566	AAAAA
		AAAAAAGAAA AGGCATT		
		TTTTTTCTTT TCCGTAA		
		AC—		
GAM3694	FLJ23132	3' AAAAAAAAAAAAAAAAAACA	83527	
		AAAAAGAAAAAAAAAAGGCA		
		TTTTTTTTTTTTTTTTTGT		
GAM3694	FLJ23518	3' AAGAAAAGGAAAAAAGCATT	83567	—
		AAGAAAA AAAAAGGCATT		
		TTCTTTT TTTTTCGTAA		
		CC		
GAM3694	HGRG8	3' AAAAAGACAAAAAACATAGCAT	83568	— AA_
	T	AAAAAGA AAAAAA GGCATT		
		TTTTTCT TTTTTT TCGTAA		
		G GTA		
GAM3694	HIP-55	3' AAAAAGAAAAAAGGCA	83569	AAA
		AAAAAGAAAAA AGGCA		
		TTTTTCTTTTT TCCGT		
		—		
GAM3694	HNRPU	3' AAAAAAAAAAAAAAGTCAC	83570	G
		AAAAGAAAAAAAAAAG CAT		
		TTTTTTTTTTTTTTTC GTG		
		A		
GAM3694	HNRPU	3' AAAAAAAAAAAAAAGTCAC	83570	G
		AAAAGAAAAAAAAAAG CAT		

		TTTTTTTTTTTTTTC GTG	
		A	
GAM3694	HSU53209	3' AAAAAAAAAAAGGAAC	83571 C
		AAAGAAAAAAAAAGG AT	
		TTTTTTTTTTTTTCC TG	
		T	
GAM3694	HTR3A	3' AAGAAAAAAAAAGACACT	83572 A
		AAGAAAAAAAA GGCATT	
		TTCTTTTTTT CTGTGA	
		—	
GAM3694	KIAA0087	3' AAAAAAAAAAAAAAAAAAC	83573
		AAAAAGAAAAAAAAAGGC	
		TTTTTTTTTTTTTTTTTG	
GAM3694	KIAA0217	3' AAAGAAAATTTGAGGCATT	83574 AAA_
		AAAGAAAA AGGCATT	
		TTTCTTTT TCCGTAA	
		AAAC	
GAM3694	KIAA0261	3' TAAAAAGGAAAAAAAAAAG	83575 A
		TAAAAA GAAAAAAAAAGG	
		ATTTTT CTTTTTTTTTC	
		C	
GAM3694	KIAA0318	3' TGAAAGAAAAAAAAAAAC	83576 A
		A AAAGAAAAAAAAAGGC	
		A TTTCTTTTTTTTTTG	
		C	
GAM3694	KIAA0349	3' AAAAAAGAAAAAAAAAA	83536
		AAAAAAGAAAAAAAAAGG	
		TTTTTTCTTTTTTTTTT	
GAM3694	KIAA0561	3' AAAAAAGAAAAAAAAAAG	83558
		AAAAAAGAAAAAAAAAAG	
		TTTTTTCTTTTTTTTTC	
GAM3694	KIAA0828	3' AAAAGAAAGAAAGAGGCA	83577 _ A
		AAAAGAAA AAA AAGGCA	
		TTTCTTT TTT TTCCGT	
		C C	
GAM3694	KIAA0907	3' AAAAAAGAAAAAAAAAAG	83558
		AAAAAAGAAAAAAAAAAG	

TTTTTTCTTTTTTTTC

GAM3694 KIAA0971 3' AAAGAAAGAAAAAAAAAAGACA 83578 A _
TT AAA AAAGAAAAAAAAAAGG CATT

|||||
TTT TTTCTTTTTTTTTTC GTAA
C T

GAM3694 KIAA1155 3' AAAAAAAGAAAAAAAAA 83478
AAAAAAAGAAAAAAAAAAG
|||||
TTTTTTCTTTTTTTTTT

GAM3694 KIAA1238 3' AAAAAAAAAAAAAAAAAAGCA 83579
AAAAAGAAAAAAAAAAGGCA
|||||
TTTTTTTTTTTTTTTTTCGT

GAM3694 KIAA1265 3' TGAAAAAAAAAAAAACAGCATT 83580 A A
A AAAGAAAAAAAAA GGCATT
| |||||
A TTTTTTTTTTTT TCGTAA
C G

GAM3694 KIAA1332 3' AAAAAAAGAAAAGAAAAAAGG 83581 _
AAAAAAAGAAAAA AAAAAGG
|||||
TTTTTTCTTTT TTTTCC
CT

GAM3694 KIAA1391 3' TGAAAAAAAAAAAAAAAAAGGCA 83582 A
A AAAAGAAAAAAAAAAGGCA
| |||||
A TTTTTTTTTTTTTTCCGT
C

GAM3694 KIAA1557 3' AAAAAAAGAAAAAAAAA 83478
AAAAAAAGAAAAAAAAAAG
|||||
TTTTTTCTTTTTTTTTT

GAM3694 KIAA1627 3' AAAAAAAGAAGAAAAAAGC 83583 AA
AAAAAAAGAA AAAAAGGC
|||||
TTTTTTCTT TTTTTCG
C_

GAM3694 KIAA1634 3' TGAAAAAAAAAAAAAAGGC 83584 A
A AAAGAAAAAAAAAAGGC
| |||||
A TTTTTTTTTTTTTCCG
C

GAM3694 KIAA1701 3' TAAAAAAAAAAAAAAAAAAAAA 83483
TAAAAAAGAAAAAAAAAAGG
|||||

ATTTTTTTTTTTTTTTTTT

GAM3694 KIAA1804 3' AAAAAAGAAAAAAAGG 83585 A
AAAAAAGAAAAAAA GG
||||||| ||
TTTTTCTTTTTTT CC

—
GAM3694 KIAA1877 3' AAAAAAGAAAAGAAAAGA 83586 A
AAAAAAGAAAA AAAAGG
||||||| |||||
TTTTTTCTTTT TTTTCT

C
GAM3694 KIAA1962 3' AAAAAAGAAAAAAAAA 83478
AAAAAAGAAAAAAAAAG
||||||| |||||
TTTTTTCTTTTTTTTT

GAM3694 KIAA1972 3' AAAAGAAGAAAAAAAAATGTGC 83587 A G__
ATT AAAA AAGAAAAAAAAA GCATT
||| ||||| |||||
TTTT TTCTTTTTTTTT CGTAA
C ACA

GAM3694 LIPG 3' AAAGAGGAAAAAAGCACT 83588 AA
AAAGA AAAAAAGGCATT
|||| |||||
TTTCT TTTTTTCGTGA
CC

GAM3694 LSFR2 3' TAAATAAGAAAAAAAAAGGC 83589 A
TAAAA AAGAAAAAAAAAGGC
|||| |||||
ATTTT TTCTTTTTTTTCCG
A

GAM3694 MGC20460 5' TAAAAAAGACAAAAAAAAAAG 83590 —
C TAAAAAAGA AAAAAAAGGC
||||| |||||
ATTTTTTTCT TTTTTTTTCG
GT

GAM3694 MGC2714 3' TAAAAAAGGAAAAAAAG 83591 A
TAAAAAAG AAAAAAAG
||||| |||||
ATTTTTTTC TTTTTTTTC
C

GAM3694 NEK1 3' AAAGAGAAATAAAGGCAT 83592 A A
AAAGA AAA AAAGGCAT
|||| ||| |||||
TTTCT TTT TTTCCGTA
C A

GAM3694 NIBAN 3' AAAGAGAAAAAAAAAAGC 83593 A
AAA AGAAAAAAAAAAGGC
||| |||||

		TTT TCTTTTTTTTTTCG		
		C		
GAM3694	NOPAR	5' AAAAAAAAAAAAAAAAAAAC	83573	
		AAAAAGAAAAAAAAAAGGC		
		TTTTTTTTTTTTTTTTTG		
GAM3694	NTT73	5' AAAAAAAAAAAAAAAAAAAC	83494	
		AAAAAGAAAAAAAAAAGGC		
		TTTTTTTTTTTTTTTTTG		
GAM3694	OATPRP4	3' AAAGAAAGAAAAGAAGGCAC	83594	A AAA
		AAA AAAGAAAA AAGGCAT		
		TTT TTTCTTTT TTCCGTG		
		C C_		
GAM3694	pcnp	3' TGAAAAAGAAAAAAAAAAG	83595	A
		A AAAAGAAAAAAAAAAG		
		A TTTTCTTTTTTTTC		
		C		
GAM3694	PDCD4	3' AAAAAAAAAAAAAAAAAAAC	83596	
		AAAAAGAAAAAAAAAAGGC		
		TTTTTTTTTTTTTTTTTG		
GAM3694	PDE7B	5' AAAAAAGAAAAAAAAAGG	83499	A
		AAAAAGAAAAAAAA GG		
		TTTTTTCTTTTTTT CC		
GAM3694	PEL12	3' TGAAAAAAAAAAAAAGACAT	83597	A
	T	A AAAAGAAAAAAAAAGGCATT		
		A TTTTTTTTTTTTTTCTGTAA		
		C		
GAM3694	PIP3-E	3' TAAAAAGAAAAAAAAAAG	83598	
		TAAAAAGAAAAAAAAAGG		
		ATTTTTCTTTTTTTTC		
GAM3694	POLR2D	3' AAAAAAAAAAAAAAGCATT	83599	
		AAAAAGAAAAAAAAAGGCATT		
		TTTTTTTTTTTTTTTCGTAA		
GAM3694	PIIB	3' TAAAAAACCCACA	83600	AAG
	TT	TAAAAAGAAAAAA GCATT		

		ATTTTTTTTTTTTTTT	TGTAA		
		GGG			
GAM3694	PRO0641	5'	AAAAAAAAAAAAAAAAAGCAC	83601	
			AAAAGAAAAAAAAAAGGCAT		
			TTTTTTTTTTTTTTTCGTG		
GAM3694	PRO2893	5'	TAAAAAAAAAAAAAAAAAGA	83602	
			TAAAAAAGAAAAAAAAAAGG		
			ATTTTTTTTTTTTTTTTCT		
GAM3694	PSPH	3'	AAAAAAAAAAAAAAAAAGCA	83603	
			AAAAGAAAAAAAAAAGGCA		
			TTTTTTTTTTTTTTTCGT		
GAM3694	PTPRT	3'	TGAAAAGAAAAAAAAAACATT	83604	A G
			A AAAAGAAAAAAAAAAG CATT		
			A TTTTCTTTTTTTTT GTAA		
			C _		
GAM3694	RAP140	3'	AAAAAAAAAAAAAAAAAAC	83494	
			AAAAAAGAAAAAAAAAAGGC		
			TTTTTTTTTTTTTTTTTG		
GAM3694	RAP2B	3'	AAAAAAAAAAAAAAAAAACATT	83605	G
			AAAAAAGAAAAAAAAAAG CATT		
			TTTTTTTTTTTTTTTT GTAA		
			G		
GAM3694	RGS13	5'	TAAATGAGAAGAGAAAAGGCA	83606	AA AAA
			TAAA AGAA AAAAGGCA		
			ATTTT TCTT TTTTCCGT		
			AC CTC		
GAM3694	RICH1	3'	AAAAAAAAAAAAAAAAAGAACA	83607	AG
			AAAAAGAAAAAAAAA GCA		
			TTTTTTTTTTTTTT TGT		
			CT		
GAM3694	RRS1	3'	AAAAGAAAAAAAAAAGGC	83608	
			AAAAGAAAAAAAAAAGGC		
			TTTTTCTTTTTTTTCCG		
GAM3694	SAMHD1	3'	AAAAAAGAAAAAAAAATAGA	83609	_
			AAAAAAGAAAAAAAAA AGG		

			TTTTTCTTTTTTT TCT		
			A		
GAM3694	SCAND2	3'	AAAAAAAAAAAAAGGCATT	83610	
			AAAGAAAAAAAAAGGCATT		
			TTTTTTTTTTTCCGTAA		
GAM3694	SDFR1	3'	AAAGGAAAAAAAAAGCA	83611	A
			AAA GAAAAAAAAAGGCA		
			TTT CTTTTTTTTTCGT		
			C		
GAM3694	SDFR1	3'	AAAGGAAAAAAAAAGCA	83611	A
			AAA GAAAAAAAAAGGCA		
			TTT CTTTTTTTTTCGT		
			C		
GAM3694	SFXN2	3'	AAAAAAAAAAAAAGAAGC	83612	A
			AAAAAGAAAAAAAA AGGC		
			TTTTTTTTTTTTT TTCG		
			C		
GAM3694	SSR3	3'	AAAAAAGAGAAAAAAGA	83613	A
			AAAAAAGA AAAAAAGG		
			TTTTTTCT TTTTTTCT		
			C		
GAM3694	STIM2	5'	TAAAAAAAAAAAAAAAAAAGG	83614	
			TAAAAAAGAAAAAAAAAAGG		
			ATTTTTTTTTTTTTTTTCC		
GAM3694	TAO1	3'	AAAAAAAAAAAAAAAAAGA	83533	
			AAAAAAGAAAAAAAAAAGG		
			TTTTTTTTTTTTTTTTTCT		
GAM3694	TGIF2	3'	AAAAAAGAAAAAAAAAAA	83536	
			AAAAAAGAAAAAAAAAAGG		
			TTTTTTCTTTTTTTTTT		
GAM3694	TOM1L1	3'	AAAAAGAGAAAAAAGGC	83615	A
			AAAAAGA AAAAAAGGC		
			TTTTTCT TTTTTTCCG		
			C		
GAM3694	TRAP150	3'	TAAAAAAGAAAAAAAAAAA	83616	
			TAAAAAAGAAAAAAAAAAG		

ATTTTTTCTTTTTTTTT

GAM3694 USP15 3' AAAAAAAGAAAAAAAAA 83478
AAAAAAAGAAAAAAAAAAG
|||||||
TTTTTTCTTTTTTTTT

GAM3694 WSB1 3' AAAAAAAAAAAAAAGACAT 83617
AAAAAGAAAAAAAAAGGCAT
|||||||
TTTTTTTTTTTTTTCTGTA

GAM3694 WSB1 3' AAAAAAAAAAAAAAGACAT 83617
AAAAAGAAAAAAAAAGGCAT
|||||||
TTTTTTTTTTTTTTCTGTA

GAM3694 ZFP106 3' TAAAAAAGAAGGCA 83618 AAAAAA
TAAAAAAGA AGGCA
||||| |||
ATTTTTTCT TCCGT

GAM3694 LOC115297 3' AAAAAAGGAAAAGGGAGGCACT 83619 A AAA
AAAAAAG AAAA AGGCATT
||||| ||| |||||
TTTTTTC TTTT TCCGTGA
C CCC

GAM3694 LOC122553 3' AAAAAAAGAAAAAAAAA 83478
AAAAAAAGAAAAAAAAAAG
|||||||
TTTTTTCTTTTTTTTT

GAM3694 LOC133686 3' AAAAAAAAAAAAAAAAAAGA 83620
AAAAAAAGAAAAAAAAAAGG
|||||||
TTTTTTTTTTTTTTTTTCT

GAM3694 LOC139673 3' AAAAAAAAAAAAAAAAAAGG 83537
AAAAAAGAAAAAAAAAAGG
|||||||
TTTTTTTTTTTTTTTTTCC

GAM3694 LOC142927 5' AAAAAAAAAAAAAAAAAAGC 83489
AAAAAGAAAAAAAAAAGGC
|||||||
TTTTTTTTTTTTTTTTTCG

GAM3694 LOC144524 5' TAAAAAAGAAAAAAAAA 83616
TAAAAAAGAAAAAAAAAAG
|||||||

ATTTTTTCTTTTTTTTT

GAM3694 LOC144587 5' TGAAAAAAAAAAAAAAGG 83490 A
A AAAAGAAAAAAAAAAGG
| |||||
A TTTTTTTTTTTTTTCC
C

GAM3694 LOC147632 5' AGAAAAAAAAAGGACCAT 83621 —
AGAAAAAAAAAAGG CAT
||||||| ||
TCTTTTTTTTCC GTA
TG

GAM3694 LOC147817 3' AAAAAAAAAAAAAAAAAAGA 83620
AAAAAAGAAAAAAAAAAGG
|||||||
TTTTTTTTTTTTTTTTCT

GAM3694 LOC148137 3' TGAAAAAAAAAAAAAGAGC 83622 A —
A AAAGAAAAAAAAAG GC
| ||||| ||
A TTTTTTTTTTTTTC CG
C T

GAM3694 LOC148198 3' AAAAAAGAAAAAGAAAAAC 83623 A
AAAAAAGAAAAA AAAGGC
||||||| |||||
TTTTTCTTTT TTTTG
C

GAM3694 LOC148898 5' TGAAGAAAAAAAAAAGCAC 83624 A G
A AAGAAAAAAAAAAG CAT
| ||||| |||
A TTCTTTTTTTTTC GTG
C —

GAM3694 LOC149722 5' TAAGAAAAGGAAATAAAAGGCA 83625 A A A
T TAA AAAAG AAA AAAAGGCAT
||| ||||| ||| |||||
ATT TTTTC TTT TTTTCCGTA
C C A

GAM3694 LOC151766 3' AAAAAAAAAAAAAAAGCA 83603
AAAAGAAAAAAAAAAGCA
|||||||
TTTTTTTTTTTTTTTCGT

GAM3694 LOC153683 3' AAAAAAAAAAAAAAAG 83626
AAAAAAGAAAAAAAAAAG
|||||||
TTTTTTTTTTTTTTTTTC

GAM3694 LOC154141 5' TAAAAAAATTCCTAAAAGGCA 83627 GAAAAA
TT TAAAAAA AAAAGGCATT
||||| |||||

	ATTTTTTT TTTTCCGTAA AAAGGA	
GAM3694 LOC202559 3'	AAAAAGAAAAAAAAAAGATT 83628 AAAAAGAAAAAAAAAAGG ATT TTTTTCTTTTTTTTTC TAA	C
GAM3694 LOC203286 5'	— AAAAAGAAAGGAAAGGCATT 83629 AAAAAGAAA AAAGGCATT TTTTTCTTT TTTCCGTAA CC_	AAA
GAM3694 LOC205327 3'	AAAAAAAAAAAAAAAAAGCCATT 83630 AAAAAGAAAAAAAAAAG CATT TTTTTTTTTTTTTTTC GTAA G	G
GAM3694 LOC221078 5'	CAAAAAAGAAAAAAATGC 83631 TAAAAAAGAAAAAAA GC GTTTTTTTCTTTTTT CG A_	AAG
GAM3694 LOC221178 3'	AAAAAGAGAGAAAGGCAT 83632 AAAAAGA AAAGGCAT TTTTTCT TTTCCGTA CTC_	AAAAA
GAM3694 LOC222001 3'	AAAGAAGGCTAAAAGGCATT 83560 AAAGAA AAAAGGCATT TTTCTT TTTTCCGTAA CCGA	AAA_
GAM3694 LOC253981 3'	AAAAAAAGAAAAAGAAAAG 83633 AAAAAAAGAAAAA AAAGG TTTTTTTCTTTT TTTTC C	A
GAM3694 LOC51107 3'	AAAAAAGAAAAAAGGCA 83634 AAAAAAGAAAAA AGGCA TTTTTTCTTTTTT TCCGT	AA
GAM3694 LOC51580 3'	— AAAAAAGAAAAGAAAAGG 83635 AAAAAAGAAAA AAAAGG TTTTTTCTTTT TTTTCC C	A
GAM3694 LOC51696 3'	TAAAAAAAAAAAAAAAAAAG 83495 TAAAAAAGAAAAAAAAAAGG 	

ATTTTTTTTTTTTTTTTTTC

GAM3694 LOC84549 3' AAAAAAAAAAAAAAAAAACA 83636
AAAAAAGAAAAAAAAAAGGCA
|||||
TTTTTTTTTTTTTTTTTGT

GAM3694 LOC90371 5' AAAAAAAGAAAAAAAAAAG 83558
AAAAAAGAAAAAAAAAAG
|||||
TTTTTTCTTTTTTTTC

GAM3694 LOC90957 3' AAAAGAAAAAAAAAAAGGC 83637 A
AAAA AGAAAAAAAAAAGGC
||| |||||
TTTT TTTTTTTTTTCCG
C

GAM3694 LOC91097 3' AAAAAAGAAAAAGAAAAGC 83564 A
AAAAAAGAAAAA AAAGGC
||||| |||||
TTTTTTCTTTTT TTTTCG
C

GAM3694 LOC91380 3' AAAAAAGAAAAAAAAAGCA 83638 AA
AAAAAAGAAAAAA GGCA
||||| |||
TTTTTTCTTTTTT TCGT

GAM3694 LOC91408 3' CAAAAGGAGAGGAAAAAAGGCA 83639 AA AA
TT TAAAA AGA AAAAAAGGCATT
|||| ||| |||||
GTTTT TCT TTTTTCCGTAA
CC CC

GAM3695 SPP1 3' AATATTAATAACAGTGATAGT 83642 T__
TT AATATTAATAATA ATAGTTT
||||| |||||
TTATAATTTTATGT TATCAAA
CAC

GAM3695 CCNG2 3' TAACATTAAAATAATACCATAG 83643 TA__
TTT TAATATTAATA TATAGTTT
||||| |||||
ATTGTAATTTTAT GTATCAAA
TATG

GAM3695 LOC121441 3' TAATATAAAAATATACATATTT 83644 T G
T TAATAT AAAATATATATA TTT
|||| ||||| |||
ATTATA TTTTATATGTAT AAA
T A

GAM3696 DKFZP564D172 3' TTTCCTCCTATATAGTTG 83647 G_
TTTCCT TGTGTAGTTG
|||| |||||

		AAAGGA ATATATCAAC		
		GG		
GAM3696 KIAA1634	3'	GCATCTTTCCTGATGACGTC	83648	T TA
		GCATCTTTCCTG GTG GTT		
		CGTAGAAAGGAC TAC CAG		
		_ TG		
GAM3696 PRO1598	3'	ATCTTTCCCACTGTGGTTG	83649	TG G A
		ATCTTTCC T TGT GTTG		
		TAGAAAGG G ACA CAAC		
		GT_ C		
GAM3696 LOC151643	3'	GCATTTTTTTCCTTGTAGTTG	83650	C__ GTG
		GCAT TTTCT TGTAGTTG		
		CGTA AAAGGA ACATCAAC		
		AAA _		
GAM3697 GPR34	3'	CTGAGTTTTGTAAATGCTAG	83653	_ A
		CTGA TTGTAAAT CTAG		
		GACT AACATTTA GATC		
		CAA C		
GAM3697 LAMP2	3'	TAAAGACTGATCTCAAAATGCT	83654	T GT_ A
		A AAGACTGATT AAAT CT		
		A TTCTGACTAG TTTA GA		
		T AGT C		
GAM3697 DIS3	3'	TAAGTATGTAAATACTA	83655	ACTGAT
		TAAG TGTAATACTA		
		ATTC ACATTTATGAT		
		AT__		
GAM3697 HABP4	3'	TATAAGTGCTTAATAAATACTA	83656	A_ GATT
G		TATAAG CT GTAAATACTAG		
		ATATTC GA TATTTATGATC		
		AC AT__		
GAM3697 PNMA5	5'	GACTGATCTAATACTAG	83657	GTA
		GACTGATT AATACTAG		
		CTGACTAG TTATGATC		
		A__		
GAM3698 CHD2	3'	TTGACATTGAAAAGGAAAAGTAT	83660	AGT CA
T		TTGACATT AA GAAAGTATT		
		AACTGTAA TT CTTTCATAA		
		CT_ TC		
GAM3698 AASDHPPT	3'	TTAATGTTAGTAACAGAAA	83661	CA
		TTGA TTAGTAACAGAAA		

AATT AATCATTGTCTTT
 AC
 GAM3698 CHUK 3' TTGACACTAATACATAGAAGGT 83662 AC_ A
 ATT TTGACATTAGTA AGAA GTATT
 ||||| ||| ||||
 AACTGTGATTAT TCTT CATAA
 GTA C
 GAM3698 DKFZp434G179 3' TTAATATTAGTAAAGTTTTAGA 83663 C_____ III
 AAGTATTA TTAGTAA AGAAAGTATT A
 ||||| ||||| I
 AATCATT TCTTTCATAA T
 TCAAAA III
 GAM3698 DKFZp564I1922 3' TTAATAAGACAGAAAGTAT 83664 ____
 TTAGTA ACAGAAAGTAT
 ||||| |||||
 AATTAT TGTCTTTCATA
 TC
 GAM3698 LOC133418 3' TTAGCAAAGGCAGAAAGTATT 83665 ____
 TTAGTAA CAGAAAGTATT
 ||||| |||||
 AATCGTT GTCTTTCATAA
 TCC
 GAM3698 LOC255098 3' TTAGCAAAGGCAGAAAGTATT 83665 ____
 TTAGTAA CAGAAAGTATT
 ||||| |||||
 AATCGTT GTCTTTCATAA
 TCC
 GAM3699 PIN 3' CAGTCTCTGGTATTTGGAATT 83668 GA AA_
 TAG TT TATTTGGAATT
 ||| || |||||
 GTC AG ATAAACCTTAA
 AG ACC
 GAM3699 MSTP031 5' TAAGTAGGATTATTGGA 83669 ATAT
 TAAGTAGGATTA TTGGA
 ||||| ||||
 ATTCATCCTAAT AACCT

 GAM3699 NESHBP 3' TAAGTAGAGATTTATGGAATT 83670 _ AATATT
 TAAGTAG GATT TGGAATT
 ||||| ||| |||||
 ATTCATC CTAA ACCTTAA
 T AT____
 GAM3699 LOC90784 5' GTAGGAACCTTTGGAATT 83671 TTAATA
 GTAGGA TTTGGAATT
 ||||| |||||
 CATCCT AAACCTTAA
 TG____
 GAM3699 LOC92360 3' GTAGGGTATCACATTGGAATT 83672 ____ ATAT
 GTAGG ATTA TTGGAATT
 ||||| ||| |||||

		CATCC TAGT AACCTTAA	
		CA GT__	
GAM3700	CLOCK	3' AAATGTATGTAACCTTGTAT 83675	CTTA
		AAGTGTATGT TGTAT	
		TTTACATACA ACATA	
		TTGA	
GAM3700	GPR85	3' TAAAGTGTGATGTTTATAT 83676	_ C
		TAAAGTGT ATGT TTATGT	
		ATTTTACA TACA AATATA	
		C _	
GAM3700	HTR2C	3' TAAAGTGTATATTTACTGT 83677	CTTA
		TAAAGTGTATGT TGT	
		ATTTTACATATA ACA	
		AATG	
GAM3700	SWAP70	3' AAAGTGTATGTTCTGGTAT 83678	_ TAT
		AAAGTGTATGT CT GTAT	
		TTTCACATACA GA CATA	
		A C__	
GAM3700	TCF3	3' CAAAGTGTATGTTTTGT 83679	CTTA
		TAAAGTGTATGT TGT	
		GTTTCACATACA ACA	
		AA__	
GAM3700	TIMM17A	3' AAGTATTATTTTATGTATATT 83680	A C
		AAGTGT TGT TTATGTATATT	
		TTCATA ATA AATACATATAA	
		_ A	
GAM3700	FLJ10989	3' AGTGTATGTTACTTGTGTAT 83681	_ A
		AGTGTATGT CTT TGTAT	
		TCACATACA GAA ACATA	
		AT C	
GAM3700	FLJ11196	3' GCGTACCGATTATGTATATT 83682	_ TC
		GTGTAT G TTATGTATATT	
		CGCATG C AATACATATAA	
		G TA	
GAM3700	KCNH7	3' AAAGTTCTTATGTATAT 83683	GTATG
		AAAGT TCTTATGTATAT	
		TTTCA AGAATACATATA	

GAM3700	KIAA1789	5' AAAGTGTGTGTCTAACACTGT 83684	A TA__
		AAAGTGT TGTCT TGT	

		TTTCACA ACAGA ACA	
		C TTGTG	
GAM3700 MYOZ2	3'	TGAATGTATTTATATGTATATT 83685	A GTCT
		A AGTGTAT TATGTATATT	
		A TTACATA ATACATATAA	
		C AAT_	
GAM3700 ZNF237	3'	GTGTACGTTTGTATATT 83686	CTTA
		GTGTATGT TGTATATT	
		CACATGCA ACATATAA	
		A__	
GAM3700 LOC158722	3'	TAAAGTGTTTATTGTATGT 83687	A CT
		TAAAGTGT TGT TATGT	
		ATTTCACA ATA ATACA	
		A AC	
GAM3701 CD2AP	3'	ATGCATTATGGAAAAAGTAGT 83690	AA TCGT
		ATGCATTAT GA GTAGT	
		TACGTAATA CT CATCA	
		C_ TTTT	
GAM3701 FREB	3'	TGCATTATAGGATGTTTAG 83691	A C G
		TGCATTATA GAT GT TAG	
		ACGTAATAT CTA CA ATC	
		C _ A	
GAM3701 PPIL1	3'	GCATTATGGTTCATGTGTAGTA 83692	AAGATC_
A		GCATTAT GTGTAGTAA	
		CGTAATA CACATCATT	
		CCAAGTA	
GAM3701 SGCG	3'	TGCATTTTGAGATCATGTAG 83693	ATA
		TGCATT AGATCGTGTAG	
		ACGTAA TCTAGTACATC	
		AAC	
GAM3701 TBR1	3'	TGCATTAGGGCACATAGTAA 83694	ATA AT TG
		TGCATT AG CG TAGTAA	
		ACGTAA TC GT ATCATT	
		_ CC GT	
GAM3701 H-plk	3'	ATGAATTATCTTATGTGTAGTA 83695	C AAG C
A		ATG ATTAT AT GTGTAGTAA	
		TAC TAATA TA CACATCATT	
		T GAA _	
GAM3701 HRH4	3'	ATGCATTAAAGACATTAAGTAA 83696	T T GT
		ATGCATTA AAGA CGT AGTAA	

TACGTAAT TTCT GTA TCATT
 _ _ AT
 GAM3701 KIAA1724 3' ATGCATTAAGATCTGTCTAG 83697 T _ G
 ATGCATTA AAGATC GT TAG
 ||||| ||||| || |||
 TACGTAAT TTCTAG CA ATC
 T A G
 GAM3701 LOC133584 3' TGCATTATAAGAAGTAG 83698 TCGT
 TGCATTATAAGA GTAG
 ||||| |||||
 ACGTAATATTCT CATC
 T__
 GAM3701 LOC147610 5' ATTATGAAACAATGTAGTAA 83699 A C
 ATTAT AGAT GTGTAGTAA
 |||| ||| |||||
 TAATA TTTG TACATCATT
 C T
 GAM3701 LOC203339 3' ATACATTATAAGGTCACCTCTAG 83700 A G_
 ATGCATTATAAG TCGT TAG
 ||||| ||||| |||
 TATGTAATATTC AGTG ATC
 C AG
 GAM3701 LOC55885 3' TGCATTATAGTGATTTTCAGTA 83701 A_ CGTG
 TGCATTATA GAT TAGTA
 ||||| ||| |||||
 ACGTAATAT CTA GTCAT
 CA AA_
 GAM3702 APPL 3' TTAGTTATTTGCCTTTGTGGAT 83704 _ A_____ III
 ATA TAGTTGTT GT TGGATAT A
 ||||| || ||||| |
 ATCAATAA CG ACCTATA T
 A GAAAC III
 GAM3702 CDKN2B 3' TCAGTTGTTCCAATGATAT 83705 G TG
 TTAGTTGTT TA GATAT
 ||||| || |||||
 AGTCAACAA GT CTATA
 G TA
 GAM3702 EHD3 3' TAGTCTGAATATGGATAT 83706 GTT
 TAGTT GTATGGATAT
 |||| |||||
 ATCAG TATACCTATA
 ACT
 GAM3702 EHHADH 3' TAGTCCATTGTATGGATAT 83707 _ TG
 TAG T TTGTATGGATAT
 ||| | |||||
 ATC G AACATACCTATA
 A GT
 GAM3702 NQO1 3' TCAGCTATTGTGGATAT 83708 AT
 TTAGTTGTTGT GGATAT
 ||||| |||||

AGTCGATAACA CCTATA

GAM3702 BCoR 3' TTAGTTGTTGTGTGGATAT 83709 A__
TTAGTTGTTGT TGGATAT
||||||| |||||
AATCAACAACA ACCTATA
CAC

GAM3702 BIRC1 3' TCAGTTGTACAACATGGAT 83710 TG__
TTAGTTGT TATGGAT
||||| |||||
AGTCAACA GTACCTA
TGTT

GAM3702 FLJ10283 3' CTAGTTGCTTATATGGAT 83711 _
TTAGTTGTT GTATGGAT
||||||| |||||
GATCAACGA TATACCTA
A

GAM3702 KIAA0831 3' TAGTTGTTACATAGGATAT 83712 _
TAGTTGTTGTAT GGATAT
||||||| |||||
ATCAACAATGTA CCTATA
T

GAM3702 KIAA1765 3' TTATTCATTGTGTGGATAT 83713 G TG A
TTA T TTGT TGGATAT
||| | ||| |||||
AAT A AACA ACCTATA
A GT C

GAM3702 LANO 3' GTGGTTGTATATCTGGATAT 83714 T ____
GT GTTGTA TGGATAT
|| ||||| |||||
CA CAACAT ACCTATA
C ATAG

GAM3702 LMOD1 3' TTAGCTGTGTGATCATGGATAT 83715 TG__
TTAGTTGT TATGGATAT
||||||| |||||
AATCGACA GTACCTATA
CACTA

GAM3702 MYT1L 5' TCAGTGAGTATGGATAT 83716 T TT
TTAGT G GTATGGATAT
||||| | |||||
AGTCA C CATACTATA
_ T _

GAM3702 PPP1R14C 3' TTAGTTGTGTGTAGATAT 83717 T A
TTAGTTGT GT TGGATAT
||||||| || |||||
AATCAACA CA ATCTATA
_ C

GAM3702 LOC221479 3' TAGTTGTTGTGAAGACAT 83718 AT
TAGTTGTTGT GGATAT
||||||| |||||

			ATCAACAACA TCTGTA		
			CT		
GAM3702	LOC92900	5'	TCACCTGTGTATGGATAT	83719	G T
			TTA TTGT GTATGGATAT		
			AGT GACA CATACTATA		
			G _		
GAM3703	ATP5B	3'	AAACGTAGTAGCAGGGG	83722	CAATC GA
			AAACGTAG GCA GGGG		
			TTTGCATC CGT CCCC		
			AT__ _		
GAM3703	CYP2F1	3'	ACGTAGCAACCCGCATGGGC	83723	_ GAG
			ACGTAGCAATC GCA GGGC		
			TGCATCGTTGG CGT CCCG		
			G A__		
GAM3703	DGAT2	3'	GTGGCAATAAAGGGGC	83724	A CGC
			GT GCAAT AGAGGGGC		
			CA CGTTA TTTCCCCG		
			C _		
GAM3703	IFNAR2	3'	ACGATAGCATCAGAGGGGC	83725	_ ATCG
			ACG TAGCA CAGAGGGGC		
			TGC ATCGT GTCTCCCCG		
			T A__		
GAM3703	LIMK1	3'	AAAACGCAGAGGACAGAGGGGC	83726	CAATC
			AAAACGTAG GCAGAGGGGC		
			TTTTGCGTC TGTCTCCCCG		
			TCC__		
GAM3703	LIMK1	3'	AAAACGCAGAGGACAGAGGGGC	83726	CAATC
			AAAACGTAG GCAGAGGGGC		
			TTTTGCGTC TGTCTCCCCG		
			TCC__		
GAM3703	USF2	3'	AAAACGCAGCTGGGGGAGGGGC	83727	AATCGCA
			AAAACGTAGC GAGGGGC		
			TTTTGCGTCG CTCCCCG		
			ACCC__		
GAM3703	AFAP	3'	CATAGGCACAGAGGGGC	83728	CAAT
			CGTAG CGCAGAGGGGC		
			GTATC GTGTCTCCCCG		
			C__		
GAM3703	ARHGEF4	3'	AACTAGAGGGCAGAGGGGC	83729	G CAATC
			AAC TAG GCAGAGGGGC		

TTG ATC CGTCTCCCCG
 _ TCC_
 GAM3703 BAG3 5' ACGTGGCCAGAGAGGGG 83730 A AAT C
 ACGT GC CG AGAGGGG
 |||| || || |||||
 TGCA CG GT TCTCCCC
 C _ C
 GAM3703 DKFZp762E1511 3' GCATGCTGGGCAGAGGGGC 83731 _ AATC
 GTA GC GCAGAGGGGC
 ||| || |||||
 CGT CG CGTCTCCCCG
 A ACC_
 GAM3703 FLJ13848 3' GTGCAGGCAGAGGGGC 83732 A ATC
 GT GCA GCAGAGGGGC
 || ||| |||||
 CA CGT CGTCTCCCCG
 _ C_
 GAM3703 FLJ20489 3' AAACGCAGGGCTGGAGGGGC 83733 CAATC A_
 AAACGTAG GC GAGGGGC
 ||||| || |||||
 TTTGCGTC CG CTCCCCG
 C _ AC
 GAM3703 KIAA1808 3' GGAACGCAGCGCATGGAGGGGC 83734 A AATC _
 A AACGTAGC GCA GAGGGGC
 | ||||| ||| |||||
 C TTGCGTCG CGT CTCCCCG
 C _ AC
 GAM3703 SCAMP5 3' ACATAGGCAGAGGGG 83735 CAATC
 ACGTAG GCAGAGGGG
 ||||| |||||
 TGTATC CGTCTCCCC

 GAM3703 TTYH2 3' GGAACGAGGACAGAGGGG 83736 A T CAATC
 A AACG AG GCAGAGGGG
 | ||| || |||||
 C TTGC TC TGTCTCCCC
 C _ C_
 GAM3703 LOC144596 3' AAAACGCAGCTGGGGGAGGGGC 83727 AATCGCA
 AAAACGTAGC GAGGGGC
 ||||| |||||
 TTTTGCCTCG CTCCCCG
 ACCCC_
 GAM3703 LOC200310 3' AACATGGCTCAGAGGGG 83737 A AATCG
 AACGT GC CAGAGGGG
 |||| || |||||
 TTGTA CG GTCTCCCC
 C A_
 GAM3703 LOC221929 5' GTGAGCTGCAGAGGGGC 83738 _ AATC
 GT AGC GCAGAGGGGC
 || ||| |||||

		CA TCG CGTCTCCCCG		
		C A__		
GAM3703	LOC91526 5'	GCAGCATGCAGAGGGG	83739	ATC
		GTAGCA GCAGAGGGG		
		CGTCGT CGTCTCCCC		
		A__		
GAM3703	LOC92223 5'	AACGTAGCAGCTGGGG	83740	ATC AGA
		AACGTAGCA GC GGGG		
		TTGCATCGT CG CCCC		
		__ A__		
GAM3704	ARHGEF7 3'	TGGTTTGATCGTCTCCATT	83743	A
		TGGTTTGA CGTCTCCATT		
		ACCAAAC TGCAGAGGTAA		
		A		
GAM3704	ETV5 3'	TGGTTTGAGCCTCCCCAAC	83744	AC A
		TGGTTTGA GTCTCC TTAAC		
		ACCAAAC TCGGAGG GGTTG		
		__ -		
GAM3704	STMN1 3'	TGGCTTGATTTATTAACC	83745	ACGTCTCC
		TGGTTTGA ATTAACC		
		ACCGAACT TAATTGG		
		AAA__		
GAM3704	TDRD1 3'	GGTTTCACTCCATTA	83746	GAA T
		GGTTT CG CTCCATTA		
		CCAAA GT GAGGTAAT		
		__ -		
GAM3704	FHR5 3'	TGGTTTGAATGTGTCCCC	83747	C__
		TGGTTTGAA GTCTCC		
		ACCAAAC TT CAGGGG		
		ACA		
GAM3704	PRO1770 5'	TGGTTTAAATGTACTATAACCC	83748	C _ CCAT
		TGGTTTGAA GT CT TAACCC		
		ACCAAATTT CA GA ATTGGG		
		A T T__		
GAM3704	LOC122726 3'	TGGTTTGATGTTCCCATAACCC	83749	AC CT T
		TGGTTTGA GT CCAT AACCC		
		ACCAAAC T CA GGTA TTGGG		
		A_ AG _		
GAM3704	LOC158427 3'	TGATTATCATTCTTTATTAACC	83750	TGAACG CC
	C	TGGTT TCT ATTAACCC		

		ACTAA AGA TAATTGGG	
		TAGTA_ AA	
GAM3705 RPS6KA1	3'	TGTGTGAGGCAAGTACTATTAG 83753	AG_ ATGT
	GG	TGTGTGA AAGTG TTAGGG	
		ACACACT TTCAT AATCCC	
		CCG GAT_	
GAM3705 B3GALT1	5'	TGTGTGAGGAGGAGATTCAAGG 83754	A A T T
		TGTGTGA GA G GA GTTTAGGG	
		ACACACT CT C CT TAAGTTCC	
		C _ _ C	
GAM3705 BAT8	3'	TGTGTGAAAGGGTGGTGGG 83755	AA A TTTA
		TGTGTGAAG GTG TG GG	
		ACACACTTT CAC AC CC	
		CC C _ _ _	
GAM3705 FLJ13114	3'	TGTGAGGGGCTGTTTAGG 83756	A AA GA
		TGTGA G GT TGTTTAGG	
		ACACT C CG ACAAATCC	
		_ CC _	
GAM3705 FLJ22655	3'	TGTGTGAAGGAGAGTGAGCAGG 83757	A_ T TT
	G	TGTGTGAAG AGTGA GT AGGG	
		ACACACTTC TCACT CG TCCC	
		CTC _ _	
GAM3705 HNRPA0	3'	TGTGTGAGGGGGTGGGGCTTAG 83758	AGAA AT
	G	TGTGTGA GTG GTTTAGG	
		ACACACT CAC CGAATCC	
		CCCC CC	
GAM3705 SCYB11	3'	ATGTGCTACATGATGTTTGGGG 83759	AAGAA A
		GTGTG GTGATGTTT GGG	
		TACAC TACTACAAA CCC	
		GATG_ C	
GAM3705 LOC201304	3'	TGTTTGAGGAAGTGGGTTGGG 83760	G A AT TA
		TGT TGA GAAGTG GTT GGG	
		ACA ACT CTTCAC CAA CCC	
		A C C_ _	
GAM3705 LOC256158	5'	TGAACCAGGTGATGTTTGGGG 83761	GA _ A
		TGAA AG TGATGTTT GGG	
		ACTT TC ACTACAAA CCC	
		GG C C	
GAM3705 LOC91050	3'	TGTTGAAGGAGTGAAG 83762	G A TGTTT
		TGT TGAAG AGTGA AG	

			ACA ACTTC TCACT TC		
			— C —		
GAM3706	C7orf2	3'	GCTTTTAAGGAAATAAGAAAC 83765	ACTC	TT
			GCT AAG AGTAAGAAAC		
			CGA TTC TTATTCTTTG		
			AAA_ CT		
GAM3706	MLH3	3'	GCTACTCAACTAGGGGAA 83766	G	TAA
			GCTACTCAA TTAG GAA		
			CGATGAGTT GATC CTT		
			— CC_		
GAM3706	NPPB	3'	CTCAAAGGTAAGAAAC 83767	TTA	
			CTCAAG GTAAGAAAC		
			GAGTTT CATTCTTTG		
			C_		
GAM3706	DKFZp434E2220	5'	ACTCAAGTCTAACAGAAAC 83768	AGTA	
			ACTCAAGTT AGAAAC		
			TGAGTTCAG TCTTTG		
			ATTG		
GAM3706	FLJ10874	3'	GCTACTCAGTCCATTAAGAAAC 83769	A	AG_
			GCTACTCA GTT TAAGAAAC		
			CGATGAGT CAG ATTCTTTG		
			— GTA		
GAM3706	FLJ20551	3'	TACTGCAGAATAGTAAGAA 83770	_	AGT
			TACT CA TAGTAAGAA		
			ATGA GT ATCATTCTT		
			C CTT		
GAM3706	FLJ20758	3'	GCTGTTCAAGTTAGAAAA 83771	AC	T
			GCT TCAAGTTAG AAGA		
			CGA AGTTCAATC TTTT		
			CA _		
GAM3706	KIAA0390	3'	TCCTGCTCAAGTTACTAAG 83772	G A	G
			TC CT CTCAAGTTA TAAG		
			AG GA GAGTTCAAT ATTC		
			_ C G		
GAM3706	KIAA1155	3'	CTACTCAGCAATAAAA 83773	A	T
			CTACTCA GT AGTAAGA		
			GATGAGT CG TTATTTT		
			_ _		
GAM3706	KIAA1344	3'	GCTACTCGGAAGTAAGAAA 83774	AAGTT	
			GCTACTC AGTAAGAAA		

CGATGAG TCATTCTTT
 CCT__
 GAM3706 KIAA1987 3' GCTCTTTAAGGTAAGAAAC 83775 ACTC TTA
 GCT AAG GTAAGAAAC
 ||| ||| |||||
 CGA TTC CATTCTTTG
 GAAA __
 GAM3706 NDUFC2 3' TACTCAAGAAAATAGAGA 83776 TT _
 TACTCAAG AGTA AGA
 ||||| ||| |||
 ATGAGTTC TTAT TCT
 TT C
 GAM3706 LOC138046 3' GCTGCTGTCCAGTAAGAAAC 83777 A CAAG
 GCT CT TTAGTAAGAAAC
 ||| ||| |||||
 CGA GA GGTCATTCTTTG
 C CA__
 GAM3707 AQP6 3' TAGCATTTTAACTTCTGAAAGT 83780 CG _
 AT TAGCAT TTAACTTTT AAAGTAT
 ||||| ||||| |||||
 ATCGTA AATTGAAGA TTTCATA
 A_ C
 GAM3707 AQP6 3' TAGCATTTTAACTTCTGAAAGT 83780 CG _
 AT TAGCAT TTAACTTTT AAAGTAT
 ||||| ||||| |||||
 ATCGTA AATTGAAGA TTTCATA
 A_ C
 GAM3707 HPGD 3' TAGCTTTCCTCTTTTAAAGTAT 83781 ATCG AA
 TAGC TT CTTTAAAGTAT
 ||| ||| |||||
 ATCG AG GAAAATTTTCATA
 AA_ GA
 GAM3707 UTX 3' GCATCTTCTTTAAAGTA 83782 GTTAAC
 GCATC TTTTAAAGTA
 ||||| |||||
 CGTAG AGAATTTTCAT
 AA____
 GAM3707 MO25 3' TAGCTCTACTGTTTAAAGTAT 83783 A GTTAAC
 TAGC TC TTTTAAAGTAT
 ||| ||| |||||
 ATCG AG AAAATTTTCATA
 _ ATGAC_
 GAM3707 LOC92223 3' GCCCAAGAAGCTTTTAAAGTAT 83784 A TT _
 GC TCG AA CTTTAAAGTAT
 || ||| ||| |||||
 CG GGT TT GAAAATTTTCATA
 _ TC C
 GAM3708 ANK3 3' GTCATTAGAGCTATGTG 83787 G TCT T
 GT CAT TGG AGCTATGTG
 || ||| ||| |||||

CA GTA ATC TCGATACAC

GAM3708 C18orf1 3' CGGCATTCTTGGTCAGTG 83788 T AGCTAT
CG GCATTCTTGGT GTG
|| ||||| |||
GC CGTAAGAACCA CAC

GT____
GAM3708 GPLD1 3' GTGTTGTTTCCCTCTATGTGT 83789 CA__ TGGTAG
GTG TTCT CTATGTGT
||| ||| |||||
CAC AAGG GATACACA
AACA GA____

GAM3708 LOC164295 5' CGTGTGTTCTGGTGGGCCA 83790 CA T A_
CGTG TTCT GGT GCTA
||| ||| ||| |||
GCAC AAGA CCA CGGT
AC _ CC

GAM3709 ADAT1 3' GCTGGAGTGCAGCGGTAC 83793 TGACCA C
GCTGGAGTGC CGG AC
||||||| ||| ||
CGACCTCACG GCC TG
TC____ A

GAM3709 AICDA 3' GCTGGAGTGC AACGGCAC 83794 TGACC
GCTGGAGTGC ACGGCAC
||||||| |||||
CGACCTCACG TGCCGTG
T____

GAM3709 AIRE 3' ACTGGAGTGCAGTGGCGCA 83795 TGACCAC A
GCTGGAGTGC GGC CA
||||||| ||| ||
TGACCTCACG CCG GT
TCA____ C

GAM3709 ANKH 3' GCTGGAGTGC GATGGC 83796 T CCAC
GCTGGAGTGC GA GGC
||||||| || |||
CGACCTCACG CT CCG
_ A____

GAM3709 ATP1A2 3' GCTGGAGTGT AATGGCAC 83797 C CCAC
GCTGGAGTG TGA GGCAC
||||||| ||| |||||
CGACCTCAC ATT CCGTG
_ A____

GAM3709 BAZ1B 5' AGCGGAACGCCACGGCC 83798 T TGC A A
AGC GGAG TG CCACGGC C
||| ||| || ||||| |
TCG CCTT GC GGTGCCG G
_ _ _ C

GAM3709 C7orf2 3' AGCTGGAGGCTTCAAATGGCA 83799 T GACCAC
AGCTGGAG GCT GGCA
||||||| ||| |||||

			TCGACCTC CGA CCGT	
			_ AGTTTA	
GAM3709	CXorf6	3'	AGCTGGGGTTGTTGGCCAGGGG 83800	A GC_ A C_
	CA		AGCTGG GT TG CCA GGCA	
			TCGACC CA AC GGT CCGT	
			C ACA C CC	
GAM3709	CYP4F3	3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_____	
GAM3709	DHFR	3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_____	
GAM3709	DNASE1	5'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_____	
GAM3709	FLRT2	5'	GCTGGAGTGCAGCGGCAC 83802	TGACCA
			GCTGGAGTGC CGGCAC	
			CGACCTCACG GCCGTG	
			TC_____	
GAM3709	FOX E1	3'	ACTGGAGTGCTGACGCAC 83803	CACG
			GCTGGAGTGCTGAC GCAC	
			TGACCTCACGACTG CGTG	

GAM3709	GP2	3'	GCTGGAGTGCAATGGCAC 83804	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TTA_____	
GAM3709	GPRC5C	3'	GCTGGAGTGTGACCGCCG 83805	C A_
			GCTGGAGTG TGACC CG	
			CGACCTCAC ACTGG GC	
			_ CG	
GAM3709	GPRC5C	3'	GCTGGAGTGTGACCGCCG 83805	C A_
			GCTGGAGTG TGACC CG	
			CGACCTCAC ACTGG GC	
			_ CG	
GAM3709	HIP1	3'	GCCGGAGTGCACTGGCAC 83806	TGACC _
			GCTGGAGTGC AC GGCAC	

			CGGCCTCACG	TG CCGTG	
			_____ A		
GAM3709	HUNK	3'	AGCTGGAGTGCAGTAGCA	83807	TGACCAC
			AGCTGGAGTGC	GGCA	
			TCGACCTCACG	TCGT	
			TCA_____		
GAM3709	IRAK4	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	KAI1	3'	GCTGGAGTGCAGTAGCAC	83808	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	TCGTG	
			TCA_____		
GAM3709	NPHP1	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	NT5C2	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	OGG1	5'	GCTGGAGTGTGATGGC	83809	C CCAC
			GCTGGAGTG TGA	GGC	
			CGACCTCAC ACT	CCG	
			_____ A_____		
GAM3709	OGG1	5'	GCTGGAGTGTGATGGC	83809	C CCAC
			GCTGGAGTG TGA	GGC	
			CGACCTCAC ACT	CCG	
			_____ A_____		
GAM3709	OGG1	5'	GCTGGAGTGTGATGGC	83809	C CCAC
			GCTGGAGTG TGA	GGC	
			CGACCTCAC ACT	CCG	
			_____ A_____		
GAM3709	PA2G4	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	PEPD	3'	ACTGGAGTGCTGACCAGCA	83810	CG
			GCTGGAGTGCTGACCA	GCA	

TGACCTCACGACTGGT CGT

GAM3709 PML 3' GCAGGAGTGCTGGCTTGGACCA 83811 T
CA GC GGAGTGCT GACCACG

|| ||||| |||||
CG CCTCACGA CTGGTGT
T CCGAAC

GAM3709 PML 3' GCAGGAGTGCTGGCTTGGACCA 83811 T
CA GC GGAGTGCT GACCACG

|| ||||| |||||
CG CCTCACGA CTGGTGT
T CCGAAC

GAM3709 PRKCG 3' AGCTGGAATGCTGGGGTGCA 83812 ACCACG
AGCTGGAGTGCTG GCA

||||||| |||
TCGACCTTACGAC CGT
CCCA__

GAM3709 PRKY 3' CTGGAGTGCAGTGGCAC 83813 TGACC _
CTGGAGTGC AC GGCAC

||||||| || |||||
GACCTCACG TG CCGTG
__ A

GAM3709 PRV1 3' AGCTGGAATGTTGGGCCACA 83814 C A_
AGCTGGAGTG TG CCACG

||||||| || |||||
TCGACCTTAC AC GGTGT
A CC

GAM3709 PSMB9 3' ACTGGAGTGCAGTGGCAC 83815 TGACCAC
GCTGGAGTGC GGCAC

||||||| |||||
TGACCTCACG CCGTG
TCA__

GAM3709 PTGIS 3' GCTGGAGTGCCGTGGCC 83816 ACCAC A
GCTGGAGTGCTG GGC C

||||||| ||| |
CGACCTCACGGC CCG G
A__ C

GAM3709 PYCR1 5' ACTGGAGTGTTGGTCATGCAGC 83817 C AC _
GCTGGAGTG TG CA CGGC

||||||| || || |||||
TGACCTCAC AC GT GTCG
A CA AC

GAM3709 RANBP2L1 3' AGCTGGAGTGCAGTGGTAC 83818 TGACCAC C
AGCTGGAGTGC GG AC

||||||| || ||
TCGACCTCACG CC TG
TCA__ A

GAM3709 RPN1 5' GCTGGAGTGTGATGGC 83809 C CCAC
GCTGGAGTG TGA GGC

||||||| ||| |||

			CGACCTCAC ACT CCG		
			— A —		
GAM3709	SLC26A4	3'	GCTGGAGTGCAGTGGCAC 83801		TGACCAC
			GCTGGAGTGC GGCAC		
			CGACCTCACG CCGTG		
			TCA —		
GAM3709	SMG1	3'	GCTGGAGTGCAGTGGCAC 83801		TGACCAC
			GCTGGAGTGC GGCAC		
			CGACCTCACG CCGTG		
			TCA —		
GAM3709	STK38	5'	GCTGGAGTGCACAGG 83819		T CAC
			GCTGGAGTGC GAC GG		
			CGACCTCACG CTG CC		
			— T —		
GAM3709	TNNC1	3'	AGTTGGAGGCTGGGCA 83820	C T	ACCAC
			AG TGGAG GCTG GGCA		
			TC ACCTC CGAC CCGT		
			A — — — —		
GAM3709	TRIM9	3'	AGCTGGCGCCTCCACGGCACA 83821	AG GA	
			AGCTGG TGCT CCACGGCACA		
			TCGACC GCGG GGTGCCGTGT		
			— A —		
GAM3709	VHL	3'	GCTGGAGTGCAGCGGCA 83822		TGACCA
			GCTGGAGTGC CGGCA		
			CGACCTCACG GCCGT		
			TC —		
GAM3709	VIL2	3'	AGCTGGAGTCTGAAAGC 83823	G	CCAC
			AGCTGGAGT CTGA GGC		
			TCGACCTCA GACT TCG		
			— T —		
GAM3709	XT3	3'	ACTGGAGTGGAGTGGCA 83824		CT CCAC
			GCTGGAGTG GA GGCA		
			TGACCTCAC CT CCGT		
			— CA —		
GAM3709	ZNF264	3'	GCTGGAGTGCAGTGGCAC 83801		TGACCAC
			GCTGGAGTGC GGCAC		
			CGACCTCACG CCGTG		
			TCA —		
GAM3709	BSPECV	5'	GCTGGGGTGACGGCAC 83825	A	CTGACC
			GCTGG GTG ACGGCAC		

			CGACC CAC	TGCCGTG	
			C _____		
GAM3709	C1orf34	3'	GCTGGAGTGCTATGGC	83826	ACCAC
			GCTGGAGTGCTG	GGC	
			CGACCTCACGAT	CCG	
			A_____		
GAM3709	C20orf12	3'	GCTGGAGTGCGATGGC	83796	T CCAC
			GCTGGAGTGC GA	GGC	
			CGACCTCACG CT	CCG	
			_ A_____		
GAM3709	C20orf150	3'	AGCTGGAGCGCTGGACCA	83827	_
			AGCTGGAGTGCTG ACCA		
			TCGACCTCGCGAC TGGT		
			C		
GAM3709	C20orf177	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	C21orf108	3'	GCTGGAGCGCAATGGCAC	83828	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCGCG	CCGTG	
			TTA_____		
GAM3709	C8orf2	3'	AGCTAGAGTGGGATGGCA	83829	CT CCAC
			AGCTGGAGTG GA	GGCA	
			TCGATCTCAC CT	CCGT	
			C_ A_____		
GAM3709	CAMKK2	5'	GCTGGAGTGCAAGTAGCAC	83808	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	TCGTG	
			TCA_____		
GAM3709	CCR6	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	CCR6	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	CPR2	3'	GCTGGAGTGCAAGTAGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	

			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	DDX34	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	DJ122O8.2	3'	GCTGAAGTGCAGTGGCAC	83830	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACTTCACG	CCGTG	
			TCA_____		
GAM3709	DKFZP434C0826	5'	AGCTGGAGGTTGGCCAGGCA	83831	TGC A C
			AGCTGGAG	TG CCA GGCA	
			TCGACCTC	AC GGT CCGT	
			CA_ C _		
GAM3709	DKFZP434I1735	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	DKFZP564I0422	3'	GCTGGAGTGCAGTCGTGCA	83832	TGACCA _
			GCTGGAGTGC	CG GCA	
			CGACCTCACG	GC CGT	
			TCA___ A		
GAM3709	DKFZp762K222	5'	AACTGGGAGCCACGGCAC	83833	AGTGCT _
			AGCTGG	GA CCACGGCAC	
			TTGACC	CT GGTGCCGTG	
			_____ C		
GAM3709	DRF1	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	ET	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	FBXO9	3'	GCTGGAGTGGAATGGCAC	83834	CT CCAC
			GCTGGAGTG	GA GGCAC	
			CGACCTCAC	CT CCGTG	
			__ TA__		
GAM3709	FKBP14	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	

			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FKSG17	3'	GCTGGAGTGCCGTGGTGCA	83835	ACCACG
			GCTGGAGTGCTG	GCA	
			CGACCTCACGGC	CGT	
			ACCA__		
GAM3709	FLJ10781	3'	GCTGGAGTGCCGTGGCAC	83836	ACCAC
			GCTGGAGTGCTG	GGCAC	
			CGACCTCACGGC	CCGTG	
			A_____		
GAM3709	FLJ10826	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ11301	3'	GCTGGAGTGCAGCGGCC	83837	TGACCA A
			GCTGGAGTGC	CGGC C	
			CGACCTCACG	GCCG G	
			TC_____	C	
GAM3709	FLJ11722	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ12078	3'	GCTGGAGCGCAGTGGCAC	83838	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCGCG	CCGTG	
			TCA_____		
GAM3709	FLJ12190	3'	GCTGGAGTGCAGTAGCAC	83808	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	TCGTG	
			TCA_____		
GAM3709	FLJ12294	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ12687	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ13117	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	

			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ13456	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ13769	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	FLJ13769	3'	AGCTGGAGTGCAGTGGCAC	83839	TGACCAC
			AGCTGGAGTGC	GGCAC	
			TCGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ14397	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	FLJ20546	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	FLJ22009	3'	AGCTGGAATGCAGTGGCC	83840	TGACCAC A
			AGCTGGAGTGC	GGC C	
			TCGACCTTACG	CCG G	
			TCA_____ C		
GAM3709	FLJ22692	3'	GCTGAAGTGCAGTGGCAC	83830	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACTTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ23040	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	FLJ23556	3'	AGCTGGAGGCGGTGGCAC	83841	T TGACCAC
			AGCTGGAG GC	GGCAC	
			TCGACCTC CG	CCGTG	
			_ CCA_____		
GAM3709	FLJ31737	3'	AGCGGAGTGCTGGAGTGCA	83842	T ACCACG
			AGC GGAGTGCTG	GCA	

			TCG CCTCACGAC	CGT	
			CTCA__		
GAM3709	FLJ32915	5'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA__		
GAM3709	GMNN	5'	GCTGGAGTGCCCGGC	83843	GACCA
			GCTGGAGTGCT	CGGC	
			CGACCTCACGG	GCCG	
GAM3709	GNB4	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA__		
GAM3709	GP5	3'	GCTAGAGTGCAGTGGCAC	83844	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGATCTCACG	CCGTG	
			TCA__		
GAM3709	GTSE1	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA__		
GAM3709	HSD17B7	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA__		
GAM3709	HSNOV1	3'	AGCTGGAGGCTCCAGGCA	83845	T GA C
			AGCTGGAG GCT CCA GGCA		
			TCGACCTC CGA GGT CCGT		
			G_ _		
GAM3709	ICAM4	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA__		
GAM3709	ICAM4	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA__		
GAM3709	IL-23R	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	

		CGACCTCACG	CCGTG		
		TCA_____			
GAM3709	IMAGE:4907098	3' GCTGGAGTGCAGTGGCAC	83801		TGACCAC
		GCTGGAGTGC	GGCAC		
		CGACCTCACG	CCGTG		
		TCA_____			
GAM3709	KBRAS2	3' GCTGGAGTGCAGTGGCAC	83801		TGACCAC
		GCTGGAGTGC	GGCAC		
		CGACCTCACG	CCGTG		
		TCA_____			
GAM3709	KIAA0057	3' GCTGGAGTGCCATGGTAC	83846		TGAC C C
		GCTGGAGTGC	CA GG AC		
		CGACCTCACG	GT CC TG		
		_____ A A			
GAM3709	KIAA0252	3' ACTGGAGTGCAGTGGCAC	83815		TGACCAC
		GCTGGAGTGC	GGCAC		
		TGACCTCACG	CCGTG		
		TCA_____			
GAM3709	KIAA0266	3' GCTAGAGTGCAGTGGCAC	83844		TGACCAC
		GCTGGAGTGC	GGCAC		
		CGATCTCACG	CCGTG		
		TCA_____			
GAM3709	KIAA0355	3' GCTGGAGTGCAGTGGCAC	83801		TGACCAC
		GCTGGAGTGC	GGCAC		
		CGACCTCACG	CCGTG		
		TCA_____			
GAM3709	KIAA0419	3' ACTGGAGTGCAATGGCAC	83847		TGACCAC
		GCTGGAGTGC	GGCAC		
		TGACCTCACG	CCGTG		
		TTA_____			
GAM3709	KIAA0447	3' GCTGGAGTGCAATGGCAC	83804		TGACCAC
		GCTGGAGTGC	GGCAC		
		CGACCTCACG	CCGTG		
		TTA_____			
GAM3709	KIAA0475	3' GCTGGAGTGCAGCAGCAC	83848		TGACCA
		GCTGGAGTGC	CGGCAC		
		CGACCTCACG	GTCGTG		
		TC_____			
GAM3709	KIAA0752	3' GCTGGAGTGCAATGGCAC	83804		TGACCAC
		GCTGGAGTGC	GGCAC		

		CGACCTCACG	CCGTG	
		TTA_____		
GAM3709	KIAA0795	3' GCTGGAATGCAGTGGCAC	83849	TGACCAC
		GCTGGAGTGC	GGCAC	
		CGACCTTACG	CCGTG	
		TCA_____		
GAM3709	KIAA0831	3' GCTGGAGTGCAATGGCAC	83804	TGACCAC
		GCTGGAGTGC	GGCAC	
		CGACCTCACG	CCGTG	
		TTA_____		
GAM3709	KIAA1160	3' GCTGGAGTGCAATGGCAC	83804	TGACCAC
		GCTGGAGTGC	GGCAC	
		CGACCTCACG	CCGTG	
		TTA_____		
GAM3709	KIAA1191	3' GCTGGAGTGTAATGGCA	83850	C CCAC
		GCTGGAGTG TGA	GGCA	
		CGACCTCAC ATT	CCGT	
		_ A_____		
GAM3709	KIAA1193	3' GCTGGAGTCTGGCCCCTGC	83851	G A ACG
		GCTGGAGT CTG CC	GC	
		CGACCTCA GAC GG	CG	
		_ C GGA		
GAM3709	KIAA1271	3' GCTGGAGCGCAGTGGCAC	83838	TGACCAC
		GCTGGAGTGC	GGCAC	
		CGACCTCGCG	CCGTG	
		TCA_____		
GAM3709	KIAA1297	5' AGCAGGCGGCCACGGCAC	83852	T A CTGA
		AGC GG GTG	CCACGGCAC	
		TCG TC CGC	GGTGCCGTG	
		_ _ C_____		
GAM3709	KIAA1328	3' GCTGGAGTGCAGCGGCA	83822	TGACCA
		GCTGGAGTGC	CGGCA	
		CGACCTCACG	GCCGT	
		TC_____		
GAM3709	KIAA1340	3' GCTGGAGTGCAATGGCAC	83804	TGACCAC
		GCTGGAGTGC	GGCAC	
		CGACCTCACG	CCGTG	
		TTA_____		
GAM3709	KIAA1559	3' GCTGGAGTGCAGTGGCAC	83801	TGACCAC
		GCTGGAGTGC	GGCAC	

			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	KIAA1641	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	KIAA1656	5'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	KIAA1724	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	KIAA1771	3'	GCTGGAGTGCAGCAGCA	83853	TGACCA
			GCTGGAGTGC	CGGCA	
			CGACCTCACG	GTCGT	
			TC_____		
GAM3709	KIAA1872	3'	GCGTGGGTGGGCCACGGCA	83854	_ A CTGA
			GC TGG GTG	CCACGGCA	
			CG ACC CAC	GGTGCCGT	
			C _ CC_		
GAM3709	KIAA1872	3'	GCTGGAATGCAGTGGCAC	83849	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTTACG	CCGTG	
			TCA_____		
GAM3709	KIAA1878	3'	GCTGAGCTTCTGTGGCAC	83855	G G_ ACCAC
			GCTG AGT CTG	GGCAC	
			CGAC TCG GAC	CCGTG	
			_ AA A_		
GAM3709	KIAA1948	3'	AGCTGGAGTGCAGTGGTAC	83818	TGACCAC C
			AGCTGGAGTGC	GG AC	
			TCGACCTCACG	CC TG	
			TCA_____ A		
GAM3709	KIAA1969	3'	AACTGGAGTGCAGTGGTAC	83856	TGACCAC C
			AGCTGGAGTGC	GG AC	
			TTGACCTCACG	CC TG	
			TCA_____ A		
GAM3709	LRG	3'	GCTAGAGTGCAGTGGCAC	83844	TGACCAC
			GCTGGAGTGC	GGCAC	

		CGATCTCACG	CCGTG		
		TCA_____			
GAM3709	LYPLA3	3' AGCTGGGTGCTGGCCAGGG	83857	A	A C
		AGCTGG GTGCTG CCA GG			
		TCGACC CACGAC GGT CC			
		— C C			
GAM3709	MCAM	3' GCTGGAGTGCAGTGGCAC	83801	TGACCAC	
		GCTGGAGTGC GGCAC			
		CGACCTCACG CCGTG			
		TCA_____			
GAM3709	MGC10200	3' ACTGGAGTGCAGTGGCAC	83815	TGACCAC	
		GCTGGAGTGC GGCAC			
		TGACCTCACG CCGTG			
		TCA_____			
GAM3709	MGC10814	3' GCTGGAGCGCAATGGCAC	83828	TGACCAC	
		GCTGGAGTGC GGCAC			
		CGACCTCGCG CCGTG			
		TTA_____			
GAM3709	MGC13017	3' GCTGGAGTGCATGGCAC	83804	TGACCAC	
		GCTGGAGTGC GGCAC			
		CGACCTCACG CCGTG			
		TTA_____			
GAM3709	MGC14407	3' GCTGGAGTGCAGTGGCAC	83801	TGACCAC	
		GCTGGAGTGC GGCAC			
		CGACCTCACG CCGTG			
		TCA_____			
GAM3709	MGC16332	3' GCTGGAGTGCAGTGGCAC	83801	TGACCAC	
		GCTGGAGTGC GGCAC			
		CGACCTCACG CCGTG			
		TCA_____			
GAM3709	MGC29891	3' GCTGGAGTGCAGTGGCAC	83801	TGACCAC	
		GCTGGAGTGC GGCAC			
		CGACCTCACG CCGTG			
		TCA_____			
GAM3709	MGC29937	3' GCTGGAGTGC AACGGC	83858	TGACC	
		GCTGGAGTGC ACGGC			
		CGACCTCACG TGCCG			
		T_____			
GAM3709	MGC5457	3' GCTGGAGTGCATGGCAC	83804	TGACCAC	
		GCTGGAGTGC GGCAC			

			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	MOST2	5'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	MRP63	3'	GCTGGAGTGCAGCGGCA	83822	TGACCA
			GCTGGAGTGC	CGGCA	
			CGACCTCACG	GCCGT	
			TC_____		
GAM3709	NMNAT	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	NMNAT	3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TTA_____		
GAM3709	Nup43	3'	AGCTGGGCGTGGTGGCC	83859	A C ACCAC A
			AGCTGG GTG TG	GGC C	
			TCGACC CGC AC	CCG G	
			_ _ CA_ _ C		
GAM3709	PDCD7	3'	GCTGGAGTGCCGTGGC	83860	ACCAC
			GCTGGAGTGCTG	GGC	
			CGACCTCACGGC	CCG	
			A_____		
GAM3709	PNPASE	3'	AGCTGGAGTGCAATGGCC	83861	TGACCAC A
			AGCTGGAGTGC	GGC C	
			TCGACCTCACG	CCG G	
			TTA_____ C		
GAM3709	PRO2730	3'	GCCGGAGTGCAATGGCAC	83862	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGGCCTCACG	CCGTG	
			TTA_____		
GAM3709	QSCN6	3'	AGCTGGAGGCTGGCCAGGCA	83863	T A C
			AGCTGGAG GCTG CCA GGCA		
			TCGACCTC CGAC GGT CCGT		
			_ C _		
GAM3709	RoXaN	3'	GCTGGAGTGTAATGGC	83864	C CCAC
			GCTGGAGTG TGA	GGC	

			CGACCTCAC ATT CCG		
			— A —		
GAM3709	RoXaN	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA —		
GAM3709	Rpo1-2	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA —		
GAM3709	Rpo1-2	3'	GCTGGAGTGTGGTGGCAC	83865	C ACCAC
			GCTGGAGTG TG	GGCAC	
			CGACCTCAC AC	CCGTG	
			— CA —		
GAM3709	SC65	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA —		
GAM3709	SCAND2	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA —		
GAM3709	SCIN	3'	GCTGGAGTGTGGTGGCC	83866	C ACCAC A
			GCTGGAGTG TG	GGC C	
			CGACCTCAC AC	CCG G	
			— CA — C		
GAM3709	SH3BGRL2	3'	GCGGAGTGCTGGGCA	83867	T ACCAC
			GC GGAGTGCTG	GGCA	
			CG CCTCACGAC	CCGT	
			—		
GAM3709	SNAPC1	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA —		
GAM3709	SPTLC2	3'	GCTAGAGTGCAGTGGCAC	83844	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGATCTCACG	CCGTG	
			TCA —		
GAM3709	STK36	3'	AGTTGGAGGCTGGACCGCA	83868	C T _ ACG
			AG TGGAG GCTG ACC GCA		

			TC ACCTC CGAC TGG CGT	
			A _ C _	
GAM3709	THEA	3'	GCTGGAATGCAGTGGCAC 83849	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTTACG CCGTG	
			TCA_	
GAM3709	TRIAD3	3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_	
GAM3709	ZFP106	3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_	
GAM3709	ZNF297B	5'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_	
GAM3709	LOC112687	3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_	
GAM3709	LOC113201	3'	AGCTGGAGTGCAATGGCA 83869	TGACCAC
			AGCTGGAGTGC GGCA	
			TCGACCTCACG CCGT	
			TTA_	
GAM3709	LOC114987	3'	GCTGGAGTGCAATGGCAC 83804	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TTA_	
GAM3709	LOC115129	3'	GCTGGAATGCAGTGGCAC 83849	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTTACG CCGTG	
			TCA_	
GAM3709	LOC116143	3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_	
GAM3709	LOC124222	3'	AGTTGGAGCGCCACGGC 83870	C TGAC
			AG TGGAGTGC CACGGC	

	TC ACCTCGCG GTGCCG	
	A _____	
GAM3709 LOC124739 3'	AGCTGGGGGCTGACCAGACA 83871	AGT C
	AGCTGG GCTGACCA GGCA	
	TCGACC CGACTGGT CTGT	
	CC_ _	
GAM3709 LOC126282 3'	AGCTGGAGTGCAGTGGCA 83872	TGACCAC
	AGCTGGAGTGC GGCA	
	TCGACCTCACG CCGT	
	TCA_____	
GAM3709 LOC126282 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA_____	
GAM3709 LOC127428 3'	AGCTGGAGTGTCTGGCTTGC 83873	_ ACCACG
	AGCTGGAGTG CTG GC	
	TCGACCTCAC GAC CG	
	A CGAA__	
GAM3709 LOC138389 5'	GCTGAGTGCTGGGCCACACA 83874	G A__
	GCTG AGTGCTG CCACG	
	CGAC TCACGAC GGTGT	
	_ CCG	
GAM3709 LOC142937 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA_____	
GAM3709 LOC144465 3'	GCTGGAGTGCAACGGCAC 83794	TGACC
	GCTGGAGTGC ACGGCAC	
	CGACCTCACG TGCCGTG	
	T_____	
GAM3709 LOC144563 3'	AGCTGGAGTGCAGTGGCA 83872	TGACCAC
	AGCTGGAGTGC GGCA	
	TCGACCTCACG CCGT	
	TCA_____	
GAM3709 LOC145387 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA_____	
GAM3709 LOC146880 3'	AGCTGAGTGCTGAGTTGCA 83875	G CCACG
	AGCTG AGTGCTGA GCA	

	TCGAC TCACGACT CGT	
	CAA__	
GAM3709 LOC146958 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA__	
GAM3709 LOC147664 3'	GCTGGAGTGGGAATGGCAC 83834	CT CCAC
	GCTGGAGTG GA GGCAC	
	CGACCTCAC CT CCGTG	
	TA__	
GAM3709 LOC148534 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA__	
GAM3709 LOC149073 3'	GCTGGAGTGGAGTGGCAC 83876	CT CCAC
	GCTGGAGTG GA GGCAC	
	CGACCTCAC CT CCGTG	
	CA__	
GAM3709 LOC149113 5'	GCTGGAGTGCAATGGCAC 83804	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TTA__	
GAM3709 LOC149464 5'	AGCTGAAGTGCAGTGGCAC 83877	TGACCAC
	AGCTGGAGTGC GGCAC	
	TCGACTTCACG CCGTG	
	TCA__	
GAM3709 LOC150244 3'	GCTGGAGTGC GTGCAGTGGCAC 83878	_ ACCAC
A	GCTGGAGTGC TG GGCACA	
	CGACCTCACG AC CCGTGT	
	C GTCA_	
GAM3709 LOC150889 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA__	
GAM3709 LOC150960 3'	AGCTGGAGTGCAGTGGCAC 83839	TGACCAC
	AGCTGGAGTGC GGCAC	
	TCGACCTCACG CCGTG	
	TCA__	
GAM3709 LOC151429 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	

	CGACCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC151556 3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC152263 3'	GCTGGAATGCACTGGCA	83879	TGACC _
	GCTGGAGTGC	AC GGCA	
	CGACCTTACG	TG CCGT	
	_____ A		
GAM3709 LOC152271 3'	GCTGGAGTGCAGTGGCA	83880	TGACC _
	GCTGGAGTGC	AC GGCA	
	CGACCTCACG	TG CCGT	
	_____ A		
GAM3709 LOC152283 3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC152445 3'	ACTGGAGTGCAATGGCAC	83847	TGACCAC
	GCTGGAGTGC	GGCAC	
	TGACCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC152453 3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC152627 3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC153727 3'	GCTAGAGTGCAGTGGCAC	83844	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGATCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC154403 5'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC154791 3'	GCTGGAGTGAGTGCCATGGC	83881	C_ A C
	GCTGGAGTG	TG CCA GGC	

	CGACCTCAC AC GGT CCG	
	TC _ A	
GAM3709 LOC154992 5'	GCTGGAGTGC AATGGCAC 83804	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TTA_____	
GAM3709 LOC158160 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA_____	
GAM3709 LOC158187 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA_____	
GAM3709 LOC158572 3'	AGTTGGAGTGCTGTGTCCACA 83882	C A__
	AG TGGAGTGCTG CCACG	
	TC ACCTCACGAC GGTGT	
	A ACA	
GAM3709 LOC158819 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA_____	
GAM3709 LOC158987 3'	GCTGGAGTGCAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA_____	
GAM3709 LOC159121 5'	AGCTGGAGCTGCTTGTGGTGCA 83883	_ GACCACG
	AGCTGGAG TGCT GCA	
	TCGACCTC ACGA CGT	
	G ACACCA_	
GAM3709 LOC161823 3'	GCTGGAGTGCTGTAGCA 83884	ACCAC
	GCTGGAGTGCTG GGCA	
	CGACCTCACGAC TCGT	
	A_____	
GAM3709 LOC162962 3'	GCTGGAGTGC ACTGGCAC 83885	TGACC _
	GCTGGAGTGC AC GGCAC	
	CGACCTCACG TG CCGTG	
	_____ A	
GAM3709 LOC196047 5'	GCTGGAGTGC AATGGCAC 83804	TGACCAC
	GCTGGAGTGC GGCAC	

	CGACCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC196540 3'	GCTGGAGCGCAGTGGCAC	83838	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCGCG	CCGTG	
	TCA_____		
GAM3709 LOC197132 3'	AGCTGGAGTGCAATGGCC	83861	TGACCAC A
	AGCTGGAGTGC	GGC C	
	TCGACCTCACG	CCG G	
	TTA_____ C		
GAM3709 LOC197196 3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC197201 3'	GCTAGAGTGCAATGGCAC	83886	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGATCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC197201 3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC199923 3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC200251 3'	GCTGGAGTGCAATGGCAC	83804	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC200316 3'	AACTGGAGTTCTGTGGC	83887	G ACCAC
	AGCTGGAGT CTG	GGC	
	TTGACCTCA GAC	CCG	
	A A_____		
GAM3709 LOC200731 3'	GCTGGAGTGCAGTAGCAC	83808	TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	TCGTG	
	TCA_____		
GAM3709 LOC201182 5'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
	GCTGGAGTGC	GGCAC	

	CGACCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC201868 5'	GCTGGAGTGC	AATGGCAC	83804 TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC219672 5'	GCTGGAGTGC	AATGGCAC	83804 TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TTA_____		
GAM3709 LOC220038 3'	GCTGGAATGCTGTGGCC		83888 ACCAC A
	GCTGGAGTGCTG	GGC C	
	CGACCTTACGAC	CCG G	
	A_____ C		
GAM3709 LOC220506 3'	GCTGGAGTGATGTGGCA		83889 C ACCAC
	GCTGGAGTG TG	GGCA	
	CGACCTCAC AC	CCGT	
	T A_____		
GAM3709 LOC220692 3'	AGCTGGAGTGCAGTGGTAC		83818 TGACCAC C
	AGCTGGAGTGC	GG AC	
	TCGACCTCACG	CC TG	
	TCA_____ A		
GAM3709 LOC220906 3'	AGCTGGAGTGCACTGGCC		83890 TGACC _ A
	AGCTGGAGTGC	AC GGC C	
	TCGACCTCACG	TG CCG G	
	_____ A C		
GAM3709 LOC221042 3'	GCTGGAGTGCAGTGGCAC		83801 TGACCAC
	GCTGGAGTGC	GGCAC	
	CGACCTCACG	CCGTG	
	TCA_____		
GAM3709 LOC221288 3'	GCTGGAGTGCTGTGGC		83891 ACCAC
	GCTGGAGTGCTG	GGC	
	CGACCTCACGAC	CCG	
	A_____		
GAM3709 LOC221337 3'	GCTGGAGTGCAACGGC		83858 TGACC
	GCTGGAGTGC	ACGGC	
	CGACCTCACG	TGCCG	
	T_____		
GAM3709 LOC221474 3'	GCTAGAGTGGAGTGGCC		83892 CT CCAC A
	GCTGGAGTG GA	GGC C	

	CGATCTCAC CT CCG G	
	__ CA__ C	
GAM3709 LOC222066 3'	AGCTGGAGTGCAATGGCA 83869	TGACCAC
	AGCTGGAGTGC GGCA	
	TCGACCTCACG CCGT	
	TTA__	
GAM3709 LOC222182 3'	GCTGGAGTGCAATGGCAC 83804	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TTA__	
GAM3709 LOC222256 3'	GCTAGAGTGCAAGTGGCAC 83844	TGACCAC
	GCTGGAGTGC GGCAC	
	CGATCTCACG CCGTG	
	TCA__	
GAM3709 LOC253039 3'	GCTGGAGTGCAAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA__	
GAM3709 LOC254531 5'	GCTGGAGTGCAAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA__	
GAM3709 LOC255042 3'	GCTAGAGTGCAATGGCAC 83886	TGACCAC
	GCTGGAGTGC GGCAC	
	CGATCTCACG CCGTG	
	TTA__	
GAM3709 LOC255177 3'	GCTGGAGTGCAAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA__	
GAM3709 LOC255326 3'	GCTGGAGTGCAAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TCA__	
GAM3709 LOC255328 3'	GCTGGAGTGCAATGGCAC 83804	TGACCAC
	GCTGGAGTGC GGCAC	
	CGACCTCACG CCGTG	
	TTA__	
GAM3709 LOC256980 3'	GCTGGAGTGCAAGTGGCAC 83801	TGACCAC
	GCTGGAGTGC GGCAC	

		CGACCTCACG	CCGTG	
		TCA_____		
GAM3709	LOC90092	3'	GCTGGAGTGCAATGGCAC	83804 TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TTA_____	
GAM3709	LOC90092	5'	GGATGCCACGGCACA	83893 GTGC A
			GGA TG CCACGGCACA	
			CCT AC GGTGCCGTGT	

GAM3709	LOC90141	3'	GCTGGAGTGCGACAGTGCA	83894 T CACG
			GCTGGAGTGC GAC GCA	
			CGACCTCACG CTG CGT	
			_ TCA_	
GAM3709	LOC90155	5'	GCTGGAGTGCAATGGCAC	83804 TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TTA_____	
GAM3709	LOC90538	3'	ACTGGAGTGCAAGTGGCAC	83815 TGACCAC
			GCTGGAGTGC GGCAC	
			TGACCTCACG CCGTG	
			TCA_____	
GAM3709	LOC90624	3'	GCTGGAGTGCAAGTGGCAC	83801 TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_____	
GAM3709	LOC91064	3'	GCTGGAGTGCAAGTGGCAC	83801 TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_____	
GAM3709	LOC91286	3'	GCTGGAGTGCAAGTGGCAC	83801 TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_____	
GAM3709	LOC91442	3'	GCTGGAGTGCAAGTGGCAC	83801 TGACCAC
			GCTGGAGTGC GGCAC	
			CGACCTCACG CCGTG	
			TCA_____	
GAM3709	LOC91547	3'	GCTGGAGTGCAAGTGGCAC	83801 TGACCAC
			GCTGGAGTGC GGCAC	

		CGACCTCACG	CCGTG		
		TCA_____			
GAM3709	LOC91812	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	LOC91813	3'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3709	LOC92973	5'	GCTGGAGTGCAGTGGCAC	83801	TGACCAC
			GCTGGAGTGC	GGCAC	
			CGACCTCACG	CCGTG	
			TCA_____		
GAM3710	NEK4	3'	TTTAAATTTTATAATTTATCA	83897	T G
	A		TTTA AATTTTATAATTTAT AA		
			AAAT TTTAAATATTAAATA TT		
			T G		
GAM3711	CARD4	3'	GTAGCCTAGCAGAGGAGAAG	83900	CCC CC
			GTAGCC GT AGGAGAAG		
			CATCGG CG TCCTCTTC		
			AT_ TC		
GAM3711	ENPP3	3'	CACTCAGCCCTGTCTAGGAGAA	83901	AG CC C
	G		TA TAGCCC GTC AGGAGAAG		
			GT GTCGGG CAG TCCTCTTC		
			GA A_ A		
GAM3711	FGF9	3'	GCAGCCCTCCAGGAG	83902	CCG
			GTAGCCC TCCAGGAG		
			CGTCGGG AGGTCCTC		

GAM3711	MSN	3'	CAAGTAGCTCTGAGAGGGGAAG	83903	CCCCGTCC A
			TAAGTAGC AGG GAAG		
			GTTTCATCG TCC CTTC		
			AGACTC_ C		
GAM3711	NOTCH2	3'	TAAGTGGCCCAAGGAGAA	83904	CCCC _
			TAGC GTCCA GGAGAA		
			ATTG CGGGT CCTCTT		
			AC_ T		
GAM3711	PKD1	3'	AGCCAGCCCCCAGGAGGAG	83905	_ TCC
			AGT AGCCCCCG AGGAG		

		TCG TCGGGGGT TCCTC	
		G CC_	
GAM3711	SCNN1B	3' AAGTGGCCTGCCACCAGGAGA 83906	A C_ T
		AAGT GCC CCG CCAGGAGA	
		TTCA CGG GGT GGCCTCT	
		C AC _	
GAM3711	TUBG1	3' TAAATAGTCTCATAAGAGGAGA 83907	CCCC CC_
	AG	TAAGTAG CGT AGGAGAAG	
		ATTTATC GTA TCCTCTTC	
		AGA_ TTC	
GAM3711	WNT3A	3' GCCCGCCCCGTCCAGGGGGA 83908	A_ C A_
		GT GCCCC GTCCAGG GA	
		CG CGGGG CAGGTCC CT	
		GG _ CC	
GAM3711	ARHF	3' GTGGCCTCCGTGTTCTGCGGGG 83909	A C _ A_ A
	AAG	GT GCC CCG TCC GG GAAG	
		CA CGG GGC AGG CC CTTC	
		C A ACA AC C	
GAM3711	BM-009	3' GCAGTTTTGCCATGCAGGAGAA 83910	CCC_ C
	G	GTAG CCGT CAGGAGAAG	
		CGTC GGTA GTCCTCTTC	
		AAAAC C	
GAM3711	CAPN13	3' GTGGCCGAGTAGGAGAAG 83911	A CCC CC
		GT GCC GT AGGAGAAG	
		CA CGG CA TCCTCTTC	
		C CT_ _	
GAM3711	FLJ12529	3' AAGTAGCCTTCTGGGGGAAG 83912	CCCG CA A
		AAGTAGCC TC GG GAAG	
		TTCATCGG AG CC CTTC	
		A_ AC C	
GAM3711	GDAP1L1	3' TAGTCCATGTCCAGGAGAA 83913	C CC
		TAG CC GTCCAGGAGAA	
		ATC GG CAGGTCCTCTT	
		A TA	
GAM3711	KIAA0863	3' AGTAGTTAAGTTAGGAGAAG 83914	CCCCC CC
		AGTAG GT AGGAGAAG	
		TCATC CA TCCTCTTC	
		AATT_ A_	
GAM3711	STX3A	3' TAAGTAGCCTTTGCAAAGGAA 83915	CCC CC
		TAAGTAGCC GT AGGAG	

ATTCATCGG CG TCCTT
 AAA TT
 GAM3711 UQCR 3' AGGGGCCCCCATGGGAA 83916 TA CCA A
 AG GCCCCCGT GG GAA
 || ||||| || ||
 TC CGGGGGTA CC CTT
 CC _ _
 GAM3711 LOC116411 5' AGAGTCCAGGCCAGGAGA 83917 T C CC T
 AG AG CC G CCAGGAGA
 || || | |||||
 TC TC GG C GGTCTCT
 _ A TC _
 GAM3711 LOC146433 3' GCAGCACCAGGAGAAG 83918 CCCCCG
 GTAGC CCAGGAGAAG
 |||| |||||
 CGTCG GGTCTCTTC
 T _ _
 GAM3711 LOC146599 5' GTAGCCCCCGCAGAAG 83919 TC
 GTAGCCCCCG CAGGAG
 ||||| ||||
 CATCGGGGGC GTCTTC
 _
 GAM3711 LOC153259 5' GTTGCCCCATCCAGGAGAAG 83920 A C
 GT GCCCC GTCCAGGAGAAG
 || |||| |||||
 CA CGGGG TAGGTCCTCTTC
 A _
 GAM3711 LOC155060 3' AAGTGGCCCCCAGGAGA 83921 A GTCC
 AAGT GCCCC AGGAGA
 |||| |||| ||||
 TTCA CGGGGG TCCTCT
 C _ _
 GAM3711 LOC202050 5' AGCAGTTCCTGAGGAGAAG 83922 CCC GTCC
 AGTAG CC AGGAGAAG
 |||| || |||||
 TCGTC GG TCCTCTTC
 AA_ AC_
 GAM3711 LOC92710 3' GTAGCCCCTGTCTAGGTTAAG 83923 C C AG
 GTAGCCCC GTC AGG AAG
 ||||| || || ||
 CATCGGGG CAG TCC TTC
 A A AA
 GAM3712 AKAP13 3' GCAGGGGACACAGCCAGTG 83926 AC AA
 GCA GGACACGGC TAGTG
 || ||||| ||||
 CGT CCTGTGTCG GTCAC
 CC _
 GAM3712 ITPR3 3' GCATGGACACGACAGTG 83927 AC ATA
 GCA GGACACGGCA GTG
 || ||||| ||

		CGT CCTGTGCTGT CAC		
		A_ _		
GAM3712	PPFIA4	3' ACAACGGACACACGGTG	83928	G AATA
		GCAACGGACACG C GTG		
		TGTTGCCTGTGT G CAC		
		C		
GAM3712	LOC115051	3' ACAACGGATATGCAACGTG	83929	CACG A
		GCAACGGA GCAAT GTG		
		TGTTGCCT CGTTG CAC		
		ATA_ _		
GAM3712	LOC143666	3' TAGCGGTAGAAGAAATAGTGA	83930	AAC CAC C
		TAGC GGA GG AATAGTGA		
		ATCG TCT TC TTATCACT		
		CCA _ T		
GAM3712	LOC196374	3' GCAGCGGACACGGAGT	83931	A CAAT
		GCA CGGACACGG AGT		
		CGT GCCTGTGCC TCA		
		C _		
GAM3712	LOC253258	3' TAGCGGTAGAAGAAATAGTGA	83930	AAC CAC C
		TAGC GGA GG AATAGTGA		
		ATCG TCT TC TTATCACT		
		CCA _ T		
GAM3713	ABCE1	3' CCTTGGCTGCCCAACAGAAAA	83934	CAACATT
		CCT CTCAACAGAAAA		
		GGA GGGTTGTCTTTT		
		ACCGAC_		
GAM3713	ASGR2	3' CCTCAAAATCCTCAACAGA	83935	C
		CCTCAA ATTCTCAACAGA		
		GGAGTT TAGGAGTTGTCT		
		T		
GAM3713	ASGR2	3' CCTCAAAATCCTCAACAGA	83935	C
		CCTCAA ATTCTCAACAGA		
		GGAGTT TAGGAGTTGTCT		
		T		
GAM3713	ASGR2	3' CCTCAAAATCCTCAACAGA	83935	C
		CCTCAA ATTCTCAACAGA		
		GGAGTT TAGGAGTTGTCT		
		T		
GAM3713	ASGR2	3' CCTCAAAATCCTCAACAGA	83935	C
		CCTCAA ATTCTCAACAGA		

			GGAGTT TAGGAGTTGTCT		
			T		
GAM3713	DNC1	3'	ACCTCAACAGCAGCAGA 83936	TTCT	A
			ACCTCAACA CA CAGA		
			TGGAGTTGT GT GTCT		
			C__ C		
GAM3713	FMO2	3'	CCCAGGATTTTCAACAGAAAA 83937	AC	C
			CTCA ATT TCAACAGAAAA		
			GGGT TAA AGTTGTCTTTT		
			CC A		
GAM3713	HS2ST1	3'	CACTTCAACATCAGAA 83938	C	TCTCAA
			TAC TCAACAT CAGAA		
			GTG AGTTGTA GTCTT		
			A _____		
GAM3713	HS2ST1	3'	TACCTGACTCTCAATAGAAA 83939	CAAC	C
			TACCT ATTCTCAA AGAAA		
			ATGGA TGAGAGTT TCTTT		
			C__ A		
GAM3713	OLFM1	3'	CACCTCAAGGGAATAACAGAA 83940		CATTCTC
			TACCTCAA AACAGAA		
			GTGGAGTT TTGTCTT		
			CCCTTA_		
GAM3713	PIK3CD	3'	TACCTCAGCACTCTCACAG 83941	A	A
			TACCTCA CATTCTCA CAG		
			ATGGAGT GTGAGAGT GTC		
			C _		
GAM3713	PSAP	3'	TCAACATCCATCTAGCAGA 83942	_	AA_
			TCAACATTC TC CAGA		
			AGTTGTAGG AG GTCT		
			T ATC		
GAM3713	TCEA1	3'	CTCACTCATTGACAGAAAA 83943	ACATT	____
			CTCA CTCA ACAGAAAA		
			GAGT GAGT TGTCTTTT		
			____ AAC		
GAM3713	TIM3	3'	CTCAACATTCCAAGGGAA 83944	T	CA
			CTCAACATTC CAA GAA		
			GAGTTGTAAG GTT CTT		
			_ CC		
GAM3713	TNFSF4	3'	CCTCTCATTTAACAGAAA 83945	AA	CTC
			CCTC CATT AACAGAAA		

GGAG GTAA TTGTCTTT
A_ A__
GAM3713 BAIAP1 3' CCTCAACATATCACTCAG 83946 TC A_
CCTCAACAT TCA CAG
||||||| ||| |||
GGAGTTGTA AGT GTC
T_ GA
GAM3713 DKFZP564F013 3' ACCTCAACATTAGACAATAGA 83947 CT_ C
ACCTCAACATT CAA AGA
||||||| ||| |||
TGGAGTTGTAA GTT TCT
TCT A
GAM3713 DKFZP564O0463 3' CCTTTTCTTTCAACAGAAAA 83948 CAACA C
CCT TT TCAACAGAAAA
||| || |||||||||
GGA AA AGTTGTCTTTT
AAAG_ _
GAM3713 DKFZP586M0622 5' CCTCAGCTACAAACAGAAAA 83949 ____ TTCTC
CCTCA ACA AACAGAAAA
||||| ||| |||||||
GGAGT TGT TTGTCTTTT
CGA ____
GAM3713 DKFZp761J139 5' CTCAGCTCCTAGTAACAGAAA 83950 ACA C_
CTCA TTCT AACAGAAA
||||| ||| |||||||
GAGT AGGA TTGTCTTT
CG_ TCA
GAM3713 FKBP9 3' TCAACATTTTATATCAGAAAA 83951 CTCAA_
TCAACATT CAGAAAA
||||||| |||||||
AGTTGTAA GTCTTTT
AATATA
GAM3713 FLJ10546 5' CCTCAACACTCAGTAACAGA 83952 TC_
CCTCAACATTC AACAGA
||||||| |||||||
GGAGTTGTGAG TTGTCT
TCA
GAM3713 HARS2 3' TACCTCAATATAATCATAGAAA 83953 C TC AC
A TACCTCAA AT TCA AGAAAA
||||||| || ||| |||||||
ATGGAGTT TA AGT TCTTTT
A TT A_
GAM3713 HMGN4 3' CTCGATGTCATCAACAGAAA 83954 AACAT _
CTC TC TCAACAGAAA
||| || |||||||||
GAG AG AGTTGTCTTT
CTAC_ T
GAM3713 HSHIN1 3' TACCTCAATATATGTTATAGAA 83955 C TCTCAAC
A TACCTCAA AT AGAAA
||||||| || |||||

ATGGAGTT TA TCTTT
 A TACAATA
 GAM3713 KIAA1729 5' TACTTCAACATTTTGTCTCA 83956 C _____
 A TAC TCAACAT TCTCAA
 ||| ||||| |||||
 ATG AGTTGTA AGAGTT
 A AAAACA
 GAM3713 KLF12 3' TACTCTCAAGACATCTTTCAGC 83957 _ _ C_ A
 AGA TAC CTCA ACATT TCA CAGA
 ||| ||| ||||| ||| |||||
 ATG GAGT TGTAG AGT GTCT
 A TC AA C
 GAM3713 KPNA6 3' TACCGTAATTCAAACAGAAA 83958 TCAAC TC
 TACC ATTC AACAGAAA
 |||| ||| |||||
 ATGG TAAG TTGTCTTT
 CAT__ T_
 GAM3713 MGC16175 3' TACCTCAAAGGAGATAACAGAA 83959 CATTCTC
 AA TACCTCAA AACAGAAAA
 ||||| |||||
 ATGGAGTT TTGTCTTTT
 TCCTCTA
 GAM3713 MGC4643 3' CTCAACTTCCAACAGAA 83960 A T
 CTCAAC TTC CAACAGAA
 ||||| ||| |||||
 GAGTTG AAG GTTGTCTT
 - -
 GAM3713 MGC5338 3' CTAACATTCTCCTATGCAAA 83961 C AA__
 CT AACATTCTC CAGA
 || ||||| |||
 GA TTGTAAGAG GTTT
 GATAC
 GAM3713 PRO1048 3' TCTGCATCTCAACAGAA 83962 AA T
 TC CAT CTCAACAGAA
 || ||| |||||
 AG GTA GAGTTGTCTT
 AC _
 GAM3713 SS18L1 3' CTCAACATTCATATGACAGAA 83963 TCA__
 CTCAACATTC ACAGAA
 ||||| |||||
 GAGTTGTAAG TGTCTT
 TATAC
 GAM3713 TU12B1-TY 3' CTCAACAAAACAAAACAGAAA 83964 TTCTC_
 CTCAACA AACAGAAA
 ||||| |||||
 GAGTTGT TTGTCTTT
 TTTGTT
 GAM3713 TUCAN 3' TACCTTGAAATCTGACAGAAAA 83965 CAACAT CA
 TACCT TCT ACAGAAAA
 |||| ||| |||||

		ATGGA AGA TGTCTTTT	
		ACTTT_ C_	
GAM3713	LOC149837 3'	TCAGCATCCCTCAGAAAA 83966	A CAA
		TCA CATTCT CAGAAAA	
		AGT GTAGGG GTCTTTT	
		C A_	
GAM3713	LOC150622 3'	ACCTCAATGGATGTAACAGAAA 83967	CATTCTC
		ACCTCAA AACAGAAA	
		TGGAGTT TTGTCTTT	
		ACCTACA	
GAM3713	LOC150862 3'	TACCTCAAATGCTTCAGA 83968	C T CAA
		TACCTCAA AT CT CAGA	
		ATGGAGTT TA GA GTCT	
		T C A_	
GAM3713	LOC219857 3'	CCTTACTGTACCAACAGAAA 83969	CA ATTG
		CCT AC TCAACAGAAA	
		GGA TG GGTGTCTTT	
		A_ ACAT	
GAM3713	LOC220549 3'	TCAGCATTTCAGACAGAAAA 83970	A C _
		TCA CATT TCA ACAGAAAA	
		AGT GTAA AGT TGTCTTTT	
		C _ C	
GAM3713	LOC220739 5'	TACCCAACAGAATCAGACAG 83971	T TTC _
		TACC CAACA TCA ACAG	
		ATGG GTTGT AGT TGTC	
		_ CTT C	
GAM3713	LOC257277 5'	TCAACATTTTCAGCCAAAA 83972	C A_
		TCAACATT TCA CAGAA	
		AGTTGTAA AGT GTTTT	
		A CG	
GAM3714	AICDA 3'	CATTTCTAAAGTTATAAATT 83975	_
		CATTTCTAAA TATAAATT	
		GTAAAGATTT ATATTAA	
		CA	
GAM3714	NAPB 3'	CATTTCAAATATAAATCA 83976	T
		CATTTCAAATATAAATTA	
		GTAAAG TTTATATTTAGT	
		_	
GAM3714	SPAP1 5'	CATTTCTAAACATATATT 83977	A
		CATTTCTAAATATA ATT	

		GTAAAGATTTGTAT TAA		
		A		
GAM3714	SPAP1	5' CATTTCTAAACATATATT 83977	A	
		CATTTCTAAATATA ATT		
		GTAAAGATTTGTAT TAA		
		A		
GAM3715	BCL11A	3' AGGGAGTGGGGCTGGAGGGCGA 83980	AT__ TT C	
	TGG	AGGGAGTGGG AGGG CGA GG		
		TCCCTCACCC TCCC GCT CC		
		CGACC __ A		
GAM3715	CALM3	3' GGGGGTGGGGTGGGGAGG 78259	A ATA TTC C	
		GGG GTGGG GGG GA GG		
		CCC CACCC CCC CT CC		
		C CA_ __ _		
GAM3715	CASQ2	3' AGGGAGTGGGAAAAGAGATGAT 83981	T_ TTC C	
	GG	AGGGAGTGGGA AGGG GA GG		
		TCCCTCACCT TCTC CT CC		
		TT TA_ A		
GAM3715	CHN1	5' AGAGAGTGGGGTGCCCGATGG 83982	ATAGG C	
		AGGGAGTGGG GTTCGA GG		
		TCTCTCACCC CGGGCT CC		
		CA__ A		
GAM3715	CHST1	3' AGGGAGTGGGGTGAGCT 83983	ATA	
		AGGGAGTGGG GGGTT		
		TCCCTCACCC CTCGA		
		CA_		
GAM3715	MN1	3' AGGGGGTGGGGGAGCTCAA 83984	A ATA	
		AGGG GTGGG GGGTTCGA		
		TCCC CACCC CTCGAGTT		
		C C_		
GAM3715	PTGFRN	3' AGGGGGTGGGGTAGGGTCG 83985	A A T	
		AGGG GTGGG TAGGGT CG		
		TCCC CACCC ATCCCA GC		
		C C _		
GAM3715	SELENBP1	3' AGGGAGTGTGGGTGATGAGGGT 83986	__ _ _	
		AGGGAGT GG GAT AGGGT		
		TCCCTCA CC CTA TCCCA		
		CAC A C		
GAM3715	SMT3H1	3' AGGGAGTGGGGTGGGAGGGGTG 83987	ATA TTCGAC	
	G	AGGGAGTGGG GGG GG		

		TCCCTCACCC CCC CC		
		CA_ TCCCCA		
GAM3715	SORCS3	5' GGGAGTGGGGAGGGGGCG 83988	AT	TT
		GGGAGTGGG AGGG CG		
		CCCTCACCC TCCC GC		
		C_ CC		
GAM3715	SUOX	5' GGGAATGGGGTAGGAGGGATGG 83989	A	TTC C
		GGGAGTGGG TAGGG GA GG		
		CCCTTACCC ATCCT CT CC		
		C CC_ A		
GAM3715	BCL2L1	3' AGGGGGTGGGAGGGTAGAGTGG 83990	A	TA TCGAC
		AGGG GTGGGA GGGT GG		
		TCCC CACCCT CCCA CC		
		C _ TCTCA		
GAM3715	C11orf9	3' GGGAGTGGGATGGGTGTCG 83991	A	_
		GGGAGTGGGAT GGGT TCG		
		CCCTCACCCCTA CCCA AGC		
		_ C		
GAM3715	DGKD	3' GGGAGTGGGATGGGTCTG 83992	A	T
		GGGAGTGGGAT GGGT CG		
		CCCTCACCCCTA CCCA GC		
		_ _		
GAM3715	DKFZP434P0111	3' AGGAGTGGGATGGCAGTAGG 83993		AG TCGAC
		GGGAGTGGGAT GGT GG		
		TCCTCACCCCTA CCG CC		
		_ TCAT_		
GAM3715	EPS15R	3' AGGGAGTGGGGTGGCCCGGAGG 78532	ATAG	AC
		AGGGAGTGGG GGTTCG GG		
		TCCCTCACCC CCGGGC CC		
		CA_ CT		
GAM3715	FLJ14107	5' GGGAGTGGGAGGGGACG 83994	TA	TTC _
		GGGAGTGGGA GGG GAC G		
		CCCTCACCCCT CCC CTG C		
		_ _ A		
GAM3715	KIAA1205	3' AGGGGGTGGGGCGGGGGCGAGA 83995	A	ATA TT _
	ACGG	AGGG GTGGG GGG CGA CGG		
		TCCC CACCC CCC GCT GCC		
		C CG_ CC CTT		
GAM3715	KIAA1887	5' AGGGGGTGGGAGGAGGGTCGGT 83996	A	T_ T AC
	GG	AGGG GTGGGA AGGGT CG GG		

		TCCC CACCCT TCCCA GC CC		
		C CC _ CA		
GAM3715 MCF2L	3'	GGGAGTGGAGTGGAGGTGCG 83997	ATA_ T	
		GGGAGTGGG GGGT CG		
		CCCTCACCT TCCA GC		
		CACC C		
GAM3715 NR6A1	3'	AGGGAGTGGGAAGGAGGAAGG 83998	T TTC C	
		AGGGAGTGGGA AGGG GA GG		
		TCCCTCACCT TCCT CT CC		
		_ C_ T		
GAM3715 NR6A1	3'	AGGGAGTGGGAAGGAGGAAGG 83998	T TTC C	
		AGGGAGTGGGA AGGG GA GG		
		TCCCTCACCT TCCT CT CC		
		_ C_ T		
GAM3715 NR6A1	3'	AGGGAGTGGGAAGGAGGAAGG 83998	T TTC C	
		AGGGAGTGGGA AGGG GA GG		
		TCCCTCACCT TCCT CT CC		
		_ C_ T		
GAM3715 P2RX5	3'	GGGAGTGGGCTGGAACCAA 83999	ATA TT	
		GGGAGTGGG GGG CGA		
		CCCTCACCC CCT GTT		
		GA_ TG		
GAM3715 SMARCF1	3'	AGAGGGTGGGGTAGGGTCC 84000	A A	
		AGGG GTGGG TAGGGTTC		
		TCTC CACCC ATCCCAGG		
		C C		
GAM3715 SMARCF1	3'	AGAGGGTGGGGTAGGGTCC 84000	A A	
		AGGG GTGGG TAGGGTTC		
		TCTC CACCC ATCCCAGG		
		C C		
GAM3715 SMARCF1	3'	AGAGGGTGGGGTAGGGTCC 84000	A A	
		AGGG GTGGG TAGGGTTC		
		TCTC CACCC ATCCCAGG		
		C C		
GAM3715 THEA	3'	GGGGTGGCTGTGTTGACGG 84001	A GATAGG	
		GGG GTGG GTTCGACGG		
		CCC CACC CAAGCTGCC		
		_ GACA_		
GAM3715 TRIM28	3'	GGGAGTGGGGATGGGGTGACAG 84002	_ A TC	
		GGGAGTGGG AT GGGT GACGG		

CCCTCACCC TA CCCA CTGTC
 C C _
 GAM3715 LOC113230 3' GGGAGTGGGGCAATCGAGGCGG 84003 A GGT _
 GGGAGTGGG TAG TCGA CGG
 ||||| ||| ||| |||
 CCCTCACCC GTT AGCT GCC
 C _ CC
 GAM3715 LOC149466 3' AGGGAGTGGGGAGGGTCTAA 84004 AT CG
 AGGGAGTGGG AGGGTT A
 ||||| ||||| |
 TCCCTCACCC TCCCAG T
 C_ AT
 GAM3715 LOC196955 3' AGGGGCTGGGATAGGAGTT 84005 AG _
 AGGG TGGGATAGG GTT
 ||| ||||| |||
 TCCC ACCCTATCC CAA
 CG T
 GAM3715 LOC254643 3' AGGCAGTGGGATGGGGTT 84006 G A
 AGG AGTGGGAT GGGTT
 ||| ||||| |||||
 TCC TCACCCTA CCCAA
 G C
 GAM3715 LOC91445 3' GGGAGTGGGAGGGGAG 84007 TA TTC C
 GGGAGTGGGA GGG GA G
 ||||| ||| |||
 CCCTCACCT CCC CT C
 _ _ T
 GAM3716 KIT 3' TTTGCCTTTTATATTG 84010 G TTTGTT
 TTTGCC TTTA TATTG
 ||||| ||| |||||
 AAACGG AAAT ATAAC
 A _
 GAM3717 AKAP13 3' TGACAAAATGAGATACTAT 84013 A A
 TGACAAAGT AGGTA TAT
 ||||| ||||| |||
 ACTGTTTTA TCTAT ATA
 C G
 GAM3717 AKAP13 3' TGACAAAATGAGATACTAT 84013 A A
 TGACAAAGT AGGTA TAT
 ||||| ||||| |||
 ACTGTTTTA TCTAT ATA
 C G
 GAM3717 AKAP13 3' TGACAAAATGAGATACTAT 84013 A A
 TGACAAAGT AGGTA TAT
 ||||| ||||| |||
 ACTGTTTTA TCTAT ATA
 C G
 GAM3717 DNMT2 3' AAAATACAGTAATATAAATT 84014 A
 AAAGTA GGTAATATAAATT
 ||||| ||||| |||||

		TTTTAT TCATTATATTTAA	
		G	
GAM3717	CHL1	3' TGACAAAGATAAGGTAAC 84015	—
		TGACAAAG TAAGGTAAT	
		ACTGTTTC ATTCCATTG	
		T	
GAM3717	FOXP1	3' ACAAAGAAAGAATATAAATT 84016	T T
		ACAAAG AAGG AATATAAATT	
		TGTTTC TTTC TTATATTTAA	
		— —	
GAM3717	LOC220477	5' GACAAGGTGGCATATAAATT 84017	A AA A
		GACAA GT GGTA TATAAATT	
		CTGTT CA CCGT ATATTTAA	
		C — —	
GAM3717	LOC51077	3' ACAAAGTGATATCATAAATT 84018	AA A
		ACAAAGT GGTA TATAAATT	
		TGTTTCA CTAT GTATTTAA	
		— A	
GAM3718	BCL7A	3' TGAGAAGTGACGCCGTTCTG 84021	AG G GA
		TGAGAAGT CGT TG CTG	
		ACTCTTCA GCG GC GAC	
		CT _ AA	
GAM3718	GLS	3' TGAGAAGAGAGGCTGGAC 84022	T_ C G
		TGAGAAG AG GT TGGAC	
		ACTCTTC TC CG ACCTG	
		TC _ —	
GAM3718	IL1F5	3' GAGGACCGTGGACTGA 84023	AAGTA G
		GAG GC TGTGGACTGA	
		CTC TG GCACCTGACT	
		C_ — —	
GAM3718	MLPH	3' TGAGCAGTGCAGGACTGAA 84024	A A TGT
		TGAG AGT GCG GGACTGAA	
		ACTC TCA CGT CCTGACTT	
		G _ — —	
GAM3718	PLD2	3' GAGAAGTGTTTGCCTG 84025	AGC G G
		GAGAAGT GT TG ACTG	
		CTCTTCA CA AC TGAC	
		C_ A G	
GAM3718	SLC2A1	3' TGAGAGGTACGTGTAAGGGACT 84026	A G —
	G	TGAGA GTA CGTGT GGACTG	

ACTCT CAT GCACA CCTGAC
 C _ TTC
 GAM3718 CYYR1 3' GAGATGGTGTGGACTGAA 84027 AGTAGC
 GAGA GTGTGGACTGAA
 ||| |||||
 CTCT CACACCTGACTT
 AC____
 GAM3718 DKFZP434F0318 3' TGGGAAGGGTGCGGACAGA 84028 A TAGC T
 TG GAAG GTGTGGAC GA
 || ||| ||||| ||
 AC CTTC CACGCCTG CT
 C C____ T
 GAM3718 EPS8R3 3' TGAGAAGGAGAGGGACTGAAC 84029 T CGTGT
 TGAGAAG AG GGAAGTGAAC
 ||||| || |||||
 ACTCTTC TC CCTGACTTG
 C TC____
 GAM3718 EPS8R3 3' TGAGAAGGAGAGGGACTGAAC 84029 T CGTGT
 TGAGAAG AG GGAAGTGAAC
 ||||| || |||||
 ACTCTTC TC CCTGACTTG
 C TC____
 GAM3718 FLJ10374 5' TGAGAAATGGTTAGGCTG 84030 AGC GT A
 TGAGAAGT GT GG CTG
 ||||| || |||
 ACTCTTTA CA CC GAC
 C__ AT _
 GAM3718 FLJ12704 3' TGAGAAGTGGTCGTGAGGAC 84031 AG_ T
 TGAGAAGT CGTG GGAC
 ||||| ||| |||
 ACTCTTCA GCAC CCTG
 CCA T
 GAM3718 FLJ13433 3' GAAAATGTGGACTGA 84032 TAGC
 GAAG GTGTGGACTGA
 ||| |||||
 CTTT TACACCTGACT

 GAM3718 FLJ13909 5' TGAGGTCTTGTGGACTG 84033 AA AGCG
 TGAG GT TGTGGACTG
 ||| || |||||
 ACTC CA ACACCTGAC
 _ GA_
 GAM3718 HT002 3' TGGGAAGCAGCGGCCTGGA 84034 A _G
 TG GAAGTAGCG T TGGA
 || ||||| | |||
 AC CTTCGTCGC G ACCT
 C C G
 GAM3718 KIAA0285 3' GAGTAGTGTGGACAGGA 84035 A GC T_
 GA GTA GTGTGGAC GA
 || ||| ||||| ||

CT CAT CACACCTG CT
 _ _ TC
 GAM3718 KIAA0601 3' GAGAGGTGGCACAACTGAAC 84036 A A GT TG
 GAGA GT GC G GACTGAAC
 |||| || | |||||
 CTCT CA CG T TTGACTTG
 C C _ GT
 GAM3718 KIAA1522 3' GAGGAGTAACTGGACTG 84037 A CGTG
 GAG AGTAG TGGACTG
 ||| ||| |||||
 CTC TCATT ACCTGAC
 C TG_
 GAM3718 MGC14288 5' TGAGGGTAGCGTCCCTGGAC 84038 AA G_
 TGAG GTAGCGT TGGAC
 ||| ||||| |||||
 ACTC CATCGCA ACCTG
 C_ GGG
 GAM3718 SP329 5' TGAGAAGCAGTGTGTGTGA 84039 C _ _
 TGAGAAGTAG GT GTG GA
 ||||| || ||| ||
 ACTCTTCGTC CA CAC CT
 A A A
 GAM3718 LOC126961 3' TGGAGGTGGCGCGGGGACTGAA 84040 A A A T
 C TG GA GT GCGTG GGACTGAAC
 || || |||| |||||
 AC CT CA CGCGC CCTGACTTG
 _ C C C
 GAM3718 LOC145376 3' GAAGCGTATGTGGGTTGAA 84041 AGC AC
 GAAGT GTGTGG TGAA
 |||| |||| ||||
 CTTCG TACACC ACTT
 CA_ CA
 GAM3718 LOC146224 5' TGAGCAGTGGCTCCAACTGA 84042 A A GTG GG
 TGAG AGT GC T ACTGA
 ||| ||| | ||||
 ACTC TCA CG G TGA
 G C AG_ TT
 GAM3718 LOC154877 3' TGATGAGTCAGTGGACTGAA 84043 GA AGCGT
 TGA AGT GTGGACTGAA
 ||| ||| |||||
 ACT TCA CACCTGACTT
 AC GT_
 GAM3718 LOC155438 3' TGGGAAGTAGCTGTGGA 84044 A G
 TG GAAGTAGC TGTGGA
 || ||||| |||||
 AC CTTTCATCG ACACCT
 C _
 GAM3718 LOC257395 3' TGGAGGTGGCGCGGGGACTGAA 84040 A A A T
 C TG GA GT GCGTG GGACTGAAC
 || || |||| |||||

		AC CT CA CGCGC CCTGACTTG		
		_ C C C		
GAM3718	LOC93496	3' TGAGAAGTGGTGTGTGA	84045	AGC GGAC
		TGAGAAGT GTGT TGA		
		ACTCTTCA CACA ACT		
		C__ AC__		
GAM3719	TRHDE	3' ATAATGCCCATCCTAGGT	84048	ATTGA A
		ATAATGCCTA TCTA GT		
		TATTACGGGT GGAT CA		
		A__ C		
GAM3719	KIAA0022	3' TAATGCCTGCATTTTCAGTAC	84049	A_ GATCTA
		TAATGCCT ATT AGTAC		
		ATTACGGA TAA TCATG		
		CG AAG__		
GAM3719	KIAA1724	3' TGCCTATTTTATCCAAGT	84050	A G
		TGCCTA TT ATCTAAGT		
		ACGGAT AA TAGGTTCA		
		A A		
GAM3719	MGC10765	3' ATGCTGGATGACCAAGTAC	84051	CTAAT T
		ATGC TGA CTAAGTAC		
		TACG ACT GGTTCATG		
		ACCT_ _		
GAM3719	LOC90509	3' CAATGCCTGGATTTAAGT	84052	AATT C
		TAATGCCT GAT TAAGT		
		GTTACGGA CTA ATTCA		
		C__ A		
GAM3720	CD3Z	3' TGTTGCGTCTTCCTGCGA	84055	C ATA
		TGTTGCGTCT CC GTGA		
		ACAACGCAGA GG CGCT		
		A A__		
GAM3720	AP4S1	3' TGGTGTGTCTCCCATACTG	84056	T C G
		TG TG GTCTCCCATA TG		
		AC AC CAGAGGGTAT AC		
		C A G		
GAM3720	DKFZp434A171	3' TGTTGCTCTTCCTCTGAAG	84057	G C ATAG
		TGTTGC TCT CC TGAAG		
		ACAACG AGA GG ACTTC		
		_ A AG__		
GAM3720	FLJ14957	3' TGTTGCGTCCTCAGAA	84058	CC TAGT
		TGTTGCGTCT CA GAA		

ACAACGCAGG GT CTT
A_ ____
GAM3720 MGC17330 3' TGTTGCGCTCCGTCAGGAAG 84059 T CA T
TGTTGCG CTCC TAG GAAG
||||| ||| ||| |||
ACAACGC GAGG GTC CTTC
_ CA _
GAM3720 MGC26914 3' TGCACCCTCTCATGGTGAAG 84060 GT_ C A
TGC C TC CAT GTGAAG
||| | || ||| |||||
ACG G AG GTA CACTTC
TG G A C
GAM3720 MLLT10 3' TGTTGCGTTTCTTCATAG 84061 C C_
TGTTGCGT TC CATAG
||||||| || |||
ACAACGCA AG GTATC
A AA
GAM3720 SDC3 3' TGTTGGGTCTCCACCTG 84062 C AG
TGTTG GTCTCCCAT TG
||||| ||||| ||
ACAAC CAGAGGGTG AC
C G_
GAM3720 LOC150759 3' GTCTGCCACTGTAGTGAAG 84063 C ____
GTCT CCAT AGTGAAG
|||| ||| |||||
CAGA GGTG TCACTTC
C ACA
GAM3720 LOC151323 3' GTCTGCCACTGTAGTGAAG 84063 C ____
GTCT CCAT AGTGAAG
|||| ||| |||||
CAGA GGTG TCACTTC
C ACA
GAM3720 LOC158527 3' TGAGTCTTTCATAGTGAAG 84064 C CC
TG GTCT CATAGTGAAG
|| ||| |||||
AC CAGA GTATCACTTC
T AA
GAM3720 LOC200399 3' GTCTGCCACTGTAGTGAAG 84063 C ____
GTCT CCAT AGTGAAG
|||| ||| |||||
CAGA GGTG TCACTTC
C ACA
GAM3721 CETN1 3' TGAGCTCCGTAAGTTTGTAAG 84067 CG ACTC
TGAGCTCCG AAG TGTAAG
||||||| || |||||
ACTCGAGGC TTC ACATTC
A_ AA_
GAM3721 DNASE1L3 5' TGGCTTCAAGACTCTGT 84068 A C CGA
TG GCT CG AGACTCTGT
|| ||| || |||||

			AC CGA GT TCTGAGACA		
			— A —		
GAM3721	RAX	3'	TGAGGTCCGCGAAGTGC 84069	C	ACTC
			TGAG TCCGCGAAG TGT		
			ACTC AGGCGCTTC ACG		
			C —		
GAM3721	SCRT1	3'	GAGTTCCGCGAAGGCTGC 84070	C	ACT
			GAG TCCGCGAAG CTGT		
			CTC AGGCGCTTC GACG		
			A C—		
GAM3721	WISP1	3'	CTCTCAAGGCTCTGTAAG 84071	CG G A	
			CTC C AAG CTCTGTAAG		
			GAG G TTC GAGACATTC		
			A— C		
GAM3721	CALN1	3'	TGAGCTCCTGAAGTCTA 84072	GC AC	
			TGAGCTCC GAAG TCTG		
			ACTCGAGG CTTC AGAT		
			A— —		
GAM3721	CLDN1	5'	TGGGCCCGCGGAGGAAGTTAA 84073	A A	ACTCTG
	G		TG GCTCCGCG AG TAAG		
			AC CGGGGCGC TC ATTC		
			C C CTTCA—		
GAM3721	DKFZP434J193	3'	AAGCTAGACTCTGTAA 84074	CCGCGA	
			GAGCT AGACTCTGTAA		
			TTCGA TCTGAGACATT		
			—		
GAM3721	FLJ12505	5'	GAGCTCCGCGGAGGCTCC 84075	A A	
			GAGCTCCGCG AG CTCT		
			CTCGAGGCGC TC GAGG		
			C C		
GAM3721	KIAA1941	3'	TGAGCTCCGTGAAGCAGCTGAA 84076	C ACT T	
	G		TGAGCTCCG GAAG CTG AAG		
			ACTCGAGGC CTTC GAC TTC		
			A GTC —		
GAM3721	MGC10200	5'	TGAGACGGGACTCTGTAAG 84077	CTCC AA	
			TGAG GCG GACTCTGTAAG		
			ACTC TGC CTGAGACATTC		
			— C—		
GAM3721	MGC24009	3'	TGAGCTTCTAATTTTCTGTAAG 84078	CCGCG GAC	
			TGAGCT AA TCTGTAAG		

ACTCGA TT AGACATTC
 AGA__ AAA
 GAM3721 LOC136345 3' TGAGCTCCTGGAGGTGACTC 84079 GC A__
 TGAGCTCC GA GACTC
 ||||| || ||||
 ACTCGAGG CT CTGAG
 AC CCA
 GAM3721 LOC148018 3' AGCTCCGCGGAGGACCAGCTG 84080 AA_ _
 AGCTCCGCG GACT CTG
 ||||| ||| ||
 TCGAGGCGC CTGG GAC
 CTC TC
 GAM3721 LOC155032 5' TGAGCTCCTGGAGGTGACTC 84079 GC A__
 TGAGCTCC GA GACTC
 ||||| || ||||
 ACTCGAGG CT CTGAG
 AC CCA
 GAM3722 IL1RAP 3' ATATATCACAGTTCTTTGT 84083 AG C
 GTATATCACA TCT TGT
 ||||| ||| ||
 TATATAGTGT AGA ACA
 CA A
 GAM3722 LARGE 3' CCTTGTCCAAGGTCTCTGT 84084 GTATA A _
 CC TC CAAG TCTCTGT
 || || ||| |||||
 GG AG GTTC AGAGACA
 AAC_ _ C
 GAM3722 LARGE 3' CCTTGTCCAAGGTCTCTGT 84084 GTATA A _
 CC TC CAAG TCTCTGT
 || || ||| |||||
 GG AG GTTC AGAGACA
 AAC_ _ C
 GAM3722 CYP2S1 3' CCTCGTATGTCCAAAGTCTCTG 84085 C A AC
 T CC CGTAT TC AAGTCTCTGT
 || ||| || |||||
 GG GCATA AG TTCAGAGACA
 A C GT
 GAM3722 DJ37E16.5 3' CCCCAGAGCATCACAAGTCTTT 84086 TA_ C
 GT CCCC G TATCACAAGTCT TGT
 ||| ||||| |||
 GGGGT GTAGTGTTCAGA ACA
 CTC A
 GAM3722 FLJ00024 5' CCCACGATGGTGCAGGTCTCTG 84087 _ TATATCA A
 T CCC CG CA GTCTCTGT
 ||| || || |||||
 GGG GC GT CAGAGACA
 T TACCAC_ C
 GAM3722 FLJ20203 3' CATCCATCTACAGGTCTCTGT 84088 A _ A
 CGT TATC ACA GTCTCTGT
 ||| ||| || |||||

GTA GTAG TGT CAGAGACA
 G A C
 GAM3722 FLJ32865 3' CATTCTCACAAGTTTCTGT 84089 ATA C
 CGT TCACAAGT TCTGT
 ||| ||||| |||||
 GTA AGTGTTCAGACA
 AG_ A
 GAM3722 KIAA0420 3' ACCTGGGCATGGGTCTCTGT 84090 CC_ ATCACAA
 ACC GTAT GTCTCTGT
 ||| ||| |||||
 TGG CGTA CAGAGACA
 ACC CC____
 GAM3722 KIAA0893 3' GTAGTCTTAAGTCTCTGT 84091 TA AC
 GTA TC AAGTCTCTGT
 ||| || |||||
 CAT AG TTCAGAGACA
 C_ AA
 GAM3722 KIAA1045 3' CCCAACCCCATGAGTCTCTGT 84092 TATA CA
 CCCG TCA AGTCTCTGT
 |||| ||| |||||
 GGGT GGT TCAGAGACA
 TGG_ AC
 GAM3722 KIAA1280 5' CCGTGTCTCCCCACCTCTGT 84093 ATA A_ AG
 CCGT TC CA TCTCTGT
 |||| || || |||||
 GGCA AG GT GGAGACA
 CAG GG ____
 GAM3722 LOC112840 3' ACCCCTGTATTTATCTTCTGT 84094 _ ATCACAA _
 ACCCC GTAT GTCT CTGT
 |||| |||| ||| |||||
 TGGGG CATA TAGA GACA
 A AA____ A
 GAM3722 LOC196047 5' CCCTGTGTACATGTGTCTCTGT 84095 C__ CACAA
 CCC GTATAT GTCTCTGT
 ||| ||||| |||||
 GGG CATGTA CAGAGACA
 ACA CA____
 GAM3722 LOC203297 5' CCCACGATGGTGCAGGTCTCTG 84087 _ TATATCA A
 T CCC CG CA GTCTCTGT
 ||| || || |||||
 GGG GC GT CAGAGACA
 T TACCAC_ C
 GAM3722 LOC221178 3' CCTGGTATTCATAAGTCTCTGT 84096 CC A C
 CC GTAT TCA AAGTCTCTGT
 || |||| || |||||
 GG CATA AGT TTCAGAGACA
 AC _ A
 GAM3722 LOC222112 3' CCTGTGTATTGACAAGTCT 84097 C A C_
 CC GT TAT ACAAGTCT
 || || || |||||

GG CA ATA TGTTCAGA
A C AC
GAM3722 LOC257354 3' ACCTGGGCATGGGTCTCTGT 84090 CC_ ATCACAA
ACC GTAT GTCTCTGT
||| ||| |||||
TGG CGTA CAGAGACA
ACC CC____
GAM3722 LOC257463 3' CATATATCAGGCTTCTGT 84098 CAA TC
CGTATATCA G TCTGT
||||||| | ||||
GTATATAGT C AGACA
C__ GA
GAM3723 OPTN 5' GAGAGAACTCCCGACCGGG 84101 C ACACGA
GAGAG AC CGACCGGG
||||| || |||||
CTCTC TG GCTGGCCC
T AGG____
GAM3723 SORCS1 3' CAGAGAGCACACATGAAATCAC 84102 C CG__ C
TGGG TAGAGAGCACACA GA AC GGG
||||||| || |||
GTCTCTCGTGTGT CT TG CCC
A TTAG A
GAM3723 ARTN 5' GAGAGGCACGGAACCGGG 84103 CACA AC
GAGAG CACG GACCGGG
||||| ||| |||||
CTCTC GTGC TTGGCCC
C__ CT
GAM3723 FGF19 5' GAGGCTGGGCGGCGACCGGG 84104 A ACACA A
GAG GC CG CGACCGGG
||| || |||||
CTC CG GC GCTGGCCC
_ ACCC_ C
GAM3723 FLJ10921 3' TAGAGAGCAGCATGTGGCACAC 84105 _____
A TAGAGAGCA CACACG
||||||| |||||
ATCTCTCGT GTGTGT
CGTACACC
GAM3723 KIAA0894 3' TAGAGAGCACACACAGTCCAAC 84106 GA__ C
GG TAGAGAGCACACAC CGAC GG
||||||| ||| ||
ATCTCTCGTGTGTG GTTG CC
TCAG _
GAM3723 KIAA1881 3' GAGAGCACGGGGCCCGGCGGCC 84107 ACA__ A A
GGG GAGAGCAC CG CG CCGGG
||||||| || |||||
CTCTCGTG GC GC GGCCC
CCCCGG C C
GAM3723 LOC120448 5' GAGAGCACAGCAGGCCGG 84108 _ CGACGA
GAGAGCACA CA CCGG
||||||| || |||

		CTCTCGTGT GT GGCC		
		C CC_____		
GAM3723	LOC138128 5'	AGAGCCACCGCGGCGACCGGG 84109	A	A_ A
		AGAGC CAC CG CGACCGGG		
		TCTCG GTG GC GCTGGCCC		
		_ GC C		
GAM3723	LOC139174 5'	TAGAGAGCATACTCGGAGTCAT 84110	C	A ACGACC_
		GGG TAGAGAGCA AC CG GGG		
		ATCTCTCGT TG GC CCC		
		A A CTCAGTA		
GAM3723	LOC196985 5'	TAGGAGCACACACGTGACGGG 84111	A	AC C
		TAG GAGCACACACG GAC GGG		
		ATC CTCGTGTGTGC CTG CCC		
		_ A_ _		
GAM3724	DPYD 5'	GGCTGTAACGCCATTGGCA 84114	ACA	
		GGCTGTGA CATTGGCA		
		CCGACATT GTAACCGT		
		GCG		
GAM3724	ITGA1 3'	TCAGGGACTGTCTCATTGGCA 84115	A	GAACA
		TCA GGGCTGT CATTGGCA		
		AGT CCTGACA GTAACCGT		
		C GA_____		
GAM3724	PGK1 3'	GGGCTGTGCACAGGAAC 84116	AA	TT
		GGGCTGTG CACA GGC		
		CCCGACAC GTGT TTG		
		_ CC		
GAM3724	SLA2 3'	TCAAGGGCTGGATTTGG 84117	T	ACACA
		TCAAGGGCTG GA TTGG		
		AGTTCCCGAC CT AACC		
		_ A_____		
GAM3724	TACC1 3'	TCCAGGGCTGTTGCATTGGCA 84118	A	GAACA
		TC AGGGCTGT CATTGGCA		
		AG TCCCGACA GTAACCGT		
		G AC_____		
GAM3724	TCTA 3'	CCAGGGGCTGTGAATAAC 84119	A	CACAT
		TCA GGGCTGTGAA TGGC		
		GGT CCCGACACTT ATTG		
		C _____		
GAM3724	TNFRSF13C 3'	TCAAGGGCTGTCAAAGATGG 84120	G	CACAT
		TCAAGGGCTGT AA TGG		

AGTTCCCGACA TT ACC
 G TCT__
 GAM3724 TRPM2 3' AGGGGTGCCAGGGCACATTGGC 84121 C GAA__
 A AGGG TGT CACATTGGCA
 |||| ||| |||||
 TCCC ACG GTGTAACCGT
 C GTCCC
 GAM3724 COTL1 3' GGGCTGTGGACACAGGG 1681 A TT
 GGGCTGTG ACACA GG
 ||||| |||| ||
 CCCGACAC TGTGT CC
 C C_
 GAM3724 DKFZp762P2111 3' TCAAAGTTTGAGCACATTGG 84122 GCTG A
 TCAAGG TGA CACATTGG
 ||||| ||| |||||
 AGTTTC ACT GTGTAACC
 AA__ C
 GAM3724 FLJ20291 3' AGGAGCCATGGAGCATATTGGC 84123 _ AA_ C
 A AGG GCTGTG CA ATTGGCA
 ||| ||||| || |||||
 TCC CGGTAC GT TAACCGT
 T CTC A
 GAM3724 KIAA0794 3' ACTGATGAACACGTTGGCA 84124 _ A
 GCTG TGAACAC TTGGCA
 |||| ||||| |||||
 TGAC ACTTGTG AACCGT
 T C
 GAM3724 MGC13251 5' TCAGGGGCTGCGGGCAGCCGGC 84125 A AA CA
 TCA GGGCTGTG CA TTGGC
 ||| ||||| || |||||
 AGT CCCGACGC GT GGCCG
 C CC C_
 GAM3724 MGC3101 3' AAGGGCCGTGGGCAGGC 84126 AA CATT
 AAGGGCTGTG CA GGC
 ||||| || |||
 TTCCCGGCAC GT CCG
 CC ____
 GAM3724 MGC4643 3' TCCTAGGTTGTGAACATATTGG 84127 AA C C
 TC GGG TGTGAACA ATTGG
 || ||| ||||| |||||
 AG TCC ACACTTGT TAACC
 GA A A
 GAM3724 PKNOX2 3' TCCAGGGCTGTGGATAGC 84128 A AACACAT
 TC AGGGCTGTG TGGC
 || ||||| |||||
 AG TCCCGACAC ATCG
 G CT____
 GAM3724 ZNF347 3' AGGATGGAGTGCATTGGCA 84129 C T ACA
 AGGG TG GA CATTGGCA
 |||| || || |||||

		TCCT AC CT GTAACCGT		
		— _ CAC		
GAM3724	LOC150605 5'	GGGCTGTGATGCACCCGTTGG	84130	A_ A__
		GGGCTGTGA CAC TTGG		
		CCCGACACT GTG AACC		
		AC GGC		
GAM3724	LOC150848 3'	AGAGTTGTGAACAAGC	84131	C CATT
		AGGG TGTGAACA GGC		
		TCTC ACACTTGT TCG		
		A _____		
GAM3725	DDOST 5'	ATCGCGGCTCGTGCCCGTGG	84134	TC _ _
		ATCGCGG CGT TCG GG		
		TAGCGCC GCA GGC CC		
		GA CG A		
GAM3725	DLK1 5'	TCGCGGTCCCGGGAGCGG	84135	GTT
		TCGCGGTCC CGGGAGCGG		
		AGCGCCAGG GCCCTCGCC		

GAM3725	DYRK2 5'	TCGGGTAGGCGGCGGGAGCGG	84136	C CC T_
		TCG GGT GT CGGGAGCGG		
		AGC CCA CG GCCCTCGCC		
		_ TC CC		
GAM3725	ENPP1 5'	ATCGCGGCCGTTCCCCGCCGG	84137	T GGGA _
		ATCGCGG CCGTTC GC GG		
		TAGCGCC GGCAAG CG CC		
		_ GGG_ G		
GAM3725	G6PD 5'	ATCGGCGGGGGCGGGGGCGG	84138	_ TCCGTT A
		ATCG CGG CGGG GCGG		
		TAGC GCC GCCC CGCC		
		C CCC_ C		
GAM3725	GUCY1A2 5'	ACCGCGGTCTGGCGGGGCGG	84139	CGTT A
		ATCGCGGTC CGGG GCGG		
		TGGCGCCAG GCCC CGCC		
		CC_ _		
GAM3725	JPH3 5'	TCGCGGCCGCCGGCG	84140	T T GGA
		TCGCGG CCGT CG GCG		
		AGCGCC GGCG GC CGC		
		— _ _		
GAM3725	MID1 5'	TCGCAGTCTTCAGAGCGG	84141	CG G
		TCGCGGTC TTCGG AGCGG		

AGCGTCAG AAGTC TCGCC

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      — —
GAM3725 NFRKB  5' TCGCGGCCGTGACGGCGG  84142  T  TC  GA
      TCGCGG CCGT  GG  GCGG
      ||||| ||| || |||
      AGCGCC GGCA  CT  CGCC
      — — GC
GAM3725 OCLN   5' GCGGCCCGAGAGGCGG  84143  TTC  A
      GCGGTCCG  GGG  GCGG
      ||||| || |||
      CGCCGGGC  CTC  CGCC
      T — —
GAM3725 THBS1  5' CGCGGCGGCCGGGAGCGG  84144  TC  TT
      CGCGG  CG  CGGGAGCGG
      |||| || |||||
      GCGCC  GC  GCCCTCGCC
      — CG
GAM3725 TRC8   5' CCGCGGCCGGGGGCG  84145  T  TTC  A
      TCGCGG CCG  GGG  GCG
      ||||| ||| ||| |||
      GGCGCC GGC  CCC  CGC
      — — —
GAM3725 ZNF174 5' CGCGGTCCCTGGGAGTGG  84146  G  C  C
      CGCGGTCC TT  GGGAG  GG
      ||||| || ||| |||
      GCGCCAGG  GA  CCCTC  CC
      — — A
GAM3725 ZNF216 5' CCGCGGGCCGGGAGCG  84147  TCC  T
      TCGCGG  GT  CGGGAGCG
      |||| || |||||
      GGCGCC  CG  GCCCTCGC
      — —
GAM3725 CECR2  5' CGCGGTCCCTCGGCGGGGGCGG 84148  GTT_  A
      CGCGGTCC  CGGG  GCGG
      ||||| ||| |||
      GCGCCAGG  GCCC  CGCC
      AGCC  C
GAM3725 CNNM2  5' TCTCGGCCACGGGGGCGG  84149  G  TT  A
      TC  CGGTCCG  CGGG  GCGG
      || ||||| ||| |||
      AG  GCCGGGT  GCCC  CGCC
      A — C
GAM3725 DKFZp586G0123 5' CGGTGGCTTGGGAGCGG  84150  CC  C
      CCGT  GTT  GGGAGCGG
      ||| || |||||
      GCCA  CGA  CCCTCGCC
      C_ A
GAM3725 FLJ20374 5' CGCGGGCGTGGGAGCG  84151  TC  TC
      CGCGG  CGT  GGGAGCG
      |||| ||| |||||
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		GCGCC GCA CCCTCGC		
		C_ _		
GAM3725	HTATSF1	5' ATCGCGGCCGCTCGGCG	84152	T GGA
		ATCGCGG CCGTTCG GCG		
		TAGCGCC GGCGAGC CGC		
		— —		
GAM3725	KIAA0513	3' TCACGGTCTGGCCAGCGG	84153	CGTTC G_
		TCGCGGTC GG AGCGG		
		AGTGCCAG CC TCGCC		
		A_ _ GG		
GAM3725	KIAA0923	5' TCACGGCCCCCGGGAGCGG	84154	GT
		TCGCGGTCC TCGGGAGCGG		
		AGTGCCGGG GGCCCTCGCC		
		—		
GAM3725	MGC21945	5' TCGCGGTCCTCCAGAGCGG	84155	G G
		TCGCGGTCC TTC GGAGCGG		
		AGCGCCAGG AGG TCTCGCC		
		_ G		
GAM3725	RAD51	5' CGCGGTCCGCCAGCG	84156	CGGG
		CGCGGTCCGTT AGCG		
		GCGCCAGGCGG TCGC		
		—		
GAM3725	RAD51	5' CGCGGTCCGCCAGCG	84156	CGGG
		CGCGGTCCGTT AGCG		
		GCGCCAGGCGG TCGC		
		—		
GAM3725	STAG1	5' TCGCCGGGGGTTTCGGGAGCGG	84157	_ TCC
		TCGC GG GTTCGGGAGCGG		
		AGCG CC CAAGCCCTCGCC		
		G CC_		
GAM3725	LOC130497	3' TCGCGGCCCGGGCG	84158	GTT GA
		TCGCGGTCC CGG GCG		
		AGCGCCGGG GCC CGC		
		— —		
GAM3725	LOC164537	5' TCGCGGCCCGGGGCG	84159	T TTC A
		TCGCGG CCG GGG GCG		
		AGCGCC GGC CCC CGC		
		— — —		
GAM3725	LOC167517	5' TCGCGGCCCGTTTCCCGCGG	84160	CGGGA
		TCGCGGTCCGTT GCGG		

			AGCGCCGGGCAA	CGCC		
			AGGG_			
GAM3725	LOC257450	5'	TCCCGGTCCGTCCATGGGCGG	84161	G	_ A
			TC CGGTCCGTTCG GG GCGG			
			AG GCCAGGCAGGT CC CGCC			
			G A _			
GAM3726	MTCP1	3'	TTTAATGTGTTTATATT	84164	T	
			TTTAATGTGTTT ATATT			
			AAATTACACAAA TATAA			
GAM3726	KIAA1586	5'	TTTAATGTGTTTATTATTGTAT	84165	TA	A
		TT	TTTAATGTGTTT TATT TATTT			
			AAATTACACAAA ATAA ATAAA			
			TA C			
GAM3726	MGC4827	3'	GTGTTTTTACTACATTT	84166	A	
			GTGTTTT TATTATATTT			
			CACAAA ATGATGTAAA			
GAM3726	PPAP2A	3'	TTTAATATGTATTATATT	84167	T	
			TTTAATGTGT TTATATT			
			AAATTATACA AATATAA			
			T			
GAM3726	STRN	3'	TTAATGTGTTTTAACCAGATTT	84168	T	T
			TTAATGTGTTTTA ATTA ATTT			
			AATTACACAAAAT TGGT TAAA			
GAM3726	LOC157292	3'	TTTAATGTGCTTAATATT	84169	T	
			TTTAATGTGTTT ATATT			
			AAATTACACGAA TATAA			
			T			
GAM3727	CASP3	3'	CATGTCTCTGCTCAGGCTCAAA	84172	CCGCC	AA
	CC		CATG GCTCA CTAAACC			
			GTAC CGAGT GAGTTTGG			
			AGAGA CC			
GAM3727	CASP3	3'	CATGTCTCTGCTCAGGCTCAAA	84172	CCGCC	AA
	CC		CATG GCTCA CTAAACC			
			GTAC CGAGT GAGTTTGG			
			AGAGA CC			
GAM3727	NEDD4	3'	ATACCCCAACAACTTAAACC	84173	G	CT
			ATGCC CCG CAACTTAAACC			

		TATGG GGT GTTTGAATTTGG	
		_ T_	
GAM3727 PTEN	5'	TGCCGCGCTTGGCTCTGGACC 84174	CAAA AA_
		TGCCGCGCT CTT ACC	
		ACGGCGGCGA GAG TGG	
		ACC_ ACC	
GAM3727 ROBO1	3'	GCCACAACAACTTAAACC 84175	T_
		GCCGC CAAACTTAAACC	
		CGGTG GTTTGAATTTGG	
		TT	
GAM3727 ROBO1	3'	GCCACAACAACTTAAACC 84175	T_
		GCCGC CAAACTTAAACC	
		CGGTG GTTTGAATTTGG	
		TT	
GAM3727 E2IG4	3'	CATGCCACTGCCCGCAGGAACT 84176	C A_____
TA		CATGCCGC GCTC AACTTA	
		GTACGGTG CGGG TTGAAT	
		A CGTCC	
GAM3727 GAL3ST2	5'	GCCGCGCTATCTCTGGACC 84177	CAAA AA_
		GCCGCGCT CTT ACC	
		CGGCGGCGA GAG TGG	
		TA__ ACC	
GAM3727 HSPC016	5'	TGCCGCGCTTCCCCAGACC 84178	CAAA A
		TGCCGCGCT CTTA ACC	
		ACGGCGGCGA GGGT TGG	
		AG__ C	
GAM3727 MGC12538	3'	GCTGCATCAAACCTTGAAC 84179	C _ A
		GC GC TCAAACCTT AAC	
		CG CG AGTTTGAA TTG	
		A T C	
GAM3727 MKRN1	3'	GCCACACAAGGCTTAAACC 84180	T A_
		GCCGC CAA CTTAAACC	
		CGGTG GTT GAATTTGG	
		T CC	
GAM3728 BCHE	3'	TATGTTCTATAAAGGGTA 84183	G_
		TATG CTGTAAAGGGTA	
		ATAC GATATTTCCCAT	
		AA	
GAM3728 CEACAM6	3'	GTATGACTATTAGGAGGGTA 84184	AA__
		GTATGGCTGT AGGGTA	

		CATACTGATA	TCCCAT		
		ATCC			
GAM3728	FPRL1	3' ATATGACTCAAGGGTA	84185	GTA	
		GTATGGCT	AAGGGTA		
		TATACTGA	TTCCCAT		
		G__			
GAM3728	FRK	3' GTAGGCCAAAGGGTA	84186	T GT	
		GTA GGCT	AAAGGGTA		
		CAT CCGG	TTTCCCAT		
		- -			
GAM3728	IL20RA	3' TATGGCTGGGATCAAAGGG	84187	_____	
		TATGGCTG	TAAAGGG		
		ATACCGAC	GTTTCCC		
		CCTA			
GAM3728	LZTFL1	3' GTATTTTGCTAAAGGGTA	84188	GGC _	
		GTAT TGT	AAAGGGTA		
		CATA ACG	TTTCCCAT		
		AA_ A			
GAM3728	POLQ	3' GTAGGTGAAAGGGTA	84189	T C T	
		GTA GG TG	AAAGGGTA		
		CAT CC AC	TTTCCCAT		
		- - -			
GAM3728	PPP6C	3' GTATATTGTAGAGGGTA	84190	GC A	
		GTATG TGTA	AGGGTA		
		CATAT ACAT	TCCCAT		
		A_ C			
GAM3728	PRKCN	3' TATGGCTGCTGTGAGGGTA	84191	AA__	
		TATGGCTGT	AGGGTA		
		ATACCGACG	TCCCAT		
		ACAC			
GAM3728	TACC1	3' GTAGGTTGAAAGGGTA	84192	T C T	
		GTA GG TG	AAAGGGTA		
		CAT CC AC	TTTCCCAT		
		- A -			
GAM3728	TNFAIP1	3' GCATGGCTGGAAGCCAAGGGTA	84193	TA_____	
		GTATGGCTG	AAGGGTA		
		CGTACCGAC	TTCCCAT		
		CTTCGG			
GAM3728	TOMM22	3' GCATGGCTGCACTCTGGTA	84194	AAG_	
		GTATGGCTGTA	GGTA		

CGTACCGACGT CCAT
GAGA
GAM3728 XK 3' GTAGGTTGGAAGGGTA 84195 T C T_
GTA GG TG AAAGGGTA
||| ||| |||||
CAT CC AC TTTCCCAT
_ A CT
GAM3728 CED-6 3' GTTAGGTAAAGGGTA 84196 A CT
GT TGG GTAAAGGGTA
|| ||| |||||
CA ATC CATTTCCTCAT
_ _
GAM3728 FLJ20127 3' GTATGGCTCTGATCAAGAAGGG 84197 TA |||
TAT TATGGCT G AAGGGTA T
||| ||| | ||||| |
ATACCGA T TTCCCAT A
GACTAG TC |||
GAM3728 HEY2 3' GTATGGCTACCTTCAGGGT 84198 AA_
GTATGGCTGT AGGGT
||| ||||| |||||
CATACCGATG TCCCA
GAAG
GAM3728 HN1L 3' ATAAAGCTTTGTAGAGGGT 84199 T _ A
GTA GGCT GTA AGGGT
||| ||||| ||| |||||
TAT TCGA CAT TCCCA
T AA C
GAM3728 KIAA0445 5' TATGGCTGTGGGACAAAGGGT 84200
TATGGCTGT AAAGGGT
||| ||||| |||||
ATACCGACA TTTCCCA
CCCTG
GAM3728 KIAA0537 3' GCATGGCCATTCAGAGGGTA 84201 AA_
GTATGGCTGT AGGGTA
||| ||||| |||||
CGTACCGGTA TCCCAT
AGTC
GAM3728 KIAA1001 3' GTGTGTTTGTAAGAGGGTA 84202 A GC _
GT TG TGTAAGGGTA
|| || ||||| |||||
CA AC ACATT TCCCAT
C AA TC
GAM3728 KIAA1724 3' GTCAGAAGTAAAGGGTA 84203 A CT
GT TGG GTAAAGGGTA
|| ||| |||||
CA GTC CATTTCCTCAT
_ TT
GAM3728 KIAA1910 3' GGAGCTACTTAAAGGGTA 84204 T _
A GGCTG TAAAGGGTA
| ||||| |||||

C TCGAT ATTTCCCAT
 C GA
 GAM3728 KIAA1924 3' GTATAGCTGCTGCAGGGT 84205 AA_
 GTATGGCTGT AGGGT
 ||||| ||||
 CATATCGACG TCCCA
 ACG
 GAM3728 MBLL39 3' GTATGGCTGAAAGAATA 84206 T
 GTATGGCTG AAAGGGTA
 ||||| |||||
 CATACCGAC TTTCTTAT
 —
 GAM3728 LOC149579 5' TATGGCTGTGGGACAAAGGGT 84200 _____
 TATGGCTGT AAAGGGT
 ||||| |||||
 ATACCGACA TTTCCCA
 CCCTG
 GAM3728 LOC163026 5' GTATGTAATAAAGGGTA 84207 GCT
 GTATG GTAAAGGGTA
 |||| |||||
 CATACTATTTCCTAT
 AT_
 GAM3728 LOC55908 3' GTAGGCATGAAAGGGTA 84208 T _ T
 GTA GGC TG AAAGGGTA
 || || || |||||
 CAT CCG AC TTTCCCAT
 _ T _
 GAM3728 LOC90155 5' GATAACTAAAGGGTA 84209 T TA
 G ATGGCTG AAGGGTA
 | ||||| |||||
 C TATTGAT TTCCCAT
 — —
 GAM3728 LOC92421 3' ATATTCTGTAAAGGGTA 84210 GG
 GTAT CTGTAAAGGGTA
 |||| |||||
 TATA GACATTTCCCAT
 A_
 GAM3729 CAPZA1 3' ATCACTCTTGTTTATAAATCAC 84213 _ TTTAGA
 ATCACTTT GTTTAT CAC
 ||||| ||||| |||
 TAGTGAGA CAAATA GTG
 A TTTA_
 GAM3729 CREB1 3' ATCACTTTGCTTTATTTGACA 84214 AT A
 ATCACTTTGTTT TTT GACA
 ||||| ||||| |||
 TAGTGAAACGAA AAA CTGT
 AT _
 GAM3729 EGR1 3' TCACTTTGTTTAAGCAAACAC 84215 TTT
 TCACTTTGTTTA TAGACAC
 ||||| |||||

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AGTGAAACAAAT GTTTGTG
TC_
GAM3729 ERBB2 3' TCGCTTTTGTCTTAGACAC 84216 A _ ATT
TC CTTT GTTT TTAGACAC
|| ||| ||| |||||
AG GAAA CAAG AATCTGTG
C A ____
GAM3729 IDS 3' CAGCTTGTTTATTTTAGA 84217 C
CA TTTGTTTATTTTAGA
|| ||||| |||||
GT GAACAAATAAAATCT
C
GAM3729 NCAM2 3' CTTTGTTTGTTTAGACAC 84218 AT
CTTTGTTT TTTAGACAC
||||| |||||
GAAACAAA AAATCTGTG
C_
GAM3729 OGN 3' ACTTTGTTTCGAACGTAGACA 84219 ATTT__
ACTTTGTTT TAGACA
||||| |||||
TGAAACAAA ATCTGT
GCTTGC
GAM3729 OGN 3' ACTTTGTTTCGAACGTAGACA 84219 ATTT__
ACTTTGTTT TAGACA
||||| |||||
TGAAACAAA ATCTGT
GCTTGC
GAM3729 OGN 3' ACTTTGTTTCGAACGTAGACA 84219 ATTT__
ACTTTGTTT TAGACA
||||| |||||
TGAAACAAA ATCTGT
GCTTGC
GAM3729 SLC16A7 3' TCACTTTGTAGGATTAGGCA 84220 TTATT A
TCACTTTGT TTAG CA
||||| ||| ||
AGTGAAACA AATC GT
TCCT_ C
GAM3729 TGFBR1 3' ATCACTTTCTTTAGTAATAAGA 84221 G TTTT__
CA ATCACTTT TTTA AGACA
||||| ||| |||||
TAGTGAAA AAAT TCTGT
G CATTAT
GAM3729 ZIC3 3' ATCACCCTGTTTATAGACA 84222 _ ATTT
ATCACT TTGTTT TAGACA
||||| ||||| |||||
TAGTGG GACAAA ATCTGT
T ____
GAM3729 AGXT2L1 3' ATCACTTGGTTTATTCTGA 84223 T A
ATCACTT GTTTATTTT GA
||||| ||||| ||

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			TAGTGAA CAAATAAGA CT		
			C _		
GAM3729	DKFZP566F2124	3'	CTTTAACTTTTAGACAC	84224	TTTA
			CTTTG TTTTAGACAC		
			GAAAT AAAATCTGTG		
			TGA_		
GAM3729	FLJ10716	3'	ACTTTGTTTATTAACA	84225	TTA
			ACTTTGTTTATT GACA		
			TGAAACAAATAA TTGT		

GAM3729	FLJ22601	3'	ACATTTGTAAATATTTTAGACA	84226	_ T__
			AC TTTGT TATTTTAGACA		
			TG AAACA ATAAAATCTGT		
			T TTT		
GAM3729	KIAA0285	3'	TCACCCTTATTTTAGA	84227	TTG
			TCACT TTTATTTTAGA		
			AGTGG GAATAAAATCT		

GAM3729	SLC19A3	3'	TTTGTTTGTTTTAGACAC	84228	A
			TTTGTTT TTTTAGACAC		
			AAACAAA AAAATCTGTG		
			C		
GAM3729	SYNJ2	3'	ACTTTGTTTATACTTACAC	84229	_ G
			ACTTTGTTTAT TTTA AC		
			TGAAACAAATA GAAT TG		
			T G		
GAM3729	TIP120A	3'	CATTTTGAAGCTTTTAGACAC	84230	C TTTA
			CA TTTG TTTTAGACAC		
			GT AAAC AAAATCTGTG		
			A TTCG		
GAM3729	LOC146056	3'	CCACTTTGTTTATGACA	84231	TTTA
			TCACTTTGTTTAT GACA		
			GGTGAAACAAATA CTGT		

GAM3729	LOC146517	3'	ACTTTGTTTATAAGAC	84232	TTT
			ACTTTGTTTAT AGAC		
			TGAAACAAATA TCTG		
			T__		
GAM3729	LOC51339	5'	ATCATTCCCGTTTTTAGACAC	84233	C_ ATT
			ATCA TTTGTTT TTAGACAC		

			TAGT GGGCAAA AATCTGTG	
			AA ____	
GAM3730	CSPG4	3'	TGAATATATTATCCTATTGGC 84236	ATG TA__
			TGAGTATATTAT CCT GC	
			ACTTATATAATA GGA CG	
			____ TAAC	
GAM3730	FCMD	3'	AGTATATCCTTCCTTAGC 84237	ATATG
			AGTATATT CCTTAGC	
			TCATATAG GGAATCG	
			GAA__	
GAM3730	RAP1A	3'	AGTATATTATATATTTTAGC 84238	CC
			AGTATATTATATG TTAGC	
			TCATATAATATAT AATCG	
			AA	
GAM3730	bA430M15.1	3'	TGAATATATACCTTAG 84239	TATAT
			TGAGTATAT GCCTTAG	
			ACTTATATA TGGAATC	

GAM3730	BCDO2	3'	TGAGTATATTGTGTGCTGC 84240	ATA CTTA
			TGAGTATATT TGC GC	
			ACTCATATAA ACG CG	
			CAC A__	
GAM3730	QKI	3'	TGAGTATTTATATGCACT 84241	A _
			TGAGTAT TTATATGC CT	
			ACTCATA AATATACG GA	
			_ T	
GAM3731	ROR2	3'	ACCGTGTTCTGTACAATACTG 84244	GC CTC C
			ACCGTGTT GT CGA ACTG	
			TGGCACAA CA GTT TGAC	
			GA T__ A	
GAM3731	BACH	3'	CACTGTGTAGCATTGATACTG 84245	C T CTCC C
			CAC GTGT GCGT GA ACTG	
			GTG CACA CGTA CT TGAC	
			A T A__ A	
GAM3731	BIKE	3'	GTGTTGCATGTTGATACTG 84246	CTCC C
			GTGTTGCGT GA ACTG	
			CACAACGTA CT TGAC	
			CAA_ A	
GAM3731	EREG	5'	GCTGTGTCCCTCTGACACTG 84247	C C__
			GTTG GTCTC GACACTG	

CGAC CAGGG CTGTGAC
A AGA
GAM3731 FLJ23233 5' CACCGTGCCTTCCGGCGCT 84248 GCGTC ACA
CACCGTGTT TCCG CT
||||||| ||| ||
GTGGCACGG AGGC GA
A____ CGC
GAM3731 FLJ23584 3' GTGTGATCTCCGATGCT 84249 T C CA
GTGT G GTCTCCGA CT
|||| | ||||| ||
CACA C TAGAGGCT GA
____ AC
GAM3731 GOLGA2LY 3' CCAGTGCTGCGTCTTTGGCACT 84250 _ CCGA
G CC GTGTTGCGTCT CACTG
|| ||||| ||||
GG CACGACGCAGA GTGAC
T AACC
GAM3731 KIAA1843 3' ATGTGACATCTCCGACACTG 84251 T
GTGT GCGTCTCCGACACTG
|||| ||||| |||||
TACA TGTAGAGGCTGTGAC
C
GAM3731 MGC3771 5' CATGTTGTTTCCGACGCTG 84252 C C A
CGTGTTG GT TCCGAC CTG
||||| || ||||| |||
GTACAAC CA AGGCTG GAC
_ A C
GAM3731 PTPRT 3' GTGCTGTGCCGCACTG 84253 C CT A
GTGTTG GT CCG CACTG
||||| || ||| |||||
CACGAC CG GGC GTGAC
A _ _
GAM3731 LOC158376 3' CACCGTGCCTCCGGCGCT 84254 TCGCT ACA
CACCGTGT CTCCG CT
||||||| ||||| ||
GTGGCACG GAGGC GA
T____ CGC
GAM3731 LOC169831 3' CCAGCACTGCGTCTCTGGCACT 84255 _TG CGA
G CC G TTGCGTCTC CACTG
|| | ||||| |||||
GG C GACGCAGAG GTGAC
T GT ACC
GAM3731 LOC245727 5' CCAGTGCTGCGTCTCTGACACT 84256 _ C
G CC GTGTTGCGTCTC GACACTG
|| ||||| ||||| |||||
GG CACGACGCAGAG CTGTGAC
T A
GAM3731 LOC257431 3' CCAGTGCTGCGTCTTTGGCACT 84250 _ CCGA
G CC GTGTTGCGTCT CACTG
|| ||||| ||||| |||||

GG CACGACGCAGA GTGAC
T AACC
GAM3731 LOC257447 3' CCAGTGCTGCGTCTCTGACACT 84256 _ C
G CC GTGTTGCGTCTC GACACTG
|| ||||| |||||
GG CACGACGCAGAG CTGTGAC
T A
GAM3731 LOC51198 3' GCATCGTTTCTGACACT 84257 CG CC
GTGTTG TCT GACACT
||||| ||| |||||
CGTAGC AGA CTGTGA
AA _
GAM3732 SLC22A5 3' TTCAATGGAGCATTTATTAT 84260 A CTGAAA
TTCAA TGGAGC ATTAT
||||| ||||| |||||
AAGTT ACCTCG TAATA
_ TAAA_
GAM3732 XPR1 3' AATTAAGCTGAAAATTATA 84261 G C
AAT GAGC TGAAAATTATA
||| ||| |||||
TTA TTCG ACTTTTAATAT
A _
GAM3732 FLJ32743 3' TTCAAAGGAAGAAAATTAT 84262 T CCT
TTCAAA GGAG GAAAATTAT
||||| ||| |||||
AAGTTT CCTT CTTTAAATA
_ _
GAM3732 GLP 3' TTCAAATGGAGTAAATGAA 84263 CC_
TTCAAATGGAG TGAA
||||||| |||
AAGTTTACCTC ACTT
ATTT
GAM3732 GOLGIN-67 3' TTCAAATGAAGTAAATGAA 84264 CC_
TTCAAATGGAG TGAA
||||||| |||
AAGTTTACTTC ACTT
ATTT
GAM3732 KIAA0855 3' TTCAAATGAAGTAAATGAA 84264 CC_
TTCAAATGGAG TGAA
||||||| |||
AAGTTTACTTC ACTT
ATTT
GAM3732 TRIP-Br2 3' TTCAAATGGATTCTTTCCTATA 84265 GC GAAAA
TTCAAATGGA CT TTATA
||||||| || |||||
AAGTTTACCT GA GATAT
AA AAG_
GAM3732 LOC145900 3' TTCAAATGAAGTAAATGAA 84264 CC_
TTCAAATGGAG TGAA
||||||| |||

	AAGTTTACTTC ACTT	
	ATTT	
GAM3732 LOC145988 3'	TTCAAATGAAGTAAATGAA 84264	CC__
	TTCAAATGGAG TGAA	
	AAGTTTACTTC ACTT	
	ATTT	
GAM3732 LOC153577 3'	TCAAGTGGTACAGAAAATTATA 84266	A A CT
	TCAA TGG GC GAAAATTATA	
	AGTT ACC TG CTTTAAATAT	
	C A T_	
GAM3732 LOC154992 5'	AAACGGAGTCTGGCTCTTATA 84267	C AAAA
	AAATGGAG CTG TTATA	
	TTTGCCTC GAC AATAT	
	A CGAG	
GAM3732 LOC196959 3'	TTCAAATGAAGTAAATGAA 84264	CC__
	TTCAAATGGAG TGAA	
	AAGTTTACTTC ACTT	
	ATTT	
GAM3732 LOC197085 3'	TTCAAATGAAGTAAATGAA 84264	CC__
	TTCAAATGGAG TGAA	
	AAGTTTACTTC ACTT	
	ATTT	
GAM3732 LOC197115 3'	TTCAAATGAAGTAAATGAA 84264	CC__
	TTCAAATGGAG TGAA	
	AAGTTTACTTC ACTT	
	ATTT	
GAM3732 LOC197116 3'	TTCAAATGAAGTAAATGAA 84264	CC__
	TTCAAATGGAG TGAA	
	AAGTTTACTTC ACTT	
	ATTT	
GAM3732 LOC197141 3'	TTCAAATGAAGTAAATGAA 84264	CC__
	TTCAAATGGAG TGAA	
	AAGTTTACTTC ACTT	
	ATTT	
GAM3732 LOC220534 3'	TTCAAATGGAGTAAATGAA 84263	CC__
	TTCAAATGGAG TGAA	
	AAGTTTACCTC ACTT	
	ATTT	
GAM3732 LOC220538 3'	TTCAAATGGAGTAAATGAA 84263	CC__
	TTCAAATGGAG TGAA	

		AAGTTTACCTC	ACTT		
		ATTT			
GAM3732	LOC254517 3'	TTCAAATGAAGTAAATGAA	84264	CC__	
		TTCAAATGGAG	TGAA		
		AAGTTTACTTC	ACTT		
		ATTT			
GAM3732	LOC257017 5'	ATGGCACTGAAAATTATA	84268	AGC	
		ATGG	CTGAAAATTATA		
		TACC	GACTTTTAATAT		
		GT_			
GAM3732	LOC257286 3'	TTCAAATGGAGTAAATGAA	84263	CC__	
		TTCAAATGGAG	TGAA		
		AAGTTTACCTC	ACTT		
		ATTT			
GAM3732	LOC51696 3'	AATGGAGCCCATCCATTATA	84269	AAA	
		AATGGAGCCTG	ATTATA		
		TTACCTCGGGT	TAATAT		
		AGG			
GAM3733	F13A1 3'	TTTAACTTTATTTTAAGCT	84272	AC	
		TTTAA	TTATTTTAAGCT		
		AAATT	AATAAAATTCGA		
		GA			
GAM3733	FLJ11017 3'	TTAAGACTTATTTTGGCCAGC	84273	_	AA
		TTAA	ACTTATTTT GCTAGC		
		AATT	TGAATAAAA CGGT		
		C	C_		
GAM3733	MGC861 3'	TTTAACTTTTTTTAGCCA	84274	A	A
		TTTAACTT	TTTTA GCTA		
		AAATTTGAA	AAAAT CGGT		
		A	_		
GAM3733	LOC151643 3'	TCAAACTAATTGAGCTAGCA	84275	T	TATT A
		TT	AACT TT AGCTAGCA		
		AG	TTTGA AA TCGATCGT		
		T	TT_ C		
GAM3733	LOC152190 5'	TTTAACTTATCTTCAAGC	84276	_	
		TTTAACTTATTT	TAAGC		
		AAATTTGAATAGA	GTT		
		A			
GAM3734	DCK 3'	TAAATTATCATCTTTGAAT	84279		
		TAAATTATCATTTTTGAAT			

ATTTAATAGTAGAAACTTA

GAM3734 SFTP2 3' TGATTATCTGGGTGAATGTATT 84280 A ATTTT
A ATTATC TGAATGTATT
||||| |||||
A TAATAG ACTTACATAA
C ACCC_

GAM3734 WNT5A 3' TAAATTATCATTTTGAA 84281 T
TAAATTATCATTTT GAA
||||||| |||
ATTTAATAGTAAAA CTT

GAM3734 ZNF195 3' TAAGCTATCATTTTGAACA 84282 A
TAA TTATCATTTTGAATG
||| |||||
ATT GATAGTAAAACTTGT
C

GAM3734 FLJ10525 3' TAAATTACTAATGAATGTATT 84283 CATTTT
TAAATTAT TGAATGTATT
||||| |||||
ATTTAATG ACTTACATAA
ATT_

GAM3734 FLJ14054 5' TAAATTATCCTTTTGAA 84284 A
TAAATTATC TTTTGAA
||||| |||||
ATTTAATAG AAAAATT
G

GAM3734 HSAJ1454 3' CTATCATTTTGTAAATATT 84285 AAT
TTATCATTTTGT GTATT
||||||| |||
GATAGTAAAAAC TATAA
ATT

GAM3734 ZAK 3' AATTATCATTTTGAATGT 84286 T
AATTATCATTTT GAATGT
||||||| |||||
TTAATAGTAAAA CTTACA

GAM3735 FLJ20758 5' CATTAAACACGGTATATGAG 84289 AT_
TATTAAACA TATATGAG
||||| |||||
GTAATTTGT ATATACTC
GCC

GAM3735 KIAA0937 3' TATTAAACATTTATTTGAG 84290 A A
TATTAAACA TTAT TGAG
||||| ||| |||
ATAATTTGT AATA ACTC
A A

GAM3736 BHLHB3 3' TGGGAATAGATGCACTTGA 66796 AAATAC GT
TGGGAATA TACT TGA
||||| ||| |||

		ACCCTTAT	GTGA	ACT		
		CTAC__	__			
GAM3736	ITK	3'	TGGGAATAATAATATTACCTCA	66797	_	C GT_
		TG	TGGGAATAA AATA TACT	TG		
			ACCCTTATT TTAT ATGG	AC		
			A A AGT			
GAM3736	MPV17	3'	TGGGAATAAGACTATTATCAAG	66798	AAT	C TG
			TGGGAATAA ACTA TGT	AG		
			ACCCTTATT TGAT ATA	TC		
			C__ A GT			
GAM3736	MSR1	3'	TGGGAATAAAAAATGCTGA	66799	TACTAC	
			TGGGAATAAAAA	TGTTGA		
			ACCCTTATTTT	ACGACT		
			T_____			
GAM3736	RNMT	3'	TGGGAATAATGGTGCTGA	66800	AATACTAC	
			TGGGAATAA	TGTTGA		
			ACCCTTATT	ACGACT		
			ACC_____			
GAM3736	SCP2	3'	TGGGAAGAAAATACTGTTTCTG	66801	T	ACTG
			TGGGAA AAAATACT	TTG		
			ACCCTT TTTTATGA	GAC		
			C CAAA			
GAM3736	SFRP4	3'	TGGGTATAAAATACTTGA	66802	A	ACTGT
			TGGG ATAAAATACT	TGA		
			ACCC TATTTTATGA	ACT		
			A _____			
GAM3736	DKFZP564K0822	3'	TGGGAATACAAAATTGTTGAG	66803	AAATACTAC	
			TGGGAATA	TGTTGAG		
			ACCCTTAT	ACAAC TC		
			GTTTTA__			
GAM3736	KIAA0564	3'	TGGGAATAAGGTACATTTTG	66804	AA	TACTG
			TGGGAATAA TAC	TTG		
			ACCCTTATT ATG	AAC		
			CC TAA__			
GAM3736	KIAA0769	3'	TGGGAATAAAATAATGCCG	66805	CTAC	
			TGGGAATAAAATA	TGTTG		
			ACCCTTATTTTAT	ACGGC		
			T_____			
GAM3736	KIAA1163	3'	TGGGAATCAAATACTAACCAAG	66806	A	CTG TG
			TGGGAAT AAATACTA	T AG		

		ACCCTTA TTTATGAT G TC	
		G T__GT	
GAM3736 KIAA1332	3'	GGAATAAAATCCTTTGTTG 66807	A AC
		GGAATAAAAT CT TGTTG	
		CCTTATTTTA GG ACAAC	
		_ AA	
GAM3736 SFRS11	3'	TGGGAATAAATTATTACT 66808	A C
		TGGGAATAAA TA TACT	
		ACCCTTATTT AT ATGA	
		A A	
GAM3736 ZNF387	3'	TGGGAGTGGAACTTACTGTTGAG 66809	ATAAAATAC
		TGGGA TACTGTTGAG	
		ACCCT ATGACAACTC	
		CACCTTA__	
GAM3736 LOC138639	3'	TGGGAATAAGGCTTGGTGTGTT 66810	AATACTAC_
		GAG TGGAATAA TGTTGAG	
		ACCCTTATT ACAACTC	
		CCGAACCAC	
GAM3736 LOC147299	3'	TGGAAATAAAATGTTG 66811	TACTAC
		TGGGAATAAAA TGTTG	
		ACCTTTATTTT ACAAC	

GAM3736 LOC90019	5'	CGGGAATAAGCAGCTGTTGAG 66812	AATACTA
		TGGGAATAA CTGTTGAG	
		GCCCTTATT GACAACTC	
		CGTC__	
GAM3737 F2RL3	3'	TGGGCACCTCCCCAGTACAG 84294	A GGA
		TG GCACCTCCCCAG AG	
		AC CGTGGAGGGGTC TC	
		C ATG	
GAM3737 GALK1	3'	TGAGCACCCGATATGGAAGAT 84295	CCCCAG
		G TGAGCACCT GGAAGATG	
		ACTCGTGGG CCTTCTAC	
		CCTATA	
GAM3737 GPR56	3'	GAGGAGAACCCAGGGAAGATG 84296	CACCT
		GAG CCCAGGGAAGATG	
		CTC GGGGTCCCTTCTAC	
		CTCTT	
GAM3737 TBX3	3'	TGAACACCTCCCCGCCTGG 84297	AG__
		TGAGCACCTCCCC GG	

ACTTGTGGAGGGG CC
 CGGA
 GAM3737 C6orf9 3' CCAGTTCCCAGGGAAGGTGA 84298 TC__ A
 CC CCCAGGGAAG TGA
 || ||||| |||
 GG GGGTCCCTTC ACT
 TCAA C
 GAM3737 Cab45 3' TGAGCACCTCCTCGGGCTCCAG 84299 _____
 G TGAGCACCTCC CCAGG
 ||||| |||
 ACTCGTGGAGG GGTCC
 AGCCCGA
 GAM3737 FLJ00058 5' CACCTCCCTGGGGTCCGGGAGA 84300 CA A____
 TG CACCTCCC GGG AGATG
 ||||| || |||
 GTGGAGGG CCC TCTAC
 AC AGGCCC
 GAM3737 FLJ10829 3' TGAGCACCTTCAGCCAGAG 84301 _C_
 TGAGCACCT C CCAGGG
 ||||| | |||
 ACTCGTGGA G GGTCTC
 A TC
 GAM3737 FLJ10970 3' TGAGACAAGGGAAGAT 84302 _ CCTCCCC
 TGAG CA AGGGAAGAT
 ||| || |||||
 ACTC GT TCCCTTCTA
 T _____
 GAM3737 FLJ20847 5' GCCAAACCCCAGGGGAGATG 84303 ACCT A
 GC CCCCAGGG AGATG
 || ||||| |||
 CG GGGGTCCC TCTAC
 GTTT C
 GAM3737 FLJ21324 5' TGAGGCTGGAGCCAGGGAAGGT 84304 CACCTCC A
 G TGAG CCAGGGAAG TG
 ||| ||||| ||
 ACTC GGTCCCTTC AC
 CGACCTC C
 GAM3737 H17 3' TGGCACAGTACTGGGGAAGATG 84305 A CTCCCCA
 TG GCAC GGGAAGATG
 || ||| |||||
 AC CGTG CCCTTCTAC
 _ TCATGAC
 GAM3737 KIAA0179 3' GCAGCCTCTAGGGAAGATG 84306 _ CCC
 GCA CCTC AGGGAAGATG
 ||| ||| |||||
 CGT GGAG TCCCTTCTAC
 C A__
 GAM3737 KIAA0377 3' TGAACATTTCCCCAGAAAAGTG 84307 CC GG A
 A TGAGCA TCCCCAG AAG TGA
 ||||| ||||| ||| |||

ACTTGT AGGGGTC TTC ACT
 AA TT _
 GAM3737 KIAA0449 3' TGAGCACCTCTCGCAGGG 84308 CC_
 TGAGCACCTC CAGGG
 ||||| ||||
 ACTCGTGGAG GTCCC
 AGC
 GAM3737 KIAA0628 3' GAGCACAGGGAAGATG 84309 CTCCCC
 GAGCAC AGGGAAGATG
 |||| |||||
 CTCGTG TCCCTTCTAC

 GAM3737 KIAA1036 3' TGGCACCTCCCAAGGTGA 84310 A C _
 TG GCACCTCCC AGG GA
 || ||||| || ||
 AC CGTGGAGGG TCC CT
 _ T A
 GAM3737 MGC3265 3' AAGCACCTTGTGAAGATGA 84311 CCCCAGG
 GAGCACCT GAAGATGA
 ||||| |||||
 TTCGTGGA CTTCTACT
 ACA____
 GAM3737 OR7E120 3' GCAGCCTTTCTCAGGGAAGATG 84312 _ CCC_
 A GCA CCT CAGGGAAGATGA
 ||| ||| |||||
 CGT GGA GTCCCTTCTACT
 C AAGA
 GAM3737 PTPN21 3' TGAGCACCTTTCCCAGGTTAGA 84313 C_ GA
 TGAGCACCT CCCAGG AGA
 ||||| ||||| |||
 ACTCGTGGA GGGTCC TCT
 AA AA
 GAM3737 TGOLN2 3' GAGCCCGGGCCCCAGGGA 84314 A T__
 GAGC CC CCCCAGGGA
 |||| || |||||
 CTCG GG GGGGTCCCT
 _ CCC
 GAM3737 LOC142972 5' GCACCTTTCCCAGGGAGATGA 84315 C_ A
 GCACCT CCCAGGGA GATGA
 |||| ||||| ||||
 CGTGGA GGGTCCCT CTACT
 AA _
 GAM3737 LOC153196 3' TGAGGGCCTGGGAGGAAGATG 84316 CA CCCC
 TGAG CCT GGGGAAGATG
 ||| ||| |||||
 ACTC GGA TCCTTCTAC
 CC CCC_
 GAM3737 LOC165229 5' TGAGAACCTCCCAAAGATG 84317 C CAGG
 TGAG ACCTCCC GAAGATG
 ||| ||||| |||||

ACTC TGGAGGG TTTCTAC
 T _____
 GAM3737 LOC200812 3' GCACCCTTTCTCGGGGAAGATG 84318 CCCC_____A
 A GCACCT GGAAGATGA
 ||||| |||||
 CGTGGG CCCTTCTACT
 AAAGAGC
 GAM3737 LOC255696 5' TGGCTGCCTTCCAGAGAAGGTG 84319 A A_ CC A
 TG GC CCT CCAGGGAAG TG
 || || || ||||| ||
 AC CG GGA GGTCTCTTC AC
 _ AC A_ C
 GAM3737 LOC91012 5' TGAACACCTTTTCAAGGA 84320 CCC
 TGAGCACCT CAGGGA
 ||||| |||||
 ACTTGTGGA GTTCCT
 AAA
 GAM3738 AARS 5' TCCCTCAGAGTCCCCCGCC 84323 GCG _C
 TCC CTCGG G CCCCCGCC
 || ||||| |||||
 AGG GAGTC C GGGGGCGG
 _ T A
 GAM3738 ABCA2 5' TCCGCGCTGGCTCCGC 84324 CG CCC
 TCCGCGCT GGC CCGC
 ||||| || |||||
 AGGCGCGA CCG GGCG
 _ A_
 GAM3738 ABCB9 3' TCCACGCTCCCTACCCGCC 84325 GGG C_
 TCCGCGCTC CC CCGGCC
 ||||| || |||||
 AGGTGCGAG GG GGGCGG
 _ AT
 GAM3738 ABCG1 3' TCCATGCTCGGACTCTCTGCC 84326 C CCCCC
 TCCG GCTCGGGC GCC
 ||||| ||||| ||
 AGGT CGAGCCTG CGG
 A AGAGA
 GAM3738 ADAM10 5' CCGCGCCCCTACCTCCCGCC 84327 GG C
 CCGCGCTC GCC CCGGCC
 ||||| || |||||
 GGCGCGGG TGG GGGCGG
 GA A
 GAM3738 ADAMTS8 5' CCCGCGCAGCCGCCTCCTGCC 84328 TCG _ _ _
 TCCGCGC GGCC CC CC GCC
 ||||| ||||| || |||||
 GGGCGCG TCGG GG GG CGG
 _ C A A
 GAM3738 AGRN 3' TCCACGCTGCCACCTCGCC 84329 CGG _ C
 TCCGCGCT GCC CC CGCC
 ||||| ||||| || |||||

AGGTGCGA CGG GG GCGG
 ____ T A
 GAM3738 AKR1C4 3' TCCACACCACAGGGCCTTCTGC 84330 C__ CCCC
 TCCGCGCT GGGCC GC
 ||||| ||| ||
 AGGTGTGG CCCGG CG
 TGT AAGA
 GAM3738 AQP2 3' TCCGGCAGCCTCCTCCCCGCC 84331 C TCGGG _
 TCCG GC CC CCCC GCC
 ||| || || |||||
 AGGC CG GG GGGGCGG
 _ TCGGA A
 GAM3738 ATP10C 5' TCCGCCGCTCAGCCCCGCC 84332 _ G C
 TCCGC GCTCG GCCC CC
 |||| |||| ||| ||
 AGGCG CGAGT CGGG GG
 G G C
 GAM3738 BAZ1B 5' CCCAGCAGCCCCCGCC 84333 C TCG
 TCCG GC GGCCCCCGCC
 ||| || |||||
 GGGT CG TCGGGGGGCGG
 _ _
 GAM3738 BRF1 3' CCCGCGAGGCCCCCTGCC 84334 CTC C
 TCCGCG GGGCCCCC GCC
 |||| | ||||| |||
 GGGCGC TCCGGGGG CGG
 ____ A
 GAM3738 CAPN10 3' TCCTGCTGCCCCCGCC 84335 GC CGG
 TCC GCT GCCCCCGCC
 ||| || |||||
 AGG CGA CGGGGGGCGG
 A_ _
 GAM3738 CASP2 5' TCGGCGCCGCCATTTCCCGC 84337 C CGG C__
 TC GCGCT GCC CCCGC
 || |||| || ||||
 AG CGCGG CGG GGGCG
 C _ TAAA
 GAM3738 CASP2 5' CCCGCGCTCGGCGCCGCC 84336 _ _
 TCCGCGCTCGG GCC CC
 ||||| ||| ||
 GGGCGCGAGCC CGG GG
 G C
 GAM3738 CASP2 5' CCCGCGCTCGGCGCCGCC 84336 _ _
 TCCGCGCTCGG GCC CC
 ||||| ||| ||
 GGGCGCGAGCC CGG GG
 G C
 GAM3738 CASP2 5' TCGGCGCCGCCATTTCCCGC 84337 C CGG C__
 TC GCGCT GCC CCCGC
 || |||| || ||||

			AG CGCGG CGG GGGCG		
			C ____ TAAA		
GAM3738	CASP7	5'	TCCGCTTCGGGCCCGC 84338	GC	CCC
			TCCGC TCGGGCCC GC		
			AGGCG AGCCCGGG CG		
			A_ ____		
GAM3738	CCND1	5'	TCCGCGCTCGGCTCTCGC 84339	G	CCCC
			TCCGCGCTCGG C CGC		
			AGGCGCGAGCC G GCG		
			AGA		
GAM3738	CDKN2D	5'	CCTGCAAAGCCCCCGCC 84340	GC	TC
			CC GC GGGCCCCCGCC		
			GG CG TTCGGGGGGCGG		
			A_ T_		
GAM3738	CDS1	5'	CCGCGCAGGCCCTCCCGCC 84341	TC	G _
			CCGCGC GG CCC CCGCC		
			GGCGCG CC GGG GGGCGG		
			T_ G A		
GAM3738	CHRNA5	5'	TCCGCGCCACAGCTCCCGCC 84342	CG	CC
			TCCGCGCT GGC CCGCC		
			AGGCGCGG TCG GGGCGG		
			TG A_		
GAM3738	CLCN7	3'	TCCGCGCCTGCCGCCTGCC 84343	T	GG C C
			TCCGCGC C GCC CC GCC		
			AGGCGCG G CGG GG CGG		
			A C A		
GAM3738	CLTB	5'	TCCGCCGGAGCCTCCGC 84344	GCT	_ CC
			TCCGC CGG GCC CCGC		
			AGGCG GCC CGG GGCG		
			____ T A_		
GAM3738	CLTB	5'	TCCGCCGGAGCCTCCGC 84344	GCT	_ CC
			TCCGC CGG GCC CCGC		
			AGGCG GCC CGG GGCG		
			____ T A_		
GAM3738	CNN1	3'	CCCCCAATGGGCCCCCGCC 84345	G	CTC
			TCC CG GGGCCCCCGCC		
			GGG GT CCCGGGGGGCGG		
			G TA_		
GAM3738	CTSZ	5'	TCCCGCTCCGGATCCCGC 84347	G	G CCC
			TCC CGCTC GG CCGC		

			AGG GCGAG CC GGGCG		
			— G TA—		
GAM3738	CTSZ	5'	TCCCGCTCTGGATCCCGCC 84348	G	G CCC
			TCC CGCTC GG CCCGCC		
			AGG GCGAG CC GGGCGG		
			— A TA—		
GAM3738	CTSZ	5'	CCCGCGCCGGCTCCCGC 84346	CG	CC
			TCCGCGCT GGC CCCGC		
			GGGCGCGG CCG GGGCG		
			— A—		
GAM3738	CXX1	5'	TCCATCGCTGCTCCTCGC 84349	—	CGG C C
			TCCG CGCT GC CC CGC		
			AGGT GCGA CG GG GCG		
			A — A A		
GAM3738	CYFIP2	5'	CCGCGCTCGGCCCCGCC 84350	GCC	
			CCGCGCTCGG CCCC GCC		
			GGCGCGAGCC GGGGCGG		
			—		
GAM3738	DDB1	3'	TCAGCAAAGGGGCCCCCTGCC 84351	C	CTC C
			TC GCG GGGCCCCC GCC		
			AG CGT CCCGGGGG CGG		
			T TTC A		
GAM3738	DDX26	5'	TCCCCGTCGTACCCCGCC 84352	G C	GGC
			TCC CG TCG CCCC GCC		
			AGG GC AGC GGGGGCGG		
			G _ AT—		
GAM3738	DHCR24	5'	TCCGCGCCTGGCCCGC 84353	CG	CCC
			TCCGCGCT GGCC GC		
			AGGCGCGG CCGGG CG		
			A— —		
GAM3738	DSCR1	5'	TCCGCCTCGGCCGCCCGCC 84354	G	GC—
			TCCGC CTCGG CCCC GCC		
			AGGCG GAGCC GGGGGCGG		
			— GGC		
GAM3738	EFNA3	5'	CCCGCGCTCCCGGCTTCTCCGC 84355	G—	CCC—
			TCCGCGCTC GGC CCGC		
			GGGCGCGAG CCG GGCG		
			GG AAGA		
GAM3738	EHD4	5'	TCCACGCTCGGATGGGACCCTG 84356	CC—	C
	C		TCCGCGCTCGGG CCC GC		

AGGTGCGAGCCT GGG CG
 ACCCT A
 GAM3738 EN1 5' CCGCGCCGGCCCCCGCC 84357 T GC
 CCGCGC CGG CCCCCGCC
 ||||| ||| |||||
 GGCGCG GCC GGGGGCGG

 — —
 GAM3738 ENO1 5' CCCGCGCCGACTTCCTGCC 84358 CG CC C
 TCCGCGCT GGC CC GCC
 ||||| ||| || |||
 GGGCGCGG CTG GG CGG

 — AA A
 GAM3738 EP300 5' GCGCCCCGGGCCCCCTGCC 84359 _ C
 GCGCTC GGGCCCCC GCC
 ||||| ||||| |||
 CGCGGG CCCGGGGG CGG
 G A
 GAM3738 EPHA2 3' CCCTGGCGGGGCCCCCTGCC 84360 GC TC C
 TCC GC GGGCCCCC GCC
 ||| || ||||| |||
 GGG CG CCCGGGGG CGG
 AC C_ A
 GAM3738 FEN1 5' TCCCCGCAGGCCCTGC 84361 G TC CC
 TCC CGC GGGCCCC GC
 ||| ||| ||||| ||
 AGG GCG TCCGGGG CG
 G _ A_
 GAM3738 FKBP10 3' CCTGGCCAGGCTCCCTGCC 84362 GC T C C
 CC GC CGGGC CCC GCC
 || || ||||| ||| |||
 GG CG GTCCG GGG CGG
 AC _ A A
 GAM3738 FOXF1 5' CCGCGCCGCCTCCCCCGCC 84363 T GGC
 CCGCGC CG CCCCCGCC
 ||||| || |||||
 GGCGCG GC GGGGGCGG
 _ GGA
 GAM3738 FZD10 5' TCCGCGCCCGGCGTCCGCC 84364 G CCC
 TCCGCGCTCGG C CCGCC
 ||||| ||| |||||
 AGGCGCGGGCC G GGCGG
 _ CA_
 GAM3738 FZD2 5' TCCTTGCGCCCCCCCCCGCC 84365 _ CGGG
 TCC GCGCT CCCCCCGCC
 ||| ||||| |||||
 AGG CGCGG GGGGGGCGG
 AAC _
 GAM3738 GNB1 5' CGCGCTCGGGCCGCGC 84366 CCC
 CGCGCTCGGGCC CGC
 ||||| ||| |||

			GCGCGAGCCCGG GCG		
			C__		
GAM3738	HCFC1	3'	CCGCCGCGGGGCTCCTTGCC 84367	_ TC	C CC
			CCGC GC GGGC CC GCC		
			GGCG CG CCCG GG CGG		
			G C_ A AA		
GAM3738	HDGF	5'	TCCGCGCCGGGCGGGAAGC 84368	T	CCCC_
			TCCGCGC CGGGCC GC		
			AGGCGCG GCCCGG CG		
			_ CCCTT		
GAM3738	HIRA	5'	CCCGCGCCCCCTCCGCC 84369	CGGG	_
			TCCGCGCT CCCC CCGCC		
			GGGCGCGG GGGG GGCGG		
			_____ A		
GAM3738	HIRA	5'	CCCGCGCTCGGCCGC 84370	GCCCC	
			TCCGCGCTCGG CCGC		
			GGGCGCGAGCC GGCG		

GAM3738	HLX1	3'	TCCACGCTGCGTCTCCTGCC 84371	_ GGCCC	C
			TCCGCGCT CG CC GCC		
			AGGTGCGA GC GG CGG		
			C AGA__ A		
GAM3738	HSF4	5'	GCGCTCGGGCCCGGCCGC 84372	C_	
			GCGCTCGGGCCC CCGC		
			CGCGAGCCCGGG GGCG		
			CC		
GAM3738	IFNGR2	5'	CCCGCGCCCCCGCCCCCGCC 84373	GG	C
			TCCGCGCTC GCCCCC GCC		
			GGGCGCGGG CGGGGG CGG		
			GG _		
GAM3738	JJAZ1	5'	TCCTGCCTCCTCCCCCGCC 84374	_ G	GGG
			TCC GC CTC CCCCCCGCC		
			AGG CG GAG GGGGGGCGG		
			A _ GA_		
GAM3738	KAL1	5'	TCCGGCCGACCTCCTCGCC 84375	C T	_ _
			TCCG GC CGGGCCC CC CGCC		
			AGGC CG GCCTGGG GG GCGG		
			_ _ A A		
GAM3738	KCNH3	5'	TCCGCGCCGGGGGAGGGCGCC 84376	T	CCCCC_
			TCCGCGC CGGG CGCC		

			AGGCGCG GCCC GCGG	
			_ CCTCCC	
GAM3738 KCNK3	3'	CCCAGCAGGGGTCCCCCGCC	84377	C TC C
		TCCG GC GGG CCCCCGCC		
		GGGT CG CCC GGGGGCGG		
		_ TC A		
GAM3738 LASS2	5'	CCCGCGCCCCGCCCTCGCC	84378	GGC C
		TCCGCGCTCG CCC CGCC		
		GGGCGCGGGC GGG GCGG		
		_____ A		
GAM3738 LHX5	5'	CCTGCCGGGCCCTCCGC	84379	GC T C
		CC GC CGGGCCC CCGC		
		GG CG GCCCGGG GGCG		
		A_ _ A		
GAM3738 LMO4	5'	CCCGCGCTCCTCCGC	84380	CGGG C
		TCCGCGCT CC CCGC		
		GGGCGCGA GG GGGCG		
		_____ A		
GAM3738 LTB	3'	CCCGTAGGCGCCCCCGCC	84381	CGCTC _
		TCCG GG GCCCCCCGCC		
		GGGC CC CGGGGGGCGG		
		AT___ G		
GAM3738 MAP7	5'	TCCCGCCGGCCCCCGC	84382	G T GC
		TCC CGC CGG CCCCCGC		
		AGG GCG GCC GGGGGCG		

GAM3738 MBNL	5'	GCGCGGCCCTCCCCCGCC	84383	TCG _____
		GCGC GGCCCC CCGCC		
		CGCG CCGGGG GGCGG		
		_____ AGGG		
GAM3738 MCM4	5'	TCCGCGCCACGCCCTCCCCGCC	84384	T G _
		TCCGCGC CG GCC CCGCC		
		AGGCGCG GT CGGG GGGCGG		
		_ G AG		
GAM3738 MGAT2	5'	CCTGCGCTCCACACATCCTCGC	84385	_ _ G CC _
C		CC GCGCTC G GC CC CGCC		
		GG CGCGAG T TG GG GCGG		
		A G G TA A		
GAM3738 MKI67	5'	CCGCGCTCACCTCCGCC	84386	GG CC
		CCGCGCTC GCC CCGCC		

		GGCGCGAG TGG GGCGG	
		— A—	
GAM3738	MMP2	5' CCCGCGCCCCAGCCCCGCC 84387	G C
		TCCGCGCTC GGCCCCC GCC	
		GGGCGCGGG TCGGGGG CGG	
		G —	
GAM3738	MYO10	5' CCCGCGGGGCTCCCCTGC 84388	CTC _ C
		TCCGCG GGGC CCCC GC	
		GGGCGC CCGG GGGG CG	
		— A A	
GAM3738	MYO1E	5' TCCGCCTCGCTCCCCTGCC 84389	G GG CC
		TCCGC CTCG CCCC GCC	
		AGGCG GAGC GGGG CGG	
		_ GA A—	
GAM3738	NFATC1	5' CCGCGCTCTGCCTCCTGCC 84390	GG C C
		CCGCGCTC GCC CC GCC	
		GGCGCGAG CGG GG CGG	
		A— A A	
GAM3738	NFRKB	5' TCCGCGCCCCTCCCGCC 84391	TCGGG _
		TCCGCGC CCC CCGGCC	
		AGGCGCG GGG GGGCGG	
		— A	
GAM3738	NRGN	5' CCCGCGCTCGGCTCCGC 84392	G CCC
		TCCGCGCTCGG C CCGC	
		GGGCGCGAGCC G GGCG	
		_ A—	
GAM3738	PACE4	5' TCCGCGCCGGGGAAGCGCC 84393	T CCCCC
		TCCGCGC CGGG CGCC	
		AGGCGCG GCCC GCGG	
		_ CTTC—	
GAM3738	PACE4	5' TCCGCGCCGGGGAAGCGCC 84393	T CCCCC
		TCCGCGC CGGG CGCC	
		AGGCGCG GCCC GCGG	
		_ CTTC—	
GAM3738	PACE4	5' TCCGCGCCGGGGAAGCGCC 84393	T CCCCC
		TCCGCGC CGGG CGCC	
		AGGCGCG GCCC GCGG	
		_ CTTC—	
GAM3738	PACE4	5' TCCGCGCCGGGGAAGCGCC 84393	T CCCCC
		TCCGCGC CGGG CGCC	

			AGGCGCG GCCC GCGG		
			_ CTTC_		
GAM3738	PACE4	5'	TCCGCGCCGGGGAAGCGCC 84393	T	CCCCC
			TCCGCGC CGGG CGCC		
			AGGCGCG GCCC GCGG		
			_ CTTC_		
GAM3738	PACE4	5'	TCCGCGCCGGGGAAGCGCC 84393	T	CCCCC
			TCCGCGC CGGG CGCC		
			AGGCGCG GCCC GCGG		
			_ CTTC_		
GAM3738	PAPPA	5'	TCCGACGTTCCCCCGCC 84394	CGCT	GG
			TCCG CG CCCCCCGCC		
			AGGC GC GGGGGGCGG		
			T__ AA		
GAM3738	PHLDA3	5'	TCCGCGCCCACCGCCCCGC 84395	GG	_
			TCCGCGCTC GCC CCCCCG		
			AGGCGCGGG TGG GGGGCG		
			_ C		
GAM3738	PITX1	3'	TCCGCGCCCGCGCCCTTCCCCG 84396	G	__
	C		TCCGCGCTCG GCC CCCGC		
			AGGCGCGGGC CGGG GGGCG		
			G AAG		
GAM3738	PPFIA3	3'	CGGCGCGAGCTCCCCCGCC 84397	C T	_
			CG GC CGGGC CCCCCGCC		
			GC CG GCTCG GGGGGCGG		
			_ C A		
GAM3738	PTBP1	3'	CCGGCCAGGCCCCCTGCC 84398	C T	C
			CCG GC CGGGCCCCC GCC		
			GGC CG GTCCGGGGG CGG		
			_ _ A		
GAM3738	PTBP1	3'	CCGGCCAGGCCCCCTGCC 84398	C T	C
			CCG GC CGGGCCCCC GCC		
			GGC CG GTCCGGGGG CGG		
			_ _ A		
GAM3738	PTPN11	5'	TCCGCCCCCGCCCTTCGCC 84400	G	GG CC
			TCCGC CTC GCC CGCC		
			AGGCG GGG CGGG GCGG		
			G _ AA		
GAM3738	PTPN11	5'	TCCTTGCTCAGGCTCCGC 84399	GC	CCC
			TCC GCTCGGGC CCGC		

			AGG CGAGTCCG GGCG		
			AA A__		
GAM3738	PTPN11	5'	TCCGCCCCCGCCCTTCGCC 84400	G GG CC	
			TCCGC CTC GCCC CGCC		
			AGGCG GGG CGGG GCGG		
			G _ AA		
GAM3738	PTPN11	5'	TCCTTGCTCAGGCTCCGC 84399	GC CCC	
			TCC GCTCGGGC CCGC		
			AGG CGAGTCCG GGCG		
			AA A__		
GAM3738	PTPRJ	5'	CCCGCGCTCGTCCCGC 84401	GGCCC	
			TCCGCGCTCG CCCGC		
			GGGCGCGAGC GGGCG		
			A__		
GAM3738	ROBO1	5'	CGCCCTCGGCCCTCGCC 84402	G G C	
			CGC CTCGG CCCC CGCC		
			GCG GAGCC GGGG GCGG		
			G _ A		
GAM3738	ROCK2	5'	TCCAAGGCGGTCCCCCGCC 84403	CGCT GC	
			TCCG CGG CCCCCGCC		
			AGGT GCC GGGGGCGG		
			TCC_ A_		
GAM3738	SIAH1	5'	TCCGTCGCCAACCCCCGCC 84404	_ T GC	
			TCCG CGC CGG CCCCCGCC		
			AGGC GCG GTT GGGGGCGG		
			A _ _		
GAM3738	SIRT3	5'	TCCGCCTCCCACCCCCGCC 84405	G GG C	
			TCCGC CTC GCCCC GCC		
			AGGCG GAG TGGGGG CGG		
			_ GG _		
GAM3738	SLC1A2	5'	CCCGCGCTCCCCTCCGCC 84406	GGG C	
			TCCGCGCTC CCC CCGCC		
			GGGCGCGAG GGG GCGG		
			_ A		
GAM3738	SMARCC2	5'	TCCGGCTCGGGCCCCGCC 84407	C _	
			TCCG GCTCGGGCCCC CC		
			AGGC CGAGCCCGGGG GG		
			_ C		
GAM3738	SMARCC2	5'	TCCGGCTCGGGCCCCGCC 84407	C _	
			TCCG GCTCGGGCCCC CC		

			AGGC CGAGCCCGGGG GG		
			— C		
GAM3738	SOLH	5'	GCTGCCCGGACGGCCTCCCGC 84408	—	— —
			GC GCTCGGGC CC CCCGC		
			CG CGGGCCTG GG GGGCG		
			A CC A		
GAM3738	SREBF1	5'	TCCTGCTGCAGGCCCCCTGCC 84409	GC	— C
			TCC GCT CGGGCCCCC GCC		
			AGG CGA GTCCGGGGG CGG		
			A_ C A		
GAM3738	TNFRSF10C	3'	TCCAGCGCCCCCGC 84410	C	TCGG
			TCCG GC GCCCCCCGC		
			AGGT CG CGGGGGGCG		
			— —		
GAM3738	TRPM7	5'	CCCGCGCCCGCCTCCGCC 84411	GGC	C
			TCCGCGCTCG CC CCGCC		
			GGGCGCGGGC GG GGCGG		
			— A		
GAM3738	UGCG	5'	CCCGCGCTCCGTTTCGCC 84412	G	CCCCC
			TCCGCGCTC GG CGCC		
			GGGCGCGAG CC GCGG		
			G AA_		
GAM3738	UMPK	5'	CCCGCGTCGGACTCCCTCCGC 84413	C	— —
			TCCGCG TCGGGC CCC CCGC		
			GGGCGC AGCCTG GGG GGCG		
			— A A		
GAM3738	VIPR2	3'	CCCGAACCGTGGGCCTCCCGCC 84414	C	C_ C
			TCCG GCT GGGCC CCCGCC		
			GGGC TGG CCCGG GGGCGG		
			T CA A		
GAM3738	WNT11	5'	CCGCGCCGAAGTCCTCCGCC 84415	CG	C C
			CCGCGCT GG CC CCGCC		
			GGCGCGG TC GG GGCGG		
			CT A A		
GAM3738	WNT2	5'	CCGCGCCCCCGCCCCCGC 84416	GG	
			CCGCGCTC GCCCCCCGC		
			GGCGCGGG CGGGGGGCG		
			GG		
GAM3738	WNT6	3'	TCCTCTCAAGCCCCTCGCC 84417	GCG	C
			TCC CTCGGGCCCC CGCC		

AGG GAGTTCGGGG GCGG
 A__ A
 GAM3738 WNT7A 5' TCCGCGCCTGAGCCTCGCC 84418 TC CCC
 TCCGCGC GGGCC CGCC
 ||||| |||| |||
 AGGCGCG CTCGG GCGG
 GA A__
 GAM3738 WRN 5' TCCACCGCCCCGCCCCCGCC 84419 _ GG
 TCCGC GCTC GCCCCCGCC
 |||| ||| |||||
 AGGTG CGGG CGGGGGGCGG
 G _
 GAM3738 XRCC3 5' TCCGCACTCCTCTTCCCGCC 84420 GGGCCC
 TCCGCGCTC CCGCC
 ||||| ||||
 AGGCGTGAG GGGCGG
 GAGAA_
 GAM3738 AAK1 5' CCGCGCTCGGCTCCCGCC 84421 G CC
 CCGCGCTCGG C CCGCC
 ||||| ||||
 GGCGCGAGCC G GGGCGG
 _ A_
 GAM3738 AHCYL1 5' CCCGCGCCGCCACCTCCGC 45043 CGG _ _
 TCCGCGCT GCC CC CCGC
 ||||| ||| ||||
 GGGCGCGG CGG GG GGCG
 _ T A
 GAM3738 AKAP9 5' TCCGGGGCTCCCCCGC 84422 CGCTC _
 TCCG GGGC CCCCCGC
 ||| ||| |||||
 AGGC CCG GGGGGCG
 _ A
 GAM3738 ARHU 5' TCCGCGCTCCGGCGGCGCC 84423 G CCCC
 TCCGCGCTC GGC CGCC
 ||||| ||| |||
 AGGCGCGAG CCG GCGG
 G CC_
 GAM3738 ASB10 3' CCTGCGGAGCTGGGCCTCCTGC 84424 _ _ C C C
 CC GC GCT GGGCC CC GC
 || || ||||| |||
 GG CG CGA CCGG GG CG
 A CCT _ A A
 GAM3738 BC022889 5' CCCGCCGCCGCCCGC 84425 G CGG
 CC CGCT GCCCCCCGC
 || ||| |||||
 GG GCGG CGGGGGGCG
 _ _
 GAM3738 C13orf1 5' TCCGTCTCCTGCCCGCC 84426 CG GG C
 TCCG CTC GCCCCG GCC
 ||| || ||||| |||

AGGC GAG CGGGGG CGG
 A_ GA _
 GAM3738 C1orf25 5' TCCGTGCCAAGCCCGCC 84427 C T C
 TCCG GC CGGGCCC CC
 |||| || ||||| ||
 AGGC CG GTTCGGG GG
 A _ C
 GAM3738 C20orf39 5' TCCCCGCCCTGCGCTCTCCGCC 84428 G GG_ CCC
 TCC CGCTC GC CCGCC
 ||| |||| || ||||
 AGG GCGGG CG GGCGG
 G ACG AGA
 GAM3738 C20orf58 5' CCCGCGCTCGGCCCCCGCC 84429 GC
 TCCGCGCTCGG CCCCCGCC
 ||||| |||||
 GGGCGCGAGCC GGGGGCGG

 GAM3738 C5orf7 5' CCCGCGCTCCCGCCCGCC 84430 GGG C
 TCCGCGCTC CC CCGCC
 ||||| || |||||
 GGGCGCGAG GG GGGCGG
 _ C
 GAM3738 C8orf13 3' CGCTCCAGCCCCTCCGCC 84432 G _
 CGCTC GGCCCC CCGCC
 |||| |||| ||||
 GCGAG TCGGGG GGCGG
 G A
 GAM3738 C8orf13 3' TCCAGCCCAAGCCCTCCGC 84431 C C
 TCCG GCTCGGGGCC CCGC
 ||| ||||| ||||
 AGGT CGGGTTCGGG GGCG
 _ A
 GAM3738 CAC-1 5' TCCGCGCTGGTCCCGC 84433 C GCCC
 TCCGCGCT GG CCCGC
 ||||| || ||||
 AGGCGCGA CC GGGCG
 _ A_ _
 GAM3738 CARM1 5' TCCGGCTCCAGGCCCGCC 84434 C _ _
 TCCG GCTC GGGCCCC CC
 ||| ||| ||||| ||
 AGGC CGAG TCCGGGG GG
 _ G C
 GAM3738 CEACAM3 3' CCCTGCAAGCCCCGC 84435 GC TC C
 TCC GC GGGCCCC GC
 ||| || ||||| ||
 GGG CG TTCGGGGG CG
 A_ _ _
 GAM3738 CEACAM4 3' TCCTTGCAAGCCCCGC 84436 GC TC C
 TCC GC GGGCCCC GC
 ||| || ||||| ||

AGG CG TTCGGGGG CG
 AA _ _
 GAM3738 CECR2 5' CCCGCGCTCTGCCCCGCC 84437 GG C
 TCCGCGCTC GCCC CC
 ||||| ||| ||
 GGGCGCGAG CGGG GG
 A_ C
 GAM3738 CENTG2 5' CCGCGCGCCCCCGC 84438 TCGG
 CCGCGC GCCCCCGC
 |||| | |||||
 GGCGCG CGGGGGGCG

 GAM3738 CHSY1 5' TCCGCACGCCCGCCCCGCC 84439 _ GGC
 TCCGC GCTCG CCCCCGCC
 |||| | |||||
 AGGCG CGGGC GGGGGCGG
 TG _
 GAM3738 CLDN1 5' TCCGCGCCCGGGGCGGCGC 84440 CCCCC
 TCCGCGCTCGGG CGC
 ||||| |||
 AGGCGCGGGCCC GCG
 CGCC_
 GAM3738 DAZAP1 3' CGCGCCCTCCCCCGCC 84443 GGG
 CGCGCTC CCCCCGCC
 |||| | |||||
 GCGCGGG GGGGGGCGG
 A_
 GAM3738 DAZAP1 5' TCCTCGCTCGCTCCCGCC 84442 G GG CC
 TCC CGCTC GC CCGCC
 || |||| | |||||
 AGG GCGAG CG GGGCGG
 A _ A_
 GAM3738 DAZAP1 5' TCGGCGCTCCCGGGCCTCCTCG 84441 C _ _ C
 C TC GCGCTC GGGCC CC CGC
 || |||| | |||| | |||
 AG CGCGAG CCCGG GG GCG
 C GG A A
 GAM3738 DKFZp434E2220 5' CCCGCGCCCTCGCCCTCGCC 84444 GG CC
 TCCGCGCTC GCCC CGCC
 ||||| ||| |||
 GGGCGCGGG CGGG GCGG
 AG A_
 GAM3738 DKFZP564K0322 5' TCCAGTAGGGTCCCCCGCC 84445 CGCTC C
 TCCG GGG CCCCCGCC
 ||| || |||||
 AGGT CCC GGGGGGCGG
 CAT_ A
 GAM3738 DMRTA2 3' GCTGCCAGGCCCTCGCC 84446 _ T C
 GC GC CGGGCCCC CGCC
 || || ||||| |||

CG CG GTCCGGGG GCGG
A _ A
GAM3738 ECE2 5' CCGCGGCCCGGTCCCCTGCC 84447 _ G C C
CCGCG CTC GG CCCC GCC
||||| ||| || |||| |||
GGCGC GGG CC GGGG CGG
C G A A
GAM3738 EIF4ENIF1 5' GCACTCGGTGCCTCCGCC 84448 _ CC
GCGCTCGG GCC CCGCC
||||||| ||| |||||
CGTGAGCC CGG GGCGG
A A_
GAM3738 FLJ10110 5' CCCGCGCTCAGCCCTCGCC 84449 G CC
TCCGCGCTCGG CCC CGCC
||||||| ||| |||||
GGGCGCGAGTC GGG GCGG
_ A_
GAM3738 FLJ10206 5' TCCGGGCCCGCCCCCTCGC 84450 C GG _
TCCG GCTC GCCCC CGC
|||| ||| ||||| |||
AGGC CGGG CGGGGG GCG
C G_ A
GAM3738 FLJ10342 5' TCCGGCCGCCCCCGC 84451 C T GGC
TCCG GC CG CCCCCG
|||| ||| |||||
AGGC CG GC GGGGGCG
_ _ _
GAM3738 FLJ10350 5' CGCGCCGCCCCCGCC 84452 T GGC
CGCGC CG CCCCCGCC
|||| || |||||
GCGCG GC GGGGGCG
_ _
GAM3738 FLJ10769 3' CCTGCCAGCTCCCTGCC 84453 GC G C C
CC GCTCGG C CCC GCC
|| ||||| | ||| |||
GG CGGGTC G GGG CGG
A_ _ A A
GAM3738 FLJ10829 3' TCCCCCAGGCCTCCTGC 84454 GCG C C
TCC CTCGGGCC CC GC
||| ||||| ||| |||
AGG GGGTCCGG GG CG
GG_ A A
GAM3738 FLJ11535 3' CGGCCCGCCCCCGC 84455 C GG
CG GCTC GCCCCCGC
|| ||| |||||
GC CGGG CGGGGGGCG
_ _
GAM3738 FLJ11535 3' CGGCCCGCCCCCGC 84455 C GG
CG GCTC GCCCCCGC
|| ||| |||||

GC CGGG CGGGGGGCG

GAM3738 FLJ11560 5' TCCACGCTCACCTGC 84456 GGCC C
TCCGCGCTCG CCC GC
||||||| |||
AGGTGCGAGT GGG CG

_____ A
GAM3738 FLJ12132 5' TCCGGCCGCTCCCCCGCC 84457 C CGG _
TCCG GCT GC CCCCCGCC
|||| ||| || |||||
AGGC CGG CG GGGGGCGG

_____ A
GAM3738 FLJ12242 5' CCCGCGCTGCTCCCGC 84458 CGG CC
TCCGCGCT GC CCCGC
|||||| || ||||
GGGCGCGA CG GGGCG

_____ A
GAM3738 FLJ12549 5' TCCCGCTCAGGCCTCCCGC 84459 G C
TCC CGCTCGGGCC CCCGC
||| ||||| ||||
AGG GCGAGTCCGG GGGCG

_____ A
GAM3738 FLJ12643 5' CCCGCGCTGCCTCCCGCC 84460 CGG C
TCCGCGCT GCC CCCGCC
|||||| ||| ||||
GGGCGCGA CGG GGGCGG

_____ A
GAM3738 FLJ13955 5' TCCGGCTCGGGCTGCGGCCGCC 84461 C CCC_
TCCG GCTCGGGC CCGCC
|||| ||||| ||||
AGGC CGAGCCCG GGCGG
_____ ACGCC

GAM3738 FLJ14466 3' TCCACGCTCTGCCCTTGC 84462 GG CC
TCCGCGCTC GCCCC GC
|||||| |||| ||
AGGTGCGAG CGGGG CG
_____ A_ AA

GAM3738 FLJ20080 5' TCCGCGGAGACCCCCCGCC 84463 CTC
TCCGCG GGGCCCCCGCC
||||| |||||
AGGCGC TCTGGGGGGCGG
_____ C_

GAM3738 FLJ20457 5' TCCGGCGCCGCCACCCCCGCC 84464 _ T GGC
TCCG CGC CG CCCCCGCC
|||| ||| || |||||
AGGC GCG GC GGGGGCGG
_____ C _ GGT

GAM3738 FLJ20551 5' TCCGCGGCTCTGCTCTCCTGCC 84465 _ GG CC_ C
TCCGCG CTC GC CC GCC
||||| ||| || |||

AGGCGC GAG CG GG CGG
 C A_ AGA A
 GAM3738 FLJ21610 5' CCCGCGCTCCCCCGC 84466 CGGGC
 TCCGCGCT CCCCCG
 ||||| |||||
 GGGCGCGA GGGGGCG

 GAM3738 FLJ21870 5' CCGCGCTGCTCCCCCGCC 84467 CGG _
 CCGCGCT GC CCCCCGCC
 ||||| || |||||
 GGCGCGA CG GGGGGCGG
 _ A
 GAM3738 FLJ22865 5' CCGTGCTTCAGGCCCGCC 84468 C _ C
 CCG GCT CGGGCCCCC GCC
 ||| ||| ||||| |||
 GGC CGA GTCCGGGGG CGG
 A A _
 GAM3738 FLJ31564 5' TCCGGCCGCCCTCCCCGC 84469 _ GGG _
 TCCG CGCTC CC CCCCCG
 ||| ||| || |||||
 AGGC GCGGG GG GGGGCG
 CG _ A
 GAM3738 FLJ32818 5' GCCGCCAGGCCTCCCGCC 84470 _ C
 GC GCTCGGGCC CCGCC
 || ||||| |||||
 CG CGGGTCCGG GGGCGG
 G A
 GAM3738 FOXJ1 5' CCGCGCTCTCTGGCCCGC 84471 G_ CCC
 CCGCGCTC GGCC GC
 ||||| ||||| ||
 GGCGCGAG CCGGG CG
 AGA _
 GAM3738 GAP1IP4BP 5' TCCGCGCCCGCCGAGCCTCGCC 84472 _ CCC
 TCCGCGCTCG GGCC CGCC
 ||||| ||| |||
 AGGCGCGGGC TCGG GCGG
 GGC A_
 GAM3738 GIOT-3 5' TCCCGCCGCCCTTCGCC 84473 G CGG C_
 TCC CGCT GCCC CGCC
 ||| ||| ||||| |||
 AGG GCGG CGGGG GCGG
 _ _ AA
 GAM3738 H2AFY 5' CCCGCGCTCTCCCCCTCCGCC 84474 GGG _
 TCCGCGCTC CCCC CCGCC
 ||||| ||| |||||
 GGGCGCGAG GGGG GGCGG
 AG_ A
 GAM3738 H2AFY 5' CCCGCGCTCTCCCCCTCCGCC 84474 GGG _
 TCCGCGCTC CCCC CCGCC
 ||||| ||| |||||

		GGGCGCGAG GGGG GGCGG	
		AG_ A	
GAM3738	HCAP-G	5' CCCGCGCTCGGCTACAGCCTGC 84475	___ CC C
	C	TCCGCGCTCGG GC CC GCC	
		GGGCGCGAGCC TG GG CGG	
		GA TC A	
GAM3738	HRK	5' CCCGCGCTCGGGCCGCCCTCG 84476	- _
	CC	TCCGCGCTCGGGCC CCCC GCC	
		GGGCGCGAGCCCGG GGGG CGG	
		C AG	
GAM3738	HSPC156	5' CCCGCGCGGCTCCTGC 84477	CG C CC
		TCCGCGCT GGC CC GC	
		GGGCGCGG CCG GG CG	
		_ A A_	
GAM3738	KATII	5' CCGCGCCCCCTCCCGCC 84478	CGGG _
		CCGCGCT CCC CCGCC	
		GGCGCGG GGG GGGCGG	
		_ A	
GAM3738	KEAP1	5' CCGCGCTCCGGCTCCGCC 84479	G CCC
		CCGCGCTC GGC CCGCC	
		GGCGCGAG CCG GGCGG	
		G A_	
GAM3738	KIAA0215	5' CCCGCGCCTCAGCTCCCGCC 84480	CG CC
		TCCGCGCT GGC CCGCC	
		GGGCGCGG TCG GGGCGG	
		AG A_	
GAM3738	KIAA0215	5' TCCTCGCCCCCGCCCCCGCC 84481	G GG
		TCC CGCTC GCCCCCGCC	
		AGG GCGGG CGGGGGGCGG	
		A GG	
GAM3738	KIAA0227	5' TCCGCGCCGCCCGCTCCCGCC 84482	CGG _
		TCCGCGCT GCCC CCGCC	
		AGGCGCGG CGGG GGGCGG	
		_ CGA	
GAM3738	KIAA0284	3' GCGCTCACCCCGCC 84483	GGC
		GCGCTCG CCCCCGCC	
		CGCGAGT GGGGGCGG	
		_	
GAM3738	KIAA0376	3' CCCGTAAGTGTTCCTCCCGCC 84484	C_ CGG CC
		TCCG GCT GC CCGCC	

		GGGC TGA CG GGGCGG	
		AT ____ AA	
GAM3738 KIAA0397	5'	CCGCGCTCCCGGCCCGCC 84485	G_ C
		CCGCGCTC GGCCC CC	
		GGCGCGAG CCGGG GG	
		GG C	
GAM3738 KIAA0427	3'	TCCAGCGGGGACCCCCGCC 84486	_ CTC
		TCC GCG GGGCCCCCGCC	
		AGG CGC CCTGGGGGGCGG	
		T C__	
GAM3738 KIAA0441	5'	CCCGCTGGCCCTCCGC 84487	G CG C
		CC CGCT GGCCC CCGC	
		GG GCGA CCGGG GGCG	
		_ _ A	
GAM3738 KIAA0603	5'	TCCGCGCTTCAGCAGCCCTGCC 13646	CG C_ C
		TCCGCGCT GGC CCC GCC	
		AGGCGCGA TCG GGG CGG	
		AG TC A	
GAM3738 KIAA0649	5'	TCCGGCCGGGCCCCCGCC 84488	C T
		TCCG GC CGGGCCCCCGCC	
		AGGC CG GCCCGGGGGGCGG	
		_ _	
GAM3738 KIAA0759	5'	CCCGCGCCCGCCTCCGC 84489	GGC C
		TCCGCGCTCG CC CCGC	
		GGGCGCGGGC GG GGCG	
		_ A	
GAM3738 KIAA0821	5'	CGAACCCGGGCCCCCGCC 84490	C
		CG GCTCGGGCCCCCGCC	
		GC TGGGCCCGGGGGGCGG	
		T	
GAM3738 KIAA1030	3'	TCCGCCTGCCCGCCCCGCC 84491	_ GGC
		TCCGC GCTCG CCCCCGCC	
		AGGCG CGGGC GGGGGCGG	
		GA _	
GAM3738 KIAA1161	5'	CGCGCTCGGGCACATCGCC 84492	CCCC
		CGCGCTCGGGC CGCC	
		GCGCGAGCCCG GCGG	
		TGTA	
GAM3738 KIAA1199	5'	CCGCGCTCAGCCCCGC 84493	GCC
		CCGCGCTCGG CCCCCG	

GGCGCGAGTC GGGGCG

GAM3738 KIAA1297 3' CCCGCGCCGAGCTCCCGCC 84494 T CC
TCCGCGC CGGGC CCCGCC
||||| |||| |||||
GGGCGCG GCTCG GGGCGG

— A—
GAM3738 KIAA1332 5' TCCACGCTCTCGGGTTCGC 84495 — CCCCC
TCCGCGCTC GGG CGC
||||||| ||| |||
AGGTGCGAG CCC GCG

AG AA—
GAM3738 KIAA1957 3' TCCGCGCCCAACCCTCG 84496 GG CC
TCCGCGCTC GCCC CG
||||||| |||| ||
AGGCGCGGG TGGG GC

— A—
GAM3738 KIAA1981 3' CCCGCGCCTCCTCCTCCGCC 84497 CGGG _ _
TCCGCGCT CC CC CCGCC
||||||| || || |||||
GGGCGCGG GG GG GGC GG

A— A A
GAM3738 LHFPL2 5' TCCACGCCGCGCGGCTCCTCG 84498 — _ C C
C TCCGCGCT CG GGC CC CGC
||||||| || ||| || |||
AGGTGCGG GC CCG GG GCG

CG G A A
GAM3738 LIP8 5' CCGTTGGCAGCCTCCCGCC 84499 C— TCG C
CCG GC GGCC CCCGCC
||| || |||| |||||
GGC CG TCGG GGGCGG

AAC — A
GAM3738 MAN1C1 5' TCCGGCCGAGCCCTCCCGCC 84500 C T _
TCCG GC CGGGCCC CCCGCC
|||| || ||||| |||||
AGGC CG GCTCGGG GGGCGG

— — AG
GAM3738 MAP3K6 5' TCCACGCTGTCCAGTCTCCGC 84501 — GCCCC
TCCGCGCT CGG CCGC
||||||| ||| |||||
AGGTGCGA GTC GGCG

CAG AGA—
GAM3738 MAPKAPK2 5' TCCGGGCCCCCTCCCGCC 84502 C GGG _
TCCG GCTC CC CCCCGCC
|||| |||| || |||||
AGGC CGGG GG GGGGCGG

C — A
GAM3738 MAPKAPK2 5' TCCGGGCCCCCTCCCGCC 84502 C GGG _
TCCG GCTC CC CCCCGCC
|||| |||| || |||||

AGGC CGGG GG GGGGCGG
 C ____ A
 GAM3738 MGC10848 3' GCACTCAGGCTTCCCGCC 84503 CC
 GCGCTCGGGC CCCGCC
 ||||| ||||
 CGTGAGTCCG GGGCGG
 AA
 GAM3738 MGC14386 5' TCCATGCCTGCCCCCGCC 84504 C T GG C
 TCCG GC C GCCCCC GCC
 ||| || ||||| ||
 AGGT CG G CGGGGG CGG
 A _ A _ _
 GAM3738 MGC15875 5' TCCGAGCCCCGCCCCTGCC 84506 C GG CC
 TCCG GCTC GCCCC GCC
 ||| ||| |||| ||
 AGGC CGGG CGGGG CGG
 T G_ A_
 GAM3738 MGC15875 5' CGCACTCGGCCCGCC 84505 GCC
 CGCGCTCGG CCCCGCC
 ||||| |||||
 GCGTGAGCC GGGGCGG

 GAM3738 MGC29643 5' CCCGCGCTCGGGCTCCCGGC 84507 C C
 TCCGCGCTCGGGC CCC GC
 ||||| ||||| ||| ||
 GGGCGCGAGCCCG GGG CG
 A C
 GAM3738 MGC4415 3' TCCGGGGATTCCCCCGCC 84508 CGCTC C_
 TCCG GGG CCCCCGCC
 ||| || |||||
 AGGC CCC GGGGGCGG
 _____ TAA
 GAM3738 MGC4701 5' CCCGCCCCAGCTCCTCGCC 84509 G G C C
 CC CGCTC GGC CC CGCC
 || |||| ||| ||||
 GG GCGGG TCG GG GCGG
 _ G A A
 GAM3738 MIG2 5' CCCGCGCTCCACCCTCTCCCG 84510 GG _____
 CC TCCGCGCTC GCC CCCGCC
 ||||| ||| |||||
 GGGCGCGAG TGGG GGGCGG
 G_ AGAG
 GAM3738 MRPL24 5' TCAGCGTCCCCTCCCCCGCC 84511 C _ GGGC
 TC GCG CTC CCCCCGCC
 || ||| || |||||
 AG CGC GGG GGGGGCGG
 T A GA_
 GAM3738 NEIL2 3' CCCTGCTCCACCCCGCC 84512 GC GGGC
 TCC GCTC CCCCCGCC
 || ||| |||||

		GGG CGAG GGGGGCGG	
		A_ GT__	
GAM3738 NESCA	5'	CCGCGCTCACCTCCCGCC 84513	GG C
		CCGCGCTC GCC CCCGCC	
		GGCGCGAG TGG GGGCGG	
		__ A	
GAM3738 NOL4	5'	CCCGCGCTCGGCCGC 84370	GCCCC
		TCCGCGCTCGG CCGC	
		GGGCGCGAGCC GGCG	

GAM3738 OSGEP	5'	TCCGCGCTGGGCCGAGC 84514	C CCCC
		TCCGCGCT GGGCC GC	
		AGGCGCGA CCCGG CG	
		_ CGT_	
GAM3738 PANX1	5'	CGCGCTCGCTGCCTCCGCC 84515	G_ CC
		CGCGCTCG GCC CCGCC	
		GCGCGAGC CGG GGCGG	
		GA A_	
GAM3738 PDE4DIP	5'	CCGCGCTCCGACCCTGCC 84516	G CCC
		CCGCGCTC GGCCC GCC	
		GGCGCGAG CTGGG CGG	
		G A__	
GAM3738 PIP5K2A	5'	CCGCGCTCCGCTCCGCC 84517	GG CCC
		CCGCGCTC GC CCGCC	
		GGCGCGAG CG GGCGG	
		G_ A__	
GAM3738 PLAGL2	5'	CCGCGCTCGGGCTCCGCC 84518	CCC
		CCGCGCTCGGGC CCGCC	
		GGCGCGAGCCCG GGCGG	
		A__	
GAM3738 PPP1R14A	5'	CCCGCGCTGTGCGCCTTCGCC 84519	CGG _ CC
		TCCGCGCT GC CC CGCC	
		GGGCGCGA CG GG GCGG	
		CA_ C AA	
GAM3738 PTK9L	5'	TCCGCGCCGTTCGGAGCCCTCCG 84520	__ _ C
C		TCCGCGC TCGG GCCC CCGC	
		AGGCGCG AGCC CGGG GGCG	
		GC T A	
GAM3738 QKI	5'	TCCGCGCCGGCTCCCGC 84521	CG CC
		TCCGCGCT GGC CCCGC	

AGGCGCGG CCG GGGCG
 — A—
 GAM3738 Rab11-FIP2 5' TCTGCGCGGACCCCGCC 84522 C TC C
 TC GCGC GGGCCCCC GCC
 || ||| ||||| |||
 AG CGCG CCTGGGGG CGG
 A — —
 GAM3738 RAB40C 3' CCGCGCCCCCTCCTCCCGCC 84523 GGG C
 CCGCGCTC CC CCGCC
 ||||| || |||||
 GGCGCGGG GG GGGCGG
 GGA A
 GAM3738 RBAK 5' TCCCGCGGCCCTTCGCC 84473 G CGG C—
 TCC CGCT GCCCC CGCC
 ||| ||| |||| |||
 AGG GCGG CGGGG GCGG
 — — AA
 GAM3738 RNPC1 3' CCCGCTGCCCCCGC 84524 G CGG
 CC CGCT GCCCCCGC
 || ||| |||||
 GG GCGA CGGGGGGCG
 — —
 GAM3738 SDS3 5' CCCGCGCTCGGTACTCGCC 84525 GCCCCC
 TCCGCGCTCGG CGCC
 ||||| |||
 GGCGCGAGCC GCGG
 ATGA—
 GAM3738 Sfmbl 5' CCCGCGCTCGCCCGC 84526 GGCCC
 TCCGCGCTCG CCCGC
 ||||| |||
 GGCGCGAGC GGGCG
 — —
 GAM3738 SLC2A10 5' TCCGGCCCGCCCCCGC 84527 C GGC
 TCCG GCTCG CCCCCG
 ||| ||| |||||
 AGGC CGGGC GGGGGCG
 — —
 GAM3738 SMARCA4 5' CCCGGCGCCTCCCCCGCC 84528 — —
 CTCGG GCC CCCCCG
 |||| ||| |||||
 GGGCC CGG GGGGCGG
 G AG
 GAM3738 SMARCE1 5' CCCGCGCTCGCCCGC 84529 GGCC
 TCCGCGCTCG CCCCCG
 ||||| |||
 GGCGCGAGC GGGGCG
 — —
 GAM3738 SOUL 5' GCGCGTCCTGCCCCCGCC 84530 — GG C
 GCGC TC GCCCCC GCC
 ||| || ||||| |||

CGCG AG CGGGGG CGG
C GA _

GAM3738 SPUVE 5' TCCGCGCCGAGCAGCCCGCC 84531 T CC
TCCGCGC CGGGC CCCGCC
||||| |||| |||||
AGGCGCG GCTCG GGGCGG
_ TC

GAM3738 STIM2 5' CCGCGGCGCATCCCCCGCC 84532 _T GG
CCGCG C CG CCCCCCGCC
||||| || |||||
GGCGC G GT GGGGGGCGG
C C A_

GAM3738 STIM2 5' TCCGGCCGCCCCCGC 84451 C T GGC
TCCG GC CG CCCCCGC
||| || |||||
AGGC CG GC GGGGGCG

GAM3738 TADA3L 5' TCCGCGCTGCAGTTAGCCCCGC 84533 _ GCC_
C TCCGCGCT CGG CCCCCGCC
||||| || |||||
AGGCGCGA GTC GGGGCGG
C AATC

GAM3738 TADA3L 5' TCCGCGCTGCAGTTAGCCCCGC 84533 _ GCC_
C TCCGCGCT CGG CCCCCGCC
||||| || |||||
AGGCGCGA GTC GGGGCGG
C AATC

GAM3738 TADA3L 5' TCCGCGCTGCAGTTAGCCCCGC 84533 _ GCC_
C TCCGCGCT CGG CCCCCGCC
||||| || |||||
AGGCGCGA GTC GGGGCGG
C AATC

GAM3738 TAF5L 5' TCCGGCTCCCCCGC 84534 C CGGG
TCCG GCT CCCCCCGC
||| || |||||
AGGC CGA GGGGGGCG

GAM3738 TMEM8 5' TCCGCGCTCGGCCCGGCGC 84535 G CC
TCCGCGCTCGG CCC CGC
||||||| || |||
AGGCGCGAGCC GGG GCG
_ CC

GAM3738 TNKS2 5' CCCTCGCTGGGCTCCCTGCC 84536 G C C C
TCC CGCT GGGC CCC GCC
||| ||| ||| ||| |||
GGG GCGA CCCG GGG CGG
A _ A A

GAM3738 TSGA 5' TCCTCCCCCGCCTCCCGCC 84537 GCG GG C
TCC CTC GCC CCCGCC
||| ||| ||| |||||

AGG GGG CGG GGGCGG
 AG_ G_ A
 GAM3738 ZDHHC2 5' TCCGCCCCCGCCGTTCCCCGCC 84538 G GG ____
 TCCGC CTC GCC CCCCCGCC
 ||||| ||| ||| |||||
 AGGCG GGG CGG GGGGCGG
 G _ CAA
 GAM3738 ZDHHC2 5' GCGCTCCGCCCCCGCC 32625 GG C
 GCGCTC GCCCCC GCC
 ||||| ||||| |||
 CGCGAG CGGGGG CGG
 G_ _
 GAM3738 ZFP91 5' TCGGCGCTGCTCCCCCGCC 84539 C CGGG
 TC GCGCT CCCCCCGCC
 || ||||| |||||
 AG CGCGA GGGGGGCGG
 C CGA_
 GAM3738 ZNF297B 5' TCAGCGCTCACATCCCCCGCC 84540 C GGC
 TC GCGCTCG CCCCCGCC
 || ||||| |||||
 AG CGCGAGT GGGGGCGG
 T GTA
 GAM3738 LOC115073 5' TCCTGCTCGGACCCCGC 84541 GC CC
 TCC GCTCGGGCCCC GC
 ||| ||||| |||
 AGG CGAGCCTGGGG CG
 A_ _
 GAM3738 LOC115548 5' TCCGCGCCCGCCCGC 84542 GGCCC
 TCCGCGCTCG CCCGC
 ||||| |||||
 AGGCGCGGGC GGGCG
 _ _
 GAM3738 LOC115574 5' CCCGCGCCGCGCCCCCTCGCC 45174 T G _
 TCCGCGC CG GCCCC CGCC
 ||||| || ||||| |||||
 GGGCGCG GC CGGGGG GCGG
 _ G A
 GAM3738 LOC126969 5' CCCGCGTCTCCCCCGC 84543 C GGGC
 TCCGCG TC CCCCCGC
 ||||| || |||||
 GGGCGC AG GGGGGCG
 _ A _
 GAM3738 LOC128844 5' CCCGCGCTGGGCTCCTGCC 84544 C C CC
 TCCGCGCT GGGC CC GCC
 ||||| ||||| |||
 GGGCGCGA CCGG GG CGG
 _ A A_
 GAM3738 LOC129408 5' CCGCGCCCCGCTCCTCGC 84545 GG C C
 CCGCGCTC GC CC CGC
 ||||| || |||

		GGCGCGGG CG GG GCG	
		G_ A A	
GAM3738	LOC130074 5'	TCCCGCTCGCTCGGCTCCGC 84546	G ____ CCC
		TCC CGCTCG GGC CCGC	
		AGG GCGAGC CCG GGCG	
		_ GAG A__	
GAM3738	LOC130367 5'	CCCGCCTCGCCCCGCC 84547	G GGC
		TCCGC CTCG CCCCCGCC	
		GGGCG GAGC GGGGGCGG	
		- -	
GAM3738	LOC130617 5'	ACTCTGGCGGGCTCCCTGCC 84548	G __ C C
		GC CT CGGGC CCC GCC	
		TG GA GCCCG GGG CGG	
		A CC A A	
GAM3738	LOC133993 5'	CCCGCGGACCCCTCTGCC 84549	GCTC CC_
		TCCGC GGGCCCC GCC	
		GGGCG CCTGGGG CGG	
		- - - AGA	
GAM3738	LOC139231 5'	CCCGCGCCCGCCCTGCC 84550	GG CC
		TCCGCGCTC GCCCC GCC	
		GGGCGCGGG CGGGG CGG	
		- - - A_	
GAM3738	LOC143666 5'	CCCGCGCTCAGGCCTCCCC 84551	-
		TCCGCGCTCGGGCC CCCC	
		GGGCGCGAGTCCGG GGGG	
		- - - A	
GAM3738	LOC145694 5'	CCGCGTCGCCCCCGCC 84552	C GG
		CCGCG TC GCCCCCGCC	
		GGCGC AG CGGGGGGCGG	
		- - -	
GAM3738	LOC145990 5'	TCCCCGCCGCCGCCCGCC 84553	G T GGC
		TCC CGC CG CCCCCGCC	
		AGG GCG GC GGGGGCGG	
		G _ GGC	
GAM3738	LOC147965 5'	TCCGCGCCCGCCTCTCGC 84554	GG CCC
		TCCGCGCTC GCC CGC	
		AGGCGCGGG CGG GCG	
		- - - AGA	
GAM3738	LOC148022 5'	TCCACACTGCCCCCGCC 84555	CGG
		TCCGCGCT GCCCCCGCC	

AGGTGTGA CGGGGGGCGG

GAM3738 LOC148479 3' TCCACGCTCGCAGCCTCCTCGC 84556 _ _ C
C TCCGCGCTCG GGCC CC CGCC

||||||| ||| || ||||
AGGTGCGAGC TCGG GG GCGG

G A A

GAM3738 LOC148753 5' TCCGGGGAGAATCCCCCGCC 84557 CGCTC C____
TCCG GGG CCCCCGCC

||| ||| |||||
AGGC CCC GGGGGCGG

_____ TCTTA

GAM3738 LOC150095 5' TCCTGCCCCATGCCCCCGCC 84558 _ G G
TCC GC CTCG GCCCCCGCC

||| || |||||
AGG CG GGGT CGGGGGGCGG

A _ A

GAM3738 LOC150142 5' TCCGCGCCCGGGCACAGGC 84559 CCCCC
TCCGCGCTCGGGC GC

||||||| ||
AGGCGCGGGCCCG CG

TGTC_

GAM3738 LOC150150 3' TCTGCGCCTCCCCCGCC 84560 C CGGGC
TC GCGCT CCCCCGCC

|| ||||| |||||
AG CGCGG GGGGGCGG

A A____

GAM3738 LOC150421 3' TCCCGCTCAGGCCCCCTGCC 84561 G C
TCC CGCTCGGGCCCCC GCC

||| ||||| |||||
AGG GCGAGTCCGGGGG CGG

_ A

GAM3738 LOC150465 3' TCAGCAAAGCCCCCTGCC 84562 C CTC C
TC GCG GGGCCCCC GCC

|| ||| ||||| |||||
AG CGT TTCGGGGG CGG

T _ A

GAM3738 LOC152559 5' CGCCGCTGGCGCCCCCGCC 84563 _ CG _
CGC GCT GGC CCCCCGCC

||| ||| ||| |||||
GCG CGA CCG GGGGGCGG

G _ C

GAM3738 LOC152917 5' CACGCTCGCCCTCCGCC 84564 GG C
CGCGCTC GCCC CCGCC

||||| ||| |||||
GTGCGAG CGGG GGCGG

_ A

GAM3738 LOC153432 5' TCCGCACCTGCCTTCGC 84565 T GG CC
TCCGCGC C GCC CCGC

||||| | ||| |||||

AGGCGTG G CGG GGCG
 A AA
 GAM3738 LOC157848 3' TCCTGCCCACTCCCCCGCC 84566 GC GG
 TCC GCTCG CCCCCCGCC
 ||| |||| |||||
 AGG CGGGT GGGGGGCGG
 A_ GA
 GAM3738 LOC161190 5' GCGGACAGGCCCCCTGCC 84567 CT C
 GCG CGGGCCCCC GCC
 ||| ||||| |||
 CGC GTCCGGGGG CGG
 CT A
 GAM3738 LOC164633 5' TCCGCGCCCGCCCGC 84542 GGCCC
 TCCGCGCTCG CCCGC
 ||||| ||||
 AGGCGCGGGC GGGCG

 GAM3738 LOC165254 5' CCGCGCTCCAGCACTCTTCGCC 84568 G CCCC_
 CCGCGCTC GGC CGCC
 ||||| || ||||
 GGCGCGAG TCG GCGG
 G TGAGAA
 GAM3738 LOC166983 5' TCCAGAAGCCCCCTGCC 84569 CGCTC C
 TCCG GGGCCCCC GCC
 ||| ||||| |||
 AGGT TTCGGGGG CGG
 C_ A
 GAM3738 LOC199745 5' CCCGCGCTCGCCGCCTGCC 84570 GG C C
 TCCGCGCTC GCC CC GCC
 ||||| ||| |||
 GGGCGCGAG CGG GG CGG
 _ C A
 GAM3738 LOC199848 5' CCGCACCGTCCCCCGCC 84571 T GGC
 CCGCGC CG CCCCCGCC
 ||||| || |||||
 GGCGTG GC GGGGGCGG
 _ A_
 GAM3738 LOC199870 5' CCGCGCTCACCGACCCGCC 84572 GG C_
 CCGCGCTC GCC CCGCC
 ||||| || |||||
 GGCGCGAG TGG GGGCGG
 _ CT
 GAM3738 LOC200084 5' TCCGGGCTCGGGCTCCGGC 84573 C CC C
 TCCG GCTCGGGC CC GC
 ||| ||||| |||
 AGGC CGAGCCCG GG CG
 C A_ C
 GAM3738 LOC200576 5' CCGCGCCGGCTGCCCCCGCC 84574 T _
 CCGCGC CGG GCCCCCGCC
 ||||| ||| |||||

GGCGCG GCC CGGGGGGCGG
_ GA
GAM3738 LOC201161 5' CCTGCGCGCGCCCCCGCC 45199 _ TCGG _
CC GCGC GC CCCCCGCC
|| ||| || |||||
GG CGCG CG GGGGGCGG
A _ C
GAM3738 LOC201514 5' CCCGCGCCTCCCTCGC 84575 CGGG C
TCCGCGCT CCCC CGC
||||| ||| ||
GGGCGCGG GGGG GCG
A _ A
GAM3738 LOC203197 5' TCACGGGCCCGCCCCCGCC 84576 _ C GG
TC CG GCTC GCCCCCGCC
|| ||| |||||
AG GC CGGG CGGGGGGCGG
T C _
GAM3738 LOC206836 5' CCGCGCGCCACCCCCCGCC 84577 T G_
CCGCGC CG GCCCCCGCC
||||| || |||||
GGCGCG GC TGGGGGGCGG
_ GG
GAM3738 LOC221773 5' CCCGCGCCCGGGGTCCTCCGCC 84578 CC _
TCCGCGCTCGGG CC CCGCC
||||||| || |||
GGGCGCGGGCCC GG GGCGG
CA A
GAM3738 LOC222166 5' CCCGCGCCCGCCTCCCGCC 84579 GG C
TCCGCGCTC GCC CCGCC
||||| || |||||
GGGCGCGGG CGG GGGCGG
_ A
GAM3738 LOC222166 5' TCCGCCCCGCCTCCCCCGCC 84581 G GG_
TCCGC CTCG CCCCCCGCC
|||| ||| |||||
AGGCG GGGC GGGGGGCGG
_ GGA
GAM3738 LOC222166 5' CCCGCGGCTCCTCCTCCGCC 84580 _ GGG CC
TCCGCG CTC CC CCGCC
|||| ||| || |||
GGGCGC GAG GG GGCGG
C GA_ A_
GAM3738 LOC253258 3' CCCGCGCTCAGGCCTCCCC 84551 _
TCCGCGCTCGGGCC CCCC
||||||| |||
GGGCGCGAGTCCGG GGGG
A
GAM3738 LOC253936 5' CCCGCGCCACCTCCCTCCGCC 84582 GG_ C
TCCGCGCTCG CCC CCGCC
|||||| || |||

GGGCGCGGGT GGG GGC GG
GGA A
GAM3738 LOC254124 3' CCGCGCCCGGCCGCCCTTGCC 84583 G _ _
CCGCGCTCGG CC CCCC GCC
||||||| || ||| ||
GGCGCGGGCC GG GGGG CGG
_ C AA
GAM3738 LOC255251 5' CGCACTCGGCCCGCC 84505 GCC
CGCGCTCGG CCCC GCC
||||||| |||||
GCGTGAGCC GGGGCGG

GAM3738 LOC255251 5' TCCGGGCCCCGCCCCTGCC 84584 C GG CC
TCCG GCTC GCCCC GCC
|||| ||| |||| ||
AGGC CGGG CGGGG CGG
C G_ A_
GAM3738 LOC255645 3' TCCGCGCCCCCACC 84585 GCTCGG
TCCGC GCCCCCGCC
|||| | |||||
AGGCG CGGGGGGTGG

GAM3738 LOC255971 3' TCCGCACCAGCCCCCGCC 84586 CG
TCCGCGCT GGCCCCCGCC
||||| |||||
AGGCGTGG TCGGGGGGCGG

GAM3738 LOC51112 5' CCCGCGTCGCCCTCGC 84587 C GGC C
TCCGCG TCG CCC CGC
||||| || ||| ||
GGGCGC AGC GGG GCG
_ _ _ A
GAM3738 LOC51125 5' CCCGCGCCGCTCCTCTGCC 84588 CGG _ CC_
TCCGCGCT GCC CC GCC
||||||| ||| || ||
GGGCGCGG CGG GG CGG
_ _ A AGA
GAM3738 LOC51334 5' TCCGCGCTCGGCCGGGC 84589 G CCCC
TCCGCGCTCGG CC GC
||||||| || ||
AGGCGCGAGCC GG CG
_ CC_
GAM3738 LOC56961 5' TCCCGCGGCCCCCGC 84590 G TCG C
TCC CGC GGCCCC GC
||| || ||||| ||
AGG GCG CCGGGGG CG

GAM3738 LOC56961 5' TCCGCCGCGTCCCCCGCC 84591 _ TCGGGC
TCCGC GC CCCCCGCC
||||| || |||||

	AGGCG CG	GGGGGCGG	
	G CA_____		
GAM3738 LOC58509	5' TCCACGCCCTGCTCCTGC	84592	GG C CC
	TCCGCGCTC GC CC GC		
	AGGTGCGGG CG GG CG		
	A_ A A_		
GAM3738 LOC84548	5' TCCACGCTGCTGCTCCCGC	84593	CGG CC
	TCCGCGCT GC CCCGC		
	AGGTGCGA CG GGGCG		
	CGA A_		
GAM3738 LOC86010	5' CCCGCGCTGCTCCTCGC	84594	CGG C C
	TCCGCGCT GC CC CGC		
	GGGCGCGA CG GG GCG		
	___ A A		
GAM3738 LOC90719	5' CCCGCGCTCGGGTTTTCCGC	84595	CCCC
	TCCGCGCTCGGG CCGC		
	GGGCGCGAGCCC GGCG		
	AAAA		
GAM3738 LOC91300	5' TCCGCGCCTTGCTCCTGCC	84596	CGG C CC
	TCCGCGCT GC CC GCC		
	AGGCGCGG CG GG CGG		
	AA_ A A_		
GAM3738 LOC91300	5' TCCGCGCCTTGCTCCTGCC	84596	CGG C CC
	TCCGCGCT GC CC GCC		
	AGGCGCGG CG GG CGG		
	AA_ A A_		
GAM3738 LOC92912	5' CCGCGCTCTCGCGGCTCCGCC	84597	___ CCC
	CCGCGCTC G GGC CCGCC		
	GGCGCGAG C CCG GGCGG		
	AG G A_		
GAM3739 C18orf1	3' TCCTGGATGTTAGGGGTATGAT	84600	C ATTT___
	TATAG TCCTGGGTGT AGG TTATAG		
	AGGACCTACA TCC AATATC		
	A CCATACT		
GAM3739 DIPA	3' CTTGGTGTGTCAGGATTTCT	84601	G
	CT GGTGTGTCAGGATTTT		
	GA CCACAGTCCTAAAGA		
	A		
GAM3739 HNRPF	5' TCTTGGGTGTGGCTTTTT	84602	C CA A
	TC TGGGTGT GG TTTTT		

AG ACCCACA CC AAAAA
 A _ G
 GAM3739 PON1 3' AGTGAGAAGGATTTTTAT 84603 TC_
 GGTG AGGATTTTTAT
 ||| |||||
 TCAC TCCTAAAAATA
 TCT
 GAM3739 DIO2 3' TGGGTGGTTTTTATA 84604 GTCA A
 TGGGT GG TTTTTATA
 ||| |||||
 ACCCA CC AAAAATAT

 GAM3739 DIO2 3' TGGGTGGTTTTTATA 84604 GTCA A
 TGGGT GG TTTTTATA
 ||| |||||
 ACCCA CC AAAAATAT

 GAM3739 FLJ10781 3' TCAGGGTGTGAGATTATA 84605 CT ATTT
 TC GGGTGTGAGG TTATA
 || ||||| |||
 AG CCCACAGTCT AATAT
 T_ _
 GAM3739 FLJ21687 3' TCCTGGGTGTGACTGTATTTAT 84606 CAG _
 AG TCCTGGGTGT GATT TTTATAG
 ||||| ||| |||||
 AGGACCCACA CTGA AAATATC
 _ CAT
 GAM3739 PRO0149 5' TGGCAAGATTTTTAT 84607 GTGT
 TGG CAGGATTTTTAT
 || |||||
 ACC GTTCTAAAAATA

 GAM3739 LOC138515 5' TCAGGGTGTTCACATTTTAT 84608 CT CAGG
 TC GGGTGT ATTTTAT
 || |||| |||||
 AG CCCACA TGAAAATA
 T_ AG_
 GAM3739 LOC154007 3' TGGGTAACAATTTTTATAG 84609 TCAG
 TGGGTG GATTTTTATAG
 |||| |||||
 ACCCAT TAAAAATATC
 TG_
 GAM3739 LOC158435 3' TCCTGGTTGCCCATTTTTAT 84610 G AGG
 TCCTGG TGTC ATTTTAT
 |||| ||| |||||
 AGGACC ACGG TAAAAATA
 A G_
 GAM3739 LOC222112 3' TCCTGGGTTTAGGAGACAATAG 84611 GTC TTTT
 TCCTGGGT AGGA ATAG
 ||||| ||| |||

			AGGACCCA TCCT TATC	
			AA_ CTGT_	
GAM3740 BCL7A	5'	CCTCCTGGGGAGGTGGC	84614	_ TCGC AAG
		CCTC TGGG GAGG TGGC		
		GGAG ACCC CTCC ACCG		
		G _ _		
GAM3740 BGN	3'	CCTCTGGGTGGCTGTGG	84615	CGCGA AA
		CCTCTGGGT GG GTGG		
		GGAGACCCA CC CACC		
		_ GA		
GAM3740 CHC1	3'	CCTCTGGGCGTGGGTCCGTG	84616	T CGA AA_
		CCTCTGGG CG GG GTG		
		GGAGACCC GC CC CAC		
		_ AC_ AGG		
GAM3740 HTRA3	3'	CCCTGGATGAGGGGGTGG	84617	CGC AA
		CTCTGGGT GAGG GTGG		
		GGGACCTA CTCC CACC		
		_ CC		
GAM3740 KLK4	3'	CCTCTGGGTCTGGGGAAG	84618	GCGA
		CCTCTGGGTC GGAAG		
		GGAGACCCAG CCTTC		
		ACC_		
GAM3740 LARS2	3'	CCTCATTCATGTGAGGAAGTGG	84619	TGGG C_
		CCTC TCG GAGGAAGTGG		
		GGAG AGT CTCCTTCACC		
		TA_ ACA		
GAM3740 OTOF	5'	CCTCTGGGCTGTGAGTCTGTG	84620	CGC GAA
		CCTCTGGGT GAG GTG		
		GGAGACCCG CTC CAC		
		ACA AGA		
GAM3740 SDC4	3'	CCCTGGGTTGCAGTGG	84621	C GAGGA
		CTCTGGGT GC AGTGG		
		GGGACCCA CG TCACC		
		A _		
GAM3740 TNFRSF8	3'	CTCTGGGTTGGTGAGGGGCG	84622	CGC_ AAGT
		CTCTGGGT GAGG GGCG		
		GAGACCCA CTCC CCGC		
		ACCA _		
GAM3740 ACAS2	5'	CCTTTGCGGTCGCGGCGGGTG	84623	C _ A_ AA
		CCT TG GGTCGCG GG GTG		

GGA AC CCAGCGC CC CAC
 A G CG ____
 GAM3740 FLJ10468 3' CTCTGGGTAGCGGTGG 84624 C AGGAA
 CTCTGGGT GCG GTGG
 ||||| || |||
 GAGACCCA CGC CACC
 T ____
 GAM3740 FLJ10563 5' CCTCCGGGTCGCCCAGGGTGG 84625 G_ AA
 CCTCTGGGTGCG AGG GTGG
 ||||| || |||
 GGAGGCCAGCG TCC CACC
 GG ____
 GAM3740 KIAA0084 3' CCTCTGGCTGGAGGAGTGG 84626 GTCGC A
 CCTCTGG GAGGA GTGG
 |||| | ||| |||
 GGAGACC CTCCT CACC
 GAC__ _
 GAM3740 KIAA0552 5' TCTGGGTCGCGGGTGGGCG 84627 A AAGT
 TCTGGGTCGCG GG GGCG
 ||||| || |||
 AGACCCAGCGC CC CCGC
 _ AC__
 GAM3740 KIAA1987 3' CCTGCTGGCAGGAAGTGG 84628 _ GGTC G
 CCT CTG GC AGGAAGTGG
 || | || |||||
 GGA GAC CG TCCTTCACC
 C ____ _
 GAM3740 KLK7 3' CTGGGTCAAAGGTGGTG 84629 C AA
 CTGGGTGCG GAGG GTG
 ||||| ||| |||
 GACCCAGT TTCC CAC
 _ AC
 GAM3740 KLK7 3' CTGGGTCAAAGGTGGTG 84629 C AA
 CTGGGTGCG GAGG GTG
 ||||| ||| |||
 GACCCAGT TTCC CAC
 _ AC
 GAM3740 MLN64 3' TCTGGCTCTGGAAGTGG 84630 G GCGA
 TCTGG TC GGAAGTGG
 |||| || |||||
 AGACC AG CCTTCACC
 G A__
 GAM3740 SPINT1 5' CCTCTGGGTTCGAGGGTG 84631 CG AA
 CCTCTGGGT CGAGG GTG
 ||||| ||| |||
 GGAGACCCA GCTCC CAC
 AG ____
 GAM3740 LOC122970 5' CCCCTGGCGGGAGGAAGTGGCG 84632 GT C
 CCTCTGG CG GAGGAAGTGGCG
 |||| | |||||

GGGGACC GC CTCCTTCACCGC
___ C
GAM3740 LOC201164 3' CTTTGGGAGGCGGAAGTGG 84633 C TC GA
CT TGGG GC GGAAGTGG
|| ||| || |||||
GA ACCC CG CCTTCACC
A TC ___
GAM3740 LOC206372 3' CTCTGGGTTCGAGGGAAG 84634 CG _
CTCTGGGT CGAGG AAG
||||| |||||
GAGACCCA GCTCC TTC
A_ C
GAM3740 LOC219404 5' TCTGGATCCTCAGGTGGTG 84635 G_ G AA
TCTGGGTC C AGG GTG
||||| | |||
AGACCTAG G TCC CAC
GA_ AC
GAM3740 LOC221692 3' CTA CTGAGAGTTGAGGAAGTGG 84636 _ TCGC
CG CT CTGGG GAGGAAGTGGCG
|| ||| |||||
GA GACTC CTCCTTCACCGC
T TCAA
GAM3740 LOC256669 5' GGGCCCTCGTGGGGAGGTGGCG 84637 G_ A_ A
GGGTC CG GGA GTGGCG
|||| || ||| |||||
CCCGG GC CCT CACCGC
GA ACC C
GAM3740 LOC51082 5' TCTGGATCCTCAGGTGGTG 84635 G_ G AA
TCTGGGTC C AGG GTG
||||| | |||
AGACCTAG G TCC CAC
GA_ AC
GAM3740 LOC92249 5' CCCTGGGTTCCGAGGTGGTG 84638 CG AA
CTCTGGGT CGAGG GTG
||||| |||||
GGGACCCA GCTCC CAC
AG AC
GAM3741 FKBP1A 3' AAGGATTTGTCATGATGGCTGT 84641 A A_____ TATA
ATACA GATTT TC CTG CA
||||| || ||| ||
CTAAA AG GAC GT
C TACTACCI ATAT
GAM3741 GALNT1 3' TGAAGATTTATTGCTGT 84642 G CA
TGAAG ATTTAT CTGT
||||| |||||
ACTTC TAAATA GACA
_ AC
GAM3741 GAS7 3' TGCAGGACAAC TGTATA 84643 A TTATC
TG AGGAT ACTGTATA
|| ||| |||||

AC TCCTG TGACATAT
 G T____
 GAM3741 RAD50 3' TGATGGATTTATCAACAGCTGT 84644 A A_____ TATA
 ATC A GGATTTATC CTG C
 ||||| ||| |
 T CCTAAATAG GAC G
 A TTGTC||| ATAT
 GAM3741 RAD50 3' TGATGGATTTATCAACAGCTGT 84644 A A_____ TATA
 ATC A GGATTTATC CTG C
 ||||| ||| |
 T CCTAAATAG GAC G
 A TTGTC||| ATAT
 GAM3741 UBE3A 3' TAAAGGATTTGTTTCATATAT 84645 A_ C
 TGAAGGATTT TCA TGTAT
 ||||| ||| ||||
 ATTTCTAAA AGT ATATA
 CA _
 GAM3741 UBE3A 3' TAAAGGATTTGTTTCATATAT 84645 A_ C
 TGAAGGATTT TCA TGTAT
 ||||| ||| ||||
 ATTTCTAAA AGT ATATA
 CA _
 GAM3741 UBE3A 3' TAAAGGATTTGTTTCATATAT 84645 A_ C
 TGAAGGATTT TCA TGTAT
 ||||| ||| ||||
 ATTTCTAAA AGT ATATA
 CA _
 GAM3741 BC022889 3' TGAAGGATTTGACGTTTGAGCT 84646 ATCA_____ TATA
 GTATACA GATTT CTG CA
 |||| ||| ||
 CTAAA GAC GT
 CTGCAAACTC||| ATAT
 GAM3741 FLJ20275 3' TGAAGGATTTACCATTAAGCTG 84647 A_____ TATA
 TATACA GGATTTATC CTG CA
 ||||| ||| ||
 CCTAAATGG GAC GT
 TAATTC||| ATAT
 GAM3741 FLJ20275 3' TGAAGATGCACCACTGTATA 84648 G T
 TGAAG AT TATCACTGTATA
 |||| || ||||| |||||
 ACTTC TA GTGGTGACATAT
 _ C
 GAM3741 FLJ21820 3' TAAAGGATCTGTGTAC 84649 TTATCA A
 TGAAGGAT CTGT TAC
 ||||| ||| |||
 ATTTCTA GACA ATG
 _____ C
 GAM3741 FLJ23441 3' AAGGATTTATCACAAAGTATA 84650 T__
 AAGGATTTATCAC GTATA
 ||||| |||||

TTCCTAAATAGTG CATAT
 TTT
 GAM3741 HARS2 3' GAGGGATTTATTGTATA 84651 A CAC
 GA GGATTTAT TGTATA
 || ||||| |||||
 CT CCTAAATA ACATAT
 C _
 GAM3741 KIAA1786 3' TGAAGAATTTATCACACAC 84652 TGT
 TGAAGGATTTATCAC ATAC
 ||||| |||||
 ACTTCTTAAATAGTG TGTG
 _
 GAM3741 LOC143196 5' GAAGGATTTATTGCGCCCAG 84653 CAC ATA
 GAAGGATTTAT TGT CAG
 ||||| ||| |||
 CTTCTTAAATA ACG GTC
 _ CGG
 GAM3742 ENTPD3 5' CTGCCGAGAGGCGGCCCGCG 84656 _ C AT
 CTGCCGCA AG GCG CCCGCG
 ||||| || ||| |||||
 GACGGCGT TC CGC GGGCGC
 C _ C_
 GAM3742 MARK3 5' TGCCTCAGGGCGCCCCGCGA 84657 GCA C A
 TGCC AG GCG TCCCGCGA
 ||| || ||| |||||
 ACGG TC CGC GGGGCGCT
 AG_ C _
 GAM3742 NEK4 5' TGCTGGGGCCCGGCCCGCGAC 84658 CGCAA G AT
 TGC GC CG CCCGCGAC
 ||| || ||| |||||
 ACG CG GC GGGCGCTG
 ACCC_ G C_
 GAM3742 TRRAP 5' CCTGCAGGCCCGGCCCGCGAC 84659 _ A G AT
 CC GCA GC CG CCCGCGAC
 || ||| || ||| |||||
 GG CGT CG GC GGGCGCTG
 A C G C_
 GAM3742 BIRC5 5' CTGCCAACGGGTCCCGCGA 84660 CAA CGA
 CTGCCG GCG TCCCGCGA
 ||||| ||| |||||
 GACGGT TGC AGGGCGCT
 _ CC_
 GAM3742 C21orf4 5' CTGCCGGCGTCCCGCG 84661 CAAGC A
 CTGCCG GCG TCCCGCG
 ||||| || |||||
 GACGGC CGC AGGGCGC
 _ _
 GAM3742 FLJ10193 3' CTGCCGCAAGTGCAAAGGC 84662 C TCCC
 CTGCCGCAAG GCGA GC
 ||||| ||| ||| ||

GACGGCGTTC CGTT CG
 A TC__
 GAM3742 HSPC182 5' GCCGCAAATCCCGCG 84663 AGCGC
 GCCGCA GATCCCGCG
 ||||| |||||
 CGGCGT TTAGGGCGC

 GAM3742 LOC151648 5' CTGCCGCAGGCGCGTCCAGAAC 84664 A A C__
 GA CTGCCGCA GCGCG TCC GCGA
 ||||| ||||| || ||||
 GACGGCGT CGCGC AGG TGCT
 C _ TCT
 GAM3742 LOC256982 3' CTGCCGGCGAGTCACCCGCGAC 84665 CAA CGAT_
 CTGCCG GCG CCCGCGAC
 ||||| || |||||
 GACGGC CGC GGGCGCTG
 ____ TCAGT
 GAM3742 LOC58525 5' CTGCCGCAGGTGGGAGCGCGCG 84666 ____ ATCCC
 TGGC CTGCCGCA AGCGCG GC
 ||||| ||||| ||
 GACGGCGT TCGCGC CG
 CCACCC GCAC_
 GAM3743 CDC25A 5' TCGGCCGCGCGCCACCGGCGCC 84669 A ACCA _ _
 CG TC GCC CGC CCGC GCGCCCG
 || ||| || ||||| |||||
 AG CGG GCG GGTG CGCGGGC
 C C__ C GC
 GAM3743 CIT 3' TCAGCCACCTGCCCTCC 84670 AC GCGCG
 TCAGCCACC GCCC CC
 ||||| ||||| ||
 AGTCGGTGG CGGG GG
 A_ GA__
 GAM3743 CNGB1 3' AGCCACCATGCCCGGCA 84671 C C
 AGCCACCA GCCCG GCG
 ||||| ||||| |||||
 TCGGTGGT CGGGC CGT
 A _
 GAM3743 COL15A1 5' AGCGCTGGCCCGCGCGCTCG 84672 CACCAC C
 AGC GCCCGCGCGC CG
 || ||||| ||||| ||
 TCG CGGGCGCGCG GC
 CGAC__ A
 GAM3743 CSPG2 5' TCGGCTGTTGCGTCCGCACGCC 84673 A CACCA C
 TC GC CG CCGCGCGCC
 || || || |||||
 AG CG GC GGC GTGCGG
 C ACAAC A
 GAM3743 G6PD 5' TCGGCCACCACCCTCG 84674 A G G
 TC GCCACCAC CCC CG
 || ||||| ||||| ||

AG CGGTGGTG GGG GC
 C _ A
 GAM3743 GNB3 5' TCAGCTGCGACGCCCGCGCCC 84675 CACC G
 TCAGC ACGCCCGCGC CC
 |||| ||||| ||
 AGTCG TCGGGGCGCG GG
 ACGC _
 GAM3743 HCN2 3' TCAGCCACTGGGCCGCCCC 84676 CAC CGC G
 TCAGCCAC GCC GC CCC
 ||||| || ||||
 AGTCGGTG CGG CG GGG
 ACC _ _
 GAM3743 HIRA 5' CAGCCGCCACCCGCGC 84677 A AC
 CAGCC CC GCCCGCGC
 |||| || |||||
 GTCGG GG TGGGCGCG
 C _
 GAM3743 IFNGR2 5' TCGGCCGCCCGCGCCCC 84678 A ACCAC G
 TC GCC GCCCGCGC CCC
 || || ||||| ||
 AG CGG CGGGCGCG GGG
 C _ _ G
 GAM3743 ILF1 5' TCGGCCGCCCGCGCACC 84679 A ACCAC C
 TC GCC GCC GCGCGCC
 || || || |||||
 AG CGG CGG CGCGTGG
 C _ _ _
 GAM3743 LRRC2 3' AGTCACCGCGCCCGGCC 84680 C A CGC
 AG CACC CGCCCG GCCC
 || |||| |||| ||
 TC GTGG GCGGGC CGGG
 A C _
 GAM3743 NESG1 5' TCAGCCACACGCCCTGACTCCG 84681 C GC GC
 TCAGCCAC ACGCCC GC CCG
 ||||| |||| || ||
 AGTCGGTG TCGGGG TG GGC
 _ AC A_
 GAM3743 ODC1 5' TCGGCCGCCCGGCCCGCGCCCG 84682 A A ACG _
 TC GCC CC CCCGC GCGCCCG
 || || || |||| |||||
 AG CGG GG GGGCG CGCGGGC
 C C _ G
 GAM3743 PSMD5 3' AGCCACCGCGCCAGCCC 84683 A CGC
 AGCCACC CGCCCG GCCC
 ||||| |||| ||
 TCGGTGG GCGGGT CGGG
 C _
 GAM3743 RENBP 5' TCAGCTGACACAGCCGCGCCCG 84684 CAC _ CGC
 TCAGC CAC GCC GCGCCCG
 |||| || || |||||

			AGTCG GTG CGG CGCGGGC		
			ACT T ____		
GAM3743	TAF1	3'	AGCCACCACGCCTGGCC 84685	CGCGC	
			AGCCACCACGCC GCC		
			TCGGTGGTGCGG CGG		
			AC____		
GAM3743	TAF1	3'	AGCCACCACGCCTGGCC 84685	CGCGC	
			AGCCACCACGCC GCC		
			TCGGTGGTGCGG CGG		
			AC____		
GAM3743	TNFRSF12	5'	TCAGCCCCGCGCCCGCAGGGCC 84686	A A C_	
			CG TCAGCC CC CGCCCGCG GCCCG		
			AGTCGG GG GCGGGCGT CGGGC		
			_ C CC		
GAM3743	ZFP103	5'	GCCGCCGCAACGCCGCGCCCG 84687	A ____ CGC	
			GCC CC ACGCC GCGCCCG		
			CGG GG TGCGG CGCGGGC		
			C CGT ____		
GAM3743	ALTE	3'	AGCCACCACGCCCGGCCACCG 84688	C GC	
			AGCCACCACGCCCG GC CCG		
			TCGGTGGTGCGGGC CG GGC		
			_ GT		
GAM3743	BNIP-S	3'	AGCCACCGCGCCCGACCACC 84689	A _ G	
			AGCCACC CGCCCG C CGCC		
			TCGGTGG GCGGGC G GTGG		
			C T_		
GAM3743	CDC14B	5'	GCCCCGCGCGCCCGCGCGCCCG 84690	A A__	
			GCC CC CGCCCGCGCGCCCG		
			CGG GG GCGGGCGCGCGGGC		
			_ CGC		
GAM3743	CDC14B	5'	GCCCCGCGCGCCCGCGCGCCCG 84690	A A__	
			GCC CC CGCCCGCGCGCCCG		
			CGG GG GCGGGCGCGCGGGC		
			_ CGC		
GAM3743	CDC14B	5'	GCCCCGCGCGCCCGCGCGCCCG 84690	A A__	
			GCC CC CGCCCGCGCGCCCG		
			CGG GG GCGGGCGCGCGGGC		
			_ CGC		
GAM3743	cerk	3'	AGCCACCGCGCCCGAGCC 84691	A CGC	
			AGCCACC CGCCCG GCC		

TCGGTGG GCGGGT CGG
C ____

GAM3743 DSIPI 5' GCCACCACGCTGGCTCCG 84692 CCGC GC
GCCACCACGC GC CCG
||||||| || |||
CGGTGGTGCG CG GGC
AC__ A_

GAM3743 EHM2 5' TCGGCCGCCCCGCGCCGCC 84693 A ACCAC _
TC GCC GCCCGCGC GCC
|| ||| ||||| |||
AG CGG CGGGCGCG CGG
C ____ G

GAM3743 FLJ10737 3' TCAGCCACCACCTGTGCGGCGC 84694 GCCC _
TCAGCCACCAC GCG CGC
||||||| ||| |||
AGTCGGTGGTG CGC GCG
GACA C

GAM3743 FLJ11637 3' AGCCACCGCGCCCGGCC 84695 A CGC
AGCCACC CGCCCG GCCC
||||| ||||| |||
TCGGTGG GCGGGC CGGG
C ____

GAM3743 FLJ12294 3' AGCCACCGCGCCCGGCC 84696 A CGC
AGCCACC CGCCCG GCC
||||| ||||| |||
TCGGTGG GCGGGC CGG
C ____

GAM3743 FLJ13952 5' CCAGCTGCTCCGCGCGCC 84697 CACCAC _ C
TCAGC GC CCGCGCGC C
|||| | ||||| |
GGTCG CG GGCGCGCG G
A____ A A

GAM3743 FLJ14345 3' AGCCACCACGCCCGGCG 84698 C
AGCCACCACGCCCG GCG
||||||| |||
TCGGTGGTGCGGGC CGC
_

GAM3743 FLJ14346 3' AGCCACCGCGCCAGCCC 84683 A CGC
AGCCACC CGCCCG GCCC
||||| ||||| |||
TCGGTGG GCGGGT CGGG
C ____

GAM3743 FLJ14547 5' TCAGCAGCCACGCGCC 84699 CACCAC C
TCAGC GCC GCGCGCC
|||| ||| |||||
AGTCG CGG TCGCGCG
T____ _

GAM3743 FLJ20059 3' AGCCACCACGCCAGCC 84700 CGC
AGCCACCACGCCCG GCC
||||||| |||

TCGGTGGTGCGGGT CGG

GAM3743 FLJ20413 3' AGCCACCGCGCCCGGCC 84696 A CGC
AGCCACC CGCCCG GCC
||||| ||||| ||
TCGGTGG GCGGGC CGG
C ____

GAM3743 FLJ20499 5' CAGCCACCGCGGACGCCC 84701 A CCCGC
CAGCCACC CG GCGCCC
||||| || |||||
GTCGGTGG GC TCGGG
C C ____

GAM3743 FLJ20700 3' AGCCACCATGCCCGGCCCA 84702 C CGC
AGCCACCA GCCCG GCCCG
||||| ||||| |||||
TCGGTGGT CGGGC CGGGT
A ____

GAM3743 FLJ21313 5' TCAGACTTCCGCGCGCC 84703 CCACC GC
TCAG AC CCGCGCGCC
||| || |||||
AGTC TG GGCGCGCGG
____ AA

GAM3743 FLJ21687 3' AGCCACCACGCTGGCC 84685 CGCGC
AGCCACCACGCC GCC
||||||| |||
TCGGTGGTGCGG CGG
AC ____

GAM3743 FLJ21777 3' AGCCACCGCGCCCGGCC 84696 A CGC
AGCCACC CGCCCG GCC
||||| ||||| |||
TCGGTGG GCGGGC CGG
C ____

GAM3743 FUSIP1 3' AGCCACCACGCCCAGCC 84700 CGC
AGCCACCACGCCCG GCC
||||||| |||
TCGGTGGTGCGGGT CGG

GAM3743 HSPC195 5' GCCGCCGCCGCCGCGCGCCCG 84704 A A_ C
GCC CC CGCC GCGCGCCCG
||| || ||||| |||||
CGG GG GCGG CGCGCGGGC
C CG _

GAM3743 KIAA0633 3' TCAGCCACCCGCCACCC 84705 A CGCGC
TCAGCCACC CGCC GCCC
||||| ||||| |||||
AGTCGGTGG GCGG TGGG

GAM3743 KIAA0720 3' TCAGCCCCGCGCCCGCAGGGCC 84686 A A C_
CG TCAGCC CC CGCCCGCG GCCCG
||||| || ||||| |||||

		AGTCGG GG GCGGGCGT CGGGC	
		_ C CC	
GAM3743 KIAA0794	3'	AGCCACCGCGCCCGGCCTTCC 84706	A C GC_
		AGCCACC CGCCCG GC CC	
		TCGGTGG GCGGGC CG GG	
		C _ GAA	
GAM3743 KIAA1198	3'	TCAGCCACCAGGTCCTCCAC 84707	CG_ CG
		TCAGCCACCA CC CGC	
		AGTCGGTGGT GG GTG	
		CCA AG	
GAM3743 KIAA1202	3'	AGCCACCATGCCCGGCC 84708	C CGC
		AGCCACCA GCCCG GCC	
		TCGGTGGT CGGGC CGG	
		A _	
GAM3743 KIAA1941	3'	AGCCACCATGCCCGGCCTCC 84709	C C GC
		AGCCACCA GCCCG GC CC	
		TCGGTGGT CGGGC CG GG	
		A _ GA	
GAM3743 KIAA1951	3'	GCCACCACAGGCGCCC 84710	CCCGC
		GCCACCACG GCGCCC	
		CGGTGGTGT CGCGGG	
		C_	
GAM3743 MGC4840	3'	AGCCATCACGCCCGGCCCA 84711	C CGC
		AGCCA CACGCCCG GCCCG	
		TCGGT GTGCGGGC CGGGT	
		A _	
GAM3743 NBR2	3'	AGCCACCATGCCTGCCC 84712	C CGCGC
		AGCCACCA GCC GCCC	
		TCGGTGGT CGG CGGG	
		A A_	
GAM3743 phorbolin-1	3'	AGCCACCGCGCCCGGCCCA 84713	A CGC
		AGCCACC CGCCCG GCCCG	
		TCGGTGG GCGGGC CGGGT	
		C _	
GAM3743 PP591	5'	AGCCACCACGCCTGGCC 84685	CGCGC
		AGCCACCACGCC GCC	
		TCGGTGGTGCGG CGG	
		AC_	
GAM3743 PRO1777	3'	AGCCACCACGCTCACCC 84714	CCGCG
		AGCCACCACGC CGCCC	

			TCGGTGGTGCG	GTGGG		
			A_____			
GAM3743	PRO1853	3'	AGCCACCACGCCCAGCC	84700		CGC
			AGCCACCACGCCCG	GCC		
			TCGGTGGTGCGGGT	CGG		

GAM3743	PRO2015	3'	AGCCACCACGCCTGGCC	84685		CGCGC
			AGCCACCACGCC	GCC		
			TCGGTGGTGCGG	CGG		
			AC_____			
GAM3743	PRO2730	3'	AGCCACCGCGCCCAGCC	84691	A	CGC
			AGCCACC	CGCCCG	GCC	
			TCGGTGG	GCGGGT	CGG	
			C_____			
GAM3743	PTD012	3'	TCAGCCACCATGCCCGGAC	84715		C C
			TCAGCCACCA	GCCCG	GC	
			AGTCGGTGGT	CGGGC	TG	
			A C			
GAM3743	QKI	5'	GCCGGCACCGCGCGCTCG	84716	ACCAC _	C
			GCC	GC	CCGCGCGC	CG
			CGG	CG	GGCGCGCG	GC
			C_____	T A		
GAM3743	RGS7	5'	CAGCCGCCACTCGCGCCC	84717	A	GCCCG
			CAGCC	CCAC	CGCGCCC	
			GTCGG	GGTG	GCGCGGG	
			C A_____			
GAM3743	RNO2	3'	AGCCACCACGCCTGGCCAGC	84718		C_ GC
			AGCCACCACGCC	GC	GC	
			TCGGTGGTGCGG	CG	CG	
			AC	GT		
GAM3743	SCYA5	3'	AGCCACCACGTCCAGCC	84719		C CGC
			AGCCACCACG	CCG	GCC	
			TCGGTGGTGC	GGT	CGG	
			A _____			
GAM3743	SLC12A5	3'	TCGGCCGCCCCGCGCCCCA	84720	A	ACCAC G
			TC	GCC	GCCCGCGC	CCCG
			AG	CGG	CGGGCGCG	GGGT
			C _____			
GAM3743	SMAP-5	3'	AGCTACCACGCCCCGGCC	84721	C	CGC
			AGC	ACCACGCCCCG	GCC	

			TCG TGGTGCGGGC CGG		
			A _		
GAM3743	SPATA1	5'	CAGCCGCGCGCCACCG 84722	A A	G
			CAGCC CC CGCCCGC CG		
			GTCGG GG GCGGGTG GC		
			C C _		
GAM3743	SSH-3	3'	GCCACCACGGCACTGCCC 84723	CCC	_
			GCCACCACG GCGC GCCC		
			CGGTGGTGC CGTG CGGG		
			_ A		
GAM3743	SYNJ2	5'	CAGCTCCCCGCGCGCCC 84724	CACCACG	
			CAGC CCCGCGCGCCC		
			GTCG GGGCGCGCGGG		
			AG_		
GAM3743	TA-LRRP	3'	AGCCACCACGCCCGGCC 84725	CGC	
			AGCCACCACGCCCG GCC		
			TCGGTGGTGCGGGC CGG		
			_		
GAM3743	ZF5128	3'	TCAGCCACCACGTCCTCCCC 84726	C GCGCG	
			TCAGCCACCACG CC CCC		
			AGTCGGTGGTGC GG GGG		
			A AGG_		
GAM3743	ZFP106	3'	AGCCACCACGCCCGGCCACG 84727	CGC	_
			AGCCACCACGCCCG GCC CG		
			TCGGTGGTGCGGGC CGG GC		
			_ T		
GAM3743	ZNF84	5'	AGCCGAGTCGCGCCCGCGCGCC 84728	ACCA_	
	CG		AGCC CGCCCGCGCGCCCG		
			TCGG GCGGGCGCGCGGGC		
			CTCAGC		
GAM3743	LOC116225	5'	CCGCCGCCGCTCGCGCCCG 84729	A A_ CG	
			CC CC CGCC CGCGCCCG		
			GG GG GCGG GCGCGGGC		
			C CG A_		
GAM3743	LOC124044	3'	TCAGCCACTGCCCGTTCC 84730	CAC CGCG	
			TCAGCCAC GCCCG CC		
			AGTCGGTG CGGGC GG		
			A_ AA_		
GAM3743	LOC145333	3'	AGCCACCGCGCCCGGCC 84696	A CGC	
			AGCCACC CGCCCG GCC		

		TCGGTGG GCGGGC CGG		
		C ____		
GAM3743	LOC145748 5'	CAGCCGCCACCGCGCC	84731	A GCCCG
		CAGCC CCAC CGCGCC		
		GTCGG GGTG GCGCGG		
		C ____		
GAM3743	LOC146713 3'	AGCCACCGCGCCCGGCCG	84732	A CGC
		AGCCACC CGCCCG GCCCG		
		TCGGTGG GCGGGC CGGGC		
		C ____		
GAM3743	LOC147165 3'	TCAGCCGCCACGCCTCTGCTC	84733	A_ C_ G
	G	TCAGCC CCACGCC GC CG		
		AGTCGG GGTGCGG CG GC		
		CG AGA A		
GAM3743	LOC149175 3'	AGCCACCACGCCCAGCC	84700	CGC
		AGCCACCACGCCCG GCC		
		TCGGTGGTGCGGGT CGG		

GAM3743	LOC150275 5'	TCGGCCGCCCGCGTCCCCAGGC	84734	A A A _ G C
	CCG	TC GCC CC CGC CC CG GCCCG		
		AG CGG GG GCG GG GT CGGGC		
		C C _ CA G C		
GAM3743	LOC150343 3'	AGCCACCATGCCTGGCCC	84735	C CGCGC
		AGCCACCA GCC GCCC		
		TCGGTGGT CGG CGGG		
		A AC__		
GAM3743	LOC151904 3'	AGCCACCACGCCCAGCC	84700	CGC
		AGCCACCACGCCCG GCC		
		TCGGTGGTGCGGGT CGG		

GAM3743	LOC152860 3'	AGCCACCGCGCCCGAGCC	84691	A CGC
		AGCCACC CGCCCG GCC		
		TCGGTGG GCGGGT CGG		
		C ____		
GAM3743	LOC153077 3'	AGCCACCATGCCCGGCA	84671	C C
		AGCCACCA GCCCG GCG		
		TCGGTGGT CGGGC CGT		
		A _		
GAM3743	LOC155066 5'	TCAGCCCCGCGCCCGCACA	84736	A A
		TCAGCC CC CGCCCGCGCG		

AGTCGG GG GCGGGCGTGT
 _ C
 GAM3743 LOC158292 5' AGTCACCGCGCCAGCTCCG 84737 C A C GC
 AG CACC CGCCCG GC CCG
 || ||| ||||| || |||
 TC GTGG GCGGGT CG GGC
 A C _ A_
 GAM3743 LOC200743 5' TCGGCACCGCCCGCGC 84738 A C AC
 TC GC ACC GCCCGCGC
 || ||| |||||
 AG CG TGG CGGGCGCG
 C _ _
 GAM3743 LOC219673 3' AGCCACCGCGCCCGGCC 84696 A CGC
 AGCCACC CGCCCG GCC
 ||||| ||||| |||
 TCGGTGG GCGGGC CGG
 C _ _
 GAM3743 LOC221042 3' TCAGCCACTGTGCACTGCCAGA 84739 _ _ CGCGC
 GCC TCAGCCAC CAC GCC GCC
 ||||| ||| ||| |||
 AGTCGGTG GTG CGG CGG
 ACAC A TCT_
 GAM3743 LOC253927 3' AGCCACCACGCCTGGCC 84685 CGCGC
 AGCCACCACGCC GCC
 ||||| |||
 TCGGTGGTGCGG CGG
 AC_
 GAM3743 LOC254387 3' AGTCACCACGCCTGGCCTCCG 84740 C CGC GC
 AG CACCACGCC GC CCG
 || ||||| || |||
 TC GTGGTGCGG CG GGC
 A AC_ GA
 GAM3743 LOC255971 3' AGCCACCGCGCCCGGCACC 84741 A C
 AGCCACC CGCCCG GCGCC
 ||||| ||||| |||||
 TCGGTGG GCGGGC CGTGG
 C _
 GAM3743 LOC256158 5' TCAGCCACGCACGTGTAGGTGC 84742 _ CCCGCGC
 CCG TCAGCCAC CACG GCCCG
 ||||| ||| |||||
 AGTCGGTG GTGC CGGGC
 C ACATCCA
 GAM3743 LOC51281 5' CAGCCACCGCGGACGCCC 84701 A CCCGC
 CAGCCACC CG GCGCCC
 ||||| || |||||
 GTCGGTGG GC TGCGGG
 C C_
 GAM3743 LOC51336 3' CCAGCCACCATGCCCGGC 84743 C C
 TCAGCCACCA GCCCG GC
 ||||| ||||| |||

GGTCGGTGGT CGGGC CG

A _

GAM3743 LOC89890 3' AGCCACCGCGCCCAGCC 84691 A CGC

AGCCACC CGCCCG GCC

||||| ||||| ||

TCGGTGG GCGGGT CGG

C _

GAM3743 LOC89958 3' AGCCACCACGCCTGGCC 84685 CGCGC

AGCCACCACGCC GCC

||||||| ||

TCGGTGGTGCGG CGG

AC _

GAM3743 LOC91547 3' AGCCACCATGCCTGGCCCA 84744 C CGCGC

AGCCACCA GCC GCCCG

||||| || ||||

TCGGTGGT CGG CGGGT

A AC _

GAM3743 LOC92231 3' TCAGCCACCGCGCCTGGC 84745 A C_

TCAGCCACC CGCC GC

||||| |||| ||

AGTCGGTGG GCGG CG

C AC

GAM3743 LOC93512 3' TCAGCCGCCACGCCTCTGCTC 84733 A_ C_ G

G TCAGCC CCACGCC GC CG

||||| ||||| ||||

AGTCGG GGTGCGG CG GC

CG AGA A

GAM3744 HS2ST1 3' TCAGAAGCACCCAATAT 84748 T TTCTC

TCAGA GC TCCAATAT

||||| || |||||

AGTCT CG GGGTTATA

T T _

GAM3744 SCA1 3' GAAGCCTCCAATGTATC 84749 T TTCT A

GA GC CTCCAAT TATC

|| || ||||| ||||

CT CG GAGGTTA ATAG

T _ C

GAM3744 FLJ12604 3' TCAGATGCTTCTTCCAA 84750 C

TCAGATGCTTCT TCCAA

||||||| ||||

AGTCTACGAAGA AGGTT

-

GAM3744 HSPCAL3 3' TCAACTTTTTTCTCCAATAT 84751 GAT C_

TCA GCTT TCTCCAATAT

|| ||| |||||

AGT TGAA AGAGGTTATA

_ AAA

GAM3744 KIAA0391 3' AATGCTCTCAATATAT 84752 T TCC

GATGCT CTC AATATAT

||||| ||| |||||

TTACGA GAG TTATATA

GAM3744 MYOZ2 3' TCATATGCTTCTTCAATTATAT 84753 G CTC _
TCA ATGCTTCT CAAT ATAT
||| ||||| ||| ||||
AGT TACGAAGA GTTA TATA
A A_ A

GAM3744 TP53INP1 3' GATGCCATTTCTAATATATC 84754 TCTC C
GATGCT TC AATATATC
||||| || |||||
CTACGG AG TTATATAG
TAA_ A

GAM3744 TP53INP1 3' GATGCCATTTCTAATATATC 84754 TCTC C
GATGCT TC AATATATC
||||| || |||||
CTACGG AG TTATATAG
TAA_ A

GAM3744 LOC147622 5' TCAGATACTTTTTGGTTTATAT 84755 CTCTCCAA
C TCAGATGCTT TATATC
||||||| |||||
AGTCTATGAA ATATAG
AAACCAA_

GAM3744 LOC150225 3' TCAGGTGCTTCTCTTACC 84756 A _
TCAG TGCTTCTCT CC
||| ||||| ||
AGTC ACGAAGAGA GG
C AT

GAM3744 LOC196484 5' CAGATGCTTTTCTCAAAC 84757 C C
CAGATGCTT TCTC AAT
||||||| ||| |||
GTCTACGAA AGAG TTG
A T

GAM3744 LOC91069 3' CAGATGCTTTTCTCAAAT 84758 C C
CAGATGCTT TCTC AAT
||||||| ||| |||
GTCTACGAA AGAG TTA
A T

GAM3745 AKAP2 3' TAAGTGGTTAACATACACA 84761 A _
TAA TGGTTAA ATATACA
||| ||||| |||||
ATT ACCAATT TATGTGT
C G

GAM3745 CRI1 3' AAATGGTTATGACAATG 84762 AATAT
AAATGGTTA ACAATG
||||||| |||||
TTTACCAAT TGTTAC
AC_

GAM3745 DHFR 3' AAATGGTTAAGTACAAT 84763 ATA
AAATGGTTAA TACAAT
||||||| |||||

		TTTACCAATT ATGTTA		
		C__		
GAM3745 DLD	3'	GGTTAAATAAAAACAAGTGA 84764	T_ _	
		GGTTAAATA ACAA TGA		
		CCAATTTAT TGTT ACT		
		TT C		
GAM3745 ITM2B	3'	TAAATAGTTAAATATATTTGA 84765	CAA	
		TAAATGGTTAAATATA TGA		
		ATTTATCAATTTATAT ACT		
		AA_		
GAM3745 NT5C2	3'	ATGGAAGAAAATATACAATG 84766	TT__	
		ATGG AAATATACAATG		
		TACC TTTATATGTTAC		
		TTCT		
GAM3745 PFN2	3'	TGGTTAACATACAAATGA 84767	A _	
		TGGTTAA TATACAA TGA		
		ACCAATT GTATGTT ACT		
		_ T		
GAM3745 PFN2	3'	TGGTTAACATACAAATGA 84767	A _	
		TGGTTAA TATACAA TGA		
		ACCAATT GTATGTT ACT		
		_ T		
GAM3745 RB1CC1	3'	TAAATGGTTAATGTGCAATGA 84768	ATATA	
		TAAATGGTTAA CAATGA		
		ATTTACCAATT GTTACT		
		ACAC_		
GAM3745 DIS3	3'	ATGGCCAAATATACGATGA 84769	A	
		ATGGTTAAATATAC ATGA		
		TACCGGTTTATATG TACT		
		C		
GAM3745 DKFZp434B0417	3'	ATGTGTTAAATGTACAATG 84770	_ A	
		ATG GTTAAAT TACAATG		
		TAC CAATTTA ATGTTAC		
		A C		
GAM3745 HSPC052	3'	TGATGGTTAAACATATTATAAT 84771	A C__	
G		A ATGGTTAAATATA AATG		
		A TACCAATTTGTAT TTAC		
		C AATA		
GAM3745 KIAA1247	3'	TAAATAGTCACATATATACAAT 84772	A__	
GA		TAAATGGTTA ATATACAATGA		

		ATTTATCAGT TATATGTTACT	
		GTA	
GAM3745 KIAA1497	5'	TGATGGACCGCATATACAATG 84773	A TTAA_
		A ATGG ATATACAATG	
		A TACC TATATGTTAC	
		C TGGCG	
GAM3745 RBM12	3'	TAAAGGTACATACAATG 84774	T TAA
		TAAA GGT ATATACAATG	
		ATTT CCA TGTATGTTAC	
GAM3745 UBE2D1	3'	CAAATGGTTTCATGGTACAATG 84775	AA A_
A		TAAATGGTT AT TACAATGA	
		GTTTACCAA TA ATGTTACT	
		AG CC	
GAM3745 LOC51133	5'	AAATGGTTATTTCAACAATG 84776	AATAT
		AAATGGTTA ACAATG	
		TTTACCAAT TGTTAC	
		AAAGT	
GAM3746 A2M	3'	GAACAGGACTCCAGCAAAGCAC 84779	AA GAACT
		GAACA AC CAAAGCAC	
		CTTGT TG GTTTCGTG	
		CC AGGTC	
GAM3746 ABCD2	5'	CGAACAAAACCGGCTCTAGC 84780	GAA AA
		CGAACAAAAC CTC AGC	
		GCTTGTTTTG GAG TCG	
		GCC A_	
GAM3746 CDKN1B	5'	CGAACAAAACAAAGCGC 84781	CTCAAA
		CGAACAAAACGAA GC	
		GCTTGTTTTGTTT CG	
		CG_	
GAM3746 CSDA	3'	GAACAAAACGGAAAAAAAGC 84782	_ AACTC_
A		GAACAAAA CG AAAGCA	
		CTTGTTTT GC TTTCGT	
		T CTTTTT	
GAM3746 GARS	5'	ACGAGAACCTTCAAAGCA 84783	ACAAAAC _
		ACGA GAAC TCAAAGCA	
		TGCT CTTG AGTTTCGT	
		GA	
GAM3746 SELP	3'	AACAGGTGAGTCAAAGCAC 84784	AAAC AC
		AACA GA TCAAAGCAC	

			TTGT CT AGTTTCGTG		
			CCA_ C_		
GAM3746	SNAP25	3'	GAACAAAAGACACAAAG 84785	C	ACT
			GAACAAAA GA CAAAG		
			CTTGTTTT CT GTTTC		
			_ GT_		
GAM3746	SNAP25	3'	GAACAAAAGACACAAAG 84785	C	ACT
			GAACAAAA GA CAAAG		
			CTTGTTTT CT GTTTC		
			_ GT_		
GAM3746	ZFP36L1	3'	GAACAAAATTAACAAAAAAAAG 84786	CG	TC__
	CA		GAACAAAA AAC AAAGCA		
			CTTGTTTT TTG TTTCGT		
			AA TTTTT		
GAM3746	DNAJC5	3'	ACCGGACGGGCCTCAAAGCAC 84787	AAA	AA_
			AC ACG CTCAAAGCAC		
			TG TGC GAGTTTCGTG		
			GCC CCG		
GAM3746	EVI5	3'	CGAACAAAAATCCCCAAAGCAC 84788	CGAA	
			CGAACAAAA CTCAAAGCAC		
			GCTTGTTTT GGGTTTCGTG		
			TAG_		
GAM3746	FIGN	3'	CAAACAAAAAATAAAGCA 84789	CGAACTC	
			CGAACAAAA AAAGCA		
			GTTTGTTTT TTTCGT		
			TTA__		
GAM3746	FLJ12526	5'	ACAAACAAAGTCCCGCGGAGCA 84790	ACGAA	AA__
	C		ACGAACAAA CTC AGCAC		
			TGTTTGTTT GGG TCGTG		
			CA__ CGCC		
GAM3746	FLJ22054	3'	ACAGACAAGGAATCAAAGCAC 84791	A	AAC C
			ACG ACAA GAA TCAAAGCAC		
			TGT TGTT CTT AGTTTCGTG		
			C C_ _		
GAM3746	gm117	3'	GACAAAACCTCAAAGCA 84792	A	GAA
			GA CAAAAC CTCAAAGCA		
			CTGTTTTG GAGTTTCGT		
			_ A_		
GAM3746	KIAA0982	3'	GAAAAGAACATATACAAAGCAC 84793	CAA	AACT
			GAA AACG CAAAGCAC		

		CTT TTGT GTTTCGTG	
		TTC ATAT	
GAM3746 LHX6	3'	ACAAATAAGACATTTACAAAGC 84794	C A AACT
	AC	ACGAA AA ACG CAAAGCAC	
		TGTTT TT TGT GTTTCGTG	
		A C AAAT	
GAM3746 MGC15437	3'	ACAAACAAAACGACAGCA 84795	A TCAA
		ACGAACAAAACGA C AGCA	
		TGTTTGTTTTGCT G TCGT	

GAM3746 VRP	5'	CGAACAGGGTCTCAAAGCAC 84796	AAACGAA
		CGAACA CTCAAAGCAC	
		GCTTGT GAGTTTCGTG	
		CCCA_____	
GAM3746 LOC120856	3'	ACGAACAAAACAGAACTTCAA 84797	- -
		ACGAACAAAAC GAACT CAA	
		TGCTTGTTTTG CTTGA GTT	
		T A	
GAM3746 LOC122700	3'	GAACAAAACATCATTTTCAAAG 84798	AAC_____
		GAACAAAACG TCAAAG	
		CTTGTTTTGT AGTTTC	
		AGTAAA	
GAM3746 LOC134218	3'	AACAAAACACAAAAGCA 84799	AACTC
		AACAAAACG AAAGCA	
		TTGTTTTGT TTTCGT	
		GT_____	
GAM3746 LOC136263	3'	AAACAAAATACATACACTCAAG 84800	CGA_____ A
	GCAC	GAACAAAA ACTCAA GCAC	
		TTTGTTTT TGAGTT CGTG	
		ATGTATG C	
GAM3746 LOC136319	3'	GAAAAAATGAACTCAAA 84801	C C
		GAA AAAA GAACTCAAA	
		CTT TTTT CTTGAGTTT	
		- A	
GAM3746 LOC145566	5'	GAACGAGGAGAGGCTCAAAGCA 84802	AAAAC A_
		GAAC GA CTCAAAGCA	
		CTTG CT GAGTTTCGT	
		CTCCT CC	
GAM3746 LOC161527	5'	GAACAAAACATCTCTAGAGCAC 84803	AA AA_
		GAACAAAACG CTC AGCAC	

		CTTGTTTTGT GAG TCGTG	
		A_ ATC	
GAM3746	LOC201848 3'	GAACAACTGATAGGGTTTAAA 84804	AC ACTC_____
		GCAC GAACAAA GA AAAGCAC	
		CTTGTTT CT TTTCGTG	
		GA ATCCCAA	
GAM3746	LOC220558 3'	GAACAAAAACGGAAAAAAAGC 84782	_ AACTC_
		A GAACAAA CG AAAGCA	
		CTTGTTTT GC TTTCGT	
		T CTTTT	
GAM3747	GALC 3'	ACTTTAAAAAGTAAGTACA 84807	CACCTC
		GCTTT AAGTAAGTACA	
		TGAAA TTCATTCATGT	
		TTT_	
GAM3747	HPGD 3'	TAGCTTTCCTCTTTTAAAGTA 84808	AC CAAGT
		TAGCTTTC CT AAGTA	
		ATCGAAAG GA TTCAT	
		GA AAAT_	
GAM3747	LARS 3'	TAGCCTTCATCAAAGTA 84809	CC _
		TAGCTTTCA TCAA GTA	
		ATCGGAAGT AGTT CAT	
		_ T	
GAM3747	NCALD 3'	TAGCTTTCAATTCAAATTAGT 84810	CC A
		TAGCTTTCA TCAAGT AGT	
		ATCGAAAGT AGTTTA TCA	
		TA A	
GAM3747	NRAS 3'	TAGCTTTCCTTCAATGGTA 84811	ACC GTAA
		TAGCTTTC TCAA GTA	
		ATCGAAAG AGTT CAT	
		GA_ AC_	
GAM3747	PTGS2 3'	GCTTTTCACTTAAAATAAGT 84812	_ CTC
		GCTTT CAC AAGTAAGT	
		CGAAA GTG TTTATTCA	
		A AAT	
GAM3747	SH2D1A 3'	GCTTTTACCTCAAGAAAT 84813	C T
		GCTTT ACCTCAAG AAGT	
		CGAAA TGGAGTTC TTTA	
		A _	
GAM3747	SLC9A6 3'	GCCTTTTCGGAGAGTAAGTACA 84814	CACCTCA
		GCTTT AGTAAGTACA	

		CGGAA TCATTCATGT	
		AGCCTC_	
GAM3747 XCL1	3'	TAGCTTTACCTCTGATAGACA 84815	AA A T
		TAGCTTTACCTC GTA G ACA	
		ATCGAAAGTGGAG TAT C TGT	
		AC _ _	
GAM3747 BPESC1	3'	GCTTTCACCACAGAGAGCA 84816	TCA TA
		GCTTTCACC AG AGTA	
		CGAAAGTGG TC TCGT	
		TG_ TC	
GAM3747 CENTG1	3'	TAGCTTCCACCCATGGGTAGGT 84817	CAA_ A
		TAGCTTTACCT GTA GT	
		ATCGAAGGTGGG CAT CA	
		TACC C	
GAM3747 KIAA0436	3'	TAACTTTCACCTTAGGCA 84818	CAA
		TAGCTTTACCT GTA	
		ATTGAAAGTGGA CGT	
		ATC	
GAM3747 KIAA1679	3'	TAGCTTTCATCTAGTCCAGCA 84819	CC A A_
		TAGCTTTC TC AGT AGTA	
		ATCGAAAGT AG TCA TCGT	
		_ A GG	
GAM3747 MRPS27	3'	TAGCTTTCTCCTCAGAACTTA 84820	A AGTAAG
CA		TAGCTTTC CCTCA TACA	
		ATCGAAAG GGAGT ATGT	
		A CTTTGA	
GAM3747 NIR3	3'	TAGCTTTCACCTCTGTA 84821	C AA
		TAGCTTTCAC TC GTA	
		ATCGAAAGTG AG CAT	
		_ A_	
GAM3747 SH3BGRL2	3'	TAGCTTTGTCTAGCAAGTA 84822	CACC A
		TAGCTTT TC AGTAAGTA	
		ATCGAAA AG TCGTTCAT	
		C_ A	
GAM3747 LOC199796	5'	GCTTCACCTTGGTAAAC 84823	T CAA GT
		GCTT CACCT GTAA AC	
		CGAA GTGGA CATT TG	
		_ AC_ _	
GAM3747 LOC90529	3'	TAGCTTTGCCCAGTAGAC 84824	A CA A T
		TAGCTTTC CCT AGTA G AC	

ATCGAAAG GGG TCAT C TG
 C _ _
 GAM3748 USH2A 5' ACAGGACCGCTGTCCCTCGT 84827 A G GC
 ATAG ACCGCTGTC CC CGT
 |||| ||||| || |||
 TGTC TGGCGACAG GG GCA
 C _ A_
 GAM3748 C22orf2 3' TAGAACTGCTGTACACAG 84828 C _
 TAGAAC GCTGTGCGC CG
 ||||| ||||| ||
 ATCTTG CGACAGTG GC
 A T
 GAM3748 DAMS 3' GAATCCGTGCCGCCGTC 84829 CCG C
 GAA CTGT GCCGCCGTC
 || ||| |||||
 CTT GGCA CGGCGGCAG
 A _ _
 GAM3748 DOC-1R 5' GCTGTGCGCAGCTGCCGTCG 84830 C__
 GCTGTGCGC GCCGTCG
 ||||| |||||
 CGACAGCG CGGCAGC
 TCGA
 GAM3748 HUMAGCGB 5' ATAGGGGCGCCACCGTCGTCG 84831 AAC GT C
 ATAG CGCT CGCCG CGTCG
 |||| ||| |||| |||||
 TATC GCGG GTGGC GCAGC
 CCC _ A
 GAM3748 KIAA1102 5' GAGGACGGCCGCCGCCGTCG 84832 ACC T
 GA GC GTCGCCGCCGTCG
 || || ||||| |||||
 CT TG CGGCGGCGGCAGC
 CC_ C
 GAM3748 RALY 5' GAGTCGTCGTCGTCGCCGTCG 84833 AC C C
 GA CG TGTCG CGCCGTCG
 || || |||| |||||
 CT GC GCAGC GCGGCAGC
 CA A A
 GAM3749 CYLD 3' TCCTGTATATTTTAATTAAATA 84836 GC
 TCTTGTAT ATTTTAATTAAATA
 ||||| ||||| |||||
 AGGACATA TAAAATTAATTTAT
 _
 GAM3749 FLJ20689 3' TCTTGTGGCATTTTTAAAAAAT 84837 AT TT
 TCTTGT GCATTTTAA AAAT
 ||||| ||||| |||||
 AGAACA CGTAAAATT TTTA
 C_ T_
 GAM3749 FLJ22670 3' TCTTGTGCTGCCAATTAAAT 84838 A_ ATTT
 TCTTGT TGC TAATTAAAT
 ||||| ||| |||||

			AGAACA ACG GTTAATTTA		
			CG ____		
GAM3749	LOC202860	3'	TCTTGGTGCATTTTAAATCA 84839	TA	
			TCTTG TGCATTTTAATTA		
			AGAAC ACGTAAAATTAGT		
			C_		
GAM3749	LOC90719	3'	TCTTGTATTGCATTTTTTTTCAA 84840	_	AA
			TCTTGTAT GCATTTT TTAA		
			AGAACATA CGTAAAA AGTT		
			A AA		
GAM3749	LOC92293	3'	TCTTGTTGCATTTTTTTAAACAAA 84841	A	AAT_
			TA TCTTGT TGCATTTT TAAATA		
			AGAACA ACGTAAAA GTTTAT		
			_ AATT		
GAM3750	PDYN	3'	TTTATGATGTGTATACTA 84844	AACA	
			TTTATGATGT TATATTA		
			AAATACTACA ATATGAT		
			C_		
GAM3751	BAT5	3'	TGAACACAGAGAATCACAAATA 84847	C	CCA
			A TGA CACAGAGA ACAAATAA		
			ACT GTGTCTCT TGTTTATT		
			T TAG		
GAM3751	CANX	3'	TGACCACAGAACAACA 84848	AC	
			TGACCACAGAG CAACA		
			ACTGGTGTCTT GTTGT		
			—		
GAM3751	CTGF	3'	TGGTCACACTCTCAACAAATAA 84849	AC	GAGAC
			A TG CACA CAACAAATAAA		
			AC GTGT GTTGTTTATTT		
			CA GAGA_		
GAM3751	FUT3	3'	TGGCCACAAAGGACTCCAGCA 84850	A	A_ A
			TG CCACAGAG CCA CA		
			AC GGTGTTTC GGT GT		
			C CTGA C		
GAM3751	HOXD4	3'	ACCACATTTCCCAACAAATAAA 84851	GAGA	
			ACCACA CCAACAAATAAA		
			TGGTGT GGTGTTTATTT		
			AAAG		
GAM3751	MBL2	3'	TGACACAAGCATCAACAAATA 84852	C G AC_	
			TGAC ACA AG CAACAAATA		

			ACTG TGT TC GTTGTTTAT		
			— — GTA		
GAM3751	MYBL1	3'	ACCACAAAAGCAAATAA 84853	ACCAA	
			ACCACAGAG CAAATAA		
			TGGTGTTTT GTTTATT		
			C_____		
GAM3751	PPP4R1	3'	TGGCCACAGAGCCCAGCAA 84854	A A A	
			TG CCACAGAG CCA CAA		
			AC GGTGTCTC GGT GTT		
			C G C		
GAM3751	SCN3A	5'	TGACCACAGAGGTTTACAAA 84855	ACCA	
			TGACCACAGAG AAAAA		
			ACTGGTGTCTC TGTTT		
			CAAA		
GAM3751	FLJ13449	3'	CACAAAGACTCCCAAATAAA 84856	CAA	
			CACAGAGAC CAAATAAA		
			GTGTTTCTG GTTTATTT		
			AGG		
GAM3751	FLJ20533	3'	TGAGCACGAACACTAACAAATA 84857	C AG G C	
			TGA CAC A AC AACAAATA		
			ACT GTG T TG TTGTTTAT		
			C CT G A		
GAM3751	FLJ22833	3'	ACTATAGACCACAAATAA 84858	AG_ A	
			AC AGACCA CAAATAA		
			TG TCTGGT GTTTATT		
			ATA _		
GAM3751	HRH4	3'	TGCCCCGGCCAACAAATAA 84859	A ACAGAGA	
			TG CC CCAACAAATAA		
			AC GG GGTGTTTATT		
			_ GCC_____		
GAM3751	ITPK1	3'	TGGCCATGGAGACCAACAGACA 84860	A CA A	
			TG CCA GAGACCAACA ATA		
			AC GGT CTCTGGTTGT TGT		
			C AC C		
GAM3751	MIC2L1	3'	TGACCACAGAGCTACAAA 84861	ACCA	
			TGACCACAGAG AAAAA		
			ACTGGTGTCTC TGTTT		
			GA__		
GAM3751	LOC145508	3'	TGGCCACAAAAAGACAAATAAA 84862	A CCA	
			TG CCACAGAGA ACAAATAAA		

		AC GGTGTTTT TGTTATTT	
		C C_	
GAM3751	LOC158046 3'	TGATCATTAGATCCCACAAATA 84863	C C_ GA A
	A	TGA CA AGA CCA CAAATAA	
		ACT GT TCT GGT GTTTATT	
		A AA AG _	
GAM3751	LOC169026 3'	ACCACAGAGCCCTAGATAAA 84864	A AACAA
		ACCACAGAG CC ATAAA	
		TGGTGTCTC GG TATTT	
		_ GATC_	
GAM3752	CLASP1 5'	TGGCACTCCCAGAGCTTTGCC 84867	A TATACCTC
		TGG ACTCCCGGA GCC	
		ACC TGAGGGTCT CGG	
		G CGAAA_	
GAM3752	LEP 3'	TGGAATTCTCAGAGGGAACCT 84868	C C TAT_
		TGGAA TC CGGA ACCT	
		ACCTT AG GTCT TGGA	
		A A CCCT	
GAM3752	KCNN1 5'	GGGCCGCCGATATGTCTTGC 84869	AA C AC C
		GG CT CCGGATAT CT GC	
		CC GG GGCCTATA GA CG	
		C_ C CA A	
GAM3752	KIAA0172 5'	TGGAAGTCCATATACCTTGC 84870	C CGG C
		TGGAA TCC ATATACCT GC	
		ACCTT AGG TATATGGA CG	
		C _ A	
GAM3752	LOC221271 3'	TGGAACTCATACCTG 84871	CCGGAT C
		TGGAACTC ATACCT G	
		ACCTTGAG TATGGA C	
		_ A	
GAM3752	LOC92379 3'	TGGAATTCCACTTTACCTCGCC 84872	C CGGATA
		TGGAA TCC TACCTCGCC	
		ACCTT AGG ATGGAGCGG	
		A TGAA_	
GAM3753	ADAR 3'	TAAGTCATGATTATCTGA 84875	CAATT GA
		TAAGTCATGA TTA TGA	
		ATTCAGTACT AAT ACT	
		_ AG	
GAM3753	ADAR 3'	TAAGTCATGATTATCTGA 84875	CAATT GA
		TAAGTCATGA TTA TGA	

		ATTCAGTACT AAT ACT	
		_____ AG	
GAM3753	ADAR	3' TAAGTCATGATTATCTGA 84875	CAATT GA
		TAAGTCATGA TTA TGA	
		ATTCAGTACT AAT ACT	
		_____ AG	
GAM3753	UCP3	3' AGTCATAATAATTTCCCGA 84876	C A_
		AGTCATGA AATTTT GA	
		TCAGTATT TTAAAG CT	
		A GG	
GAM3753	FLJ21934	3' GCCATGACATCTAGATGAG 84877	AT
		GTCATGACA TTTAGATGAG	
		CGGTACTGT AGATCTACTC	

GAM3753	LOC220115	5' CAAGTTGTCTTTT TAGATGAG 84878	CA ACAA
		TAAGT TG TTTTAGATGAG	
		GTTCA AC AAAATCTACTC	
		___ AGA_	
GAM3753	LOC257117	5' TAAGTCATGAAATATG 84879	C TTTAG
		TAAGTCATGA AAT ATG	
		ATTCAGTACT TTA TAC	

GAM3753	LOC93538	3' TAAGTCATTGCAATTTTAA 84880	GA
		TAAGTCAT CAATTTTAG	
		ATTCAGTA GTTAAAATT	
		AC	
GAM3754	C18orf1	3' CATTTTCTCATAAACTATGCA 84883	CG AACAG
		CA TTCTCATAAA GCA	
		GT AAGAGTATTT CGT	
		AA GATA_	
GAM3754	KIF3B	3' GTTCTTATTCAAACAGGCA 84884	C AA
		GTTCT AT AAACAGGCA	
		CAAGA TA TTTGTCCGT	
		A AG	
GAM3754	NRG1	3' GTTCTCATGCGACAGGCA 84885	AAAA
		GTTCTCAT ACAGGCA	
		CAAGAGTA TGTCCGT	
		CGC_	
GAM3754	NRG1	3' GTTCTCATGCGACAGGCA 84885	AAAA
		GTTCTCAT ACAGGCA	

CAAGAGTA TGTCCGT
 CGC_
 GAM3754 PODXL 3' TCCTGTTTTCCCCAAACAGGC 84886 ACG_ ATAA
 A TCC TTCTC AAACAGGCA
 ||| |||| |||||
 AGG AAGGG TTTGTCCGT
 ACAA GG_
 GAM3754 SEPN1 3' TCCACTTTGGGGAAAACAGGCA 84887 GTTCTCATA
 TCCAC AAAACAGGCA
 |||| |||||
 AGGTG TTTTGTCCGT
 AAACCCC_
 GAM3754 DKFZP434J037 3' CCCATGTACACAAGAAACAGGC 84888 C TCT _
 A TCCA GT CATAA AAACAGGCA
 ||| || |||||
 GGGT CA GTGTT TTTGTCCGT
 A T_ C
 GAM3754 ERO1L 3' TCCATTGTCCAGAAACAGGCA 84889 C_ TCATAA
 TCCA GTTC AAACAGGCA
 ||| ||| |||||
 AGGT CAGG TTTGTCCGT
 AA TC_
 GAM3754 FLJ13912 3' TCCATCTTAAACAGG 84890 CGT CATA
 TCCA TCT AAAACAGG
 ||| ||| |||||
 AGGT AGA TTTTGTCC
 _ A_
 GAM3754 FLJ20055 5' TCCATGTTTAAACAGG 84891 C CTCATA
 TCCA GTT AAAACAGG
 ||| ||| |||||
 AGGT CAA TTTTGTCC
 A A_
 GAM3754 FLJ22215 3' CGTCACTATAGAAACAGGC 84892 _ C A
 CGTT CT ATA AAACAGGC
 ||| || |||||
 GCAG GA TAT TTTGTCCG
 T _ C
 GAM3754 IL18BP 5' GTTTCATATGAACAGGCA 84893 CT AA
 GTT CATA AACAGGCA
 ||| ||| |||||
 CAA GTAT TTGTCCGT
 AG AC
 GAM3754 KIAA1209 3' GTATCGATTAGAAACAGGCA 84894 _ TCA A
 GT TC TA AAACAGGCA
 || || |||||
 CA AG AT TTTGTCCGT
 T CTA C
 GAM3754 LHFP 3' TCCACGTTTGTGCATAGGC 84895 CT_ AAAAAC
 TCCACGTT CAT AGGC
 ||||| ||| |||

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AGGTGCAA GTA TCCG
ACAC _____
GAM3754 TIGD1 5' TCCACGTCTTATAAAAGAC 84896 T C AAC
TCCACGT CT ATAAA AGGC
||||| || |||| |||
AGGTGCA GA TATTT TCTG
_ A _
GAM3754 LOC196812 3' GTTTTCATAAAAATGGCA 84897 C CA
GTT TCATAAAAA GGCA
||| ||||||| |||
CAA AGTATTTTT CCGT
A A_
GAM3754 LOC221312 3' TCTGGCAAGAAAACAGGCA 84898 _ TA
TCT CA AAAACAGGCA
||| || |||||||
AGA GT TTTTGTCCGT
CC TC
GAM3754 LOC63923 3' CAAGACCCTCATAAAGACGGGC 84899 C_ TT A A
A CA G CTCATAAA AC GGCA
|| | |||||| | |||
GT T GAGTATTT TG CCGT
TC GG C C
GAM3755 CASP7 3' TGATGGATACATATC 84902 C GTGTCC
TG ATGGA TACATATC
|| |||| |||||||
AC TACCT ATGTATAG
_ _
GAM3755 CASP7 3' TGATGGATACATATC 84902 C GTGTCC
TG ATGGA TACATATC
|| |||| |||||||
AC TACCT ATGTATAG
_ _
GAM3755 CASP7 3' TGATGGATACATATC 84902 C GTGTCC
TG ATGGA TACATATC
|| |||| |||||||
AC TACCT ATGTATAG
_ _
GAM3755 CYR61 3' CATGGAGTGTCCCCCTTCA 84903 ACATA
CATGGAGTGTCCCT TCA
||||||||| |||
GTACCTCACAGGG AGT
GGA_
GAM3755 GAS7 3' TAGAGTGCCTATGTATCAA 84904 T CA
TGGAGTG CCTA TATCAA
||||| ||| |||||
ATCTCAC GGAT ATAGTT
_ AC
GAM3755 HPGD 3' TGTATGTGAGTGTTTTACA 84905 C _ CC
TG ATG GAGTGT TACA
|| ||| ||||| |||

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AC TAC CTCACA ATGT
A A AA
GAM3755 ITPR2 3' TGCATGCAGACATATC 84906 G TGTCTT
TGCATG AG ACATATC
||||| || |||||
ACGTAC TC TGTATAG
G _____
GAM3755 ARAP3 3' CATGGAACCCCTACGTATCAA 84907 GTG A
CATGGA TCCTAC TATCAA
||||| ||||| |||||
GTACCT GGGATG ATAGTT
TG_ C
GAM3755 DCOHM 3' GAGTGGCAACTACATATCAA 84908 TC__
GAGTG CTACATATCAA
||||| ||||| |||||
CTCAC GATGTATAGTT
CGTT
GAM3755 FLJ13110 3' TGCAGTTTTCTTACATATCA 84909 G G_ C
TG AGT TC TACATATCA
|| ||| || ||||| |||||
AC TCA AG ATGTATAGT
G AA A
GAM3755 FLJ21934 3' TGTGTAGAGCTTTACATATCAA 84910 CA GTCC
TG TGGAGT TACATATCAA
|| ||||| ||||| |||||
AC ATCTCG ATGTATAGTT
AC AA__
GAM3755 KIAA1826 3' CAAGAATTGTTCTACATAT 84911 T G C
CA GGA TGT CTACATAT
|| ||| || ||||| |||||
GT CTT ACA GATGTATA
T A A
GAM3755 NPFF 3' TGCATGCAGACATATC 84906 G TGTCTT
TGCATG AG ACATATC
||||| || |||||
ACGTAC TC TGTATAG
G _____
GAM3755 PGR1 3' TGCATGGAGTCGTCTTCCA 84912 _ CTA
TGCATGGAGT GTC CA
||||||| ||| ||
ACGTACCTCA CAG GT
G AAG
GAM3755 RNAH 3' TGCTTTTTCATCTTACATATCA 84913 ATGGAG C
A TGC TGTC TACATATCAA
||| ||| ||||| |||||
ACG GTAG ATGTATAGTT
AAAAA_ A
GAM3755 LOC155438 3' TGCAGGAGTGTCTTCACCA 84914 T CTACA
TGCA GGAGTGTC TATCA
||||| ||||| |||||

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		ACGT CCTCACAG GTGGT		
		— AA—		
GAM3755	LOC197287 3'	TGCAAGGACCTGCATATCA 84915	T GTGT A	
		TGCA GGA CCT CATATCA		
		ACGT CCT GGA GTATAGT		
		T — C		
GAM3755	LOC221981 3'	GCAGAATGTCTTATATGTCAA 84916	TG C C A	
		GCA GAGTGTC TA AT TCAA		
		CGT CTTACAG AT TA AGTT		
		— A A C		
GAM3756	FGF6 3'	TCAATCGAACAGATGATGCTTT 84919	CGCAAC_	
A		TCGATCGGAT GCTTTA		
		AGTTAGCTTG CGAAAT		
		TCTACTA		
GAM3757	GABARAPL3 5'	AGGGGGACCTCGGGTGCG 84922	TGT A A	
		AGG GA TCTCG GTGCG		
		TCC CT GGAGC CACGC		
		CC_ _ C		
GAM3757	PEG10 3'	TAGGAGTGTGAATCTGGGTG 84923	AA CGA	
		TAG GGTGTGAATCT GTG		
		ATC TCACACTTAGA CAC		
		C_ CC_		
GAM3758	CASP10 3'	TGCAGGGCTGTGAAGTGAGAC 84926	AGACG _ _	
		TGCA TGTGAAGT AG C		
		ACGT ACACTTCA TC G		
		CCCG_ C T		
GAM3758	FEZ1 3'	AAGACCCTAGAAAGTAGCGA 84927	GTGT_	
		AAGAC GAAGTAGCGA		
		TTCTG TTTCATCGCT		
		GGATC		
GAM3758	FPGS 3'	TGCAAGGCATGTGAAATGCAGC 84928	A _	
		TGCAAG CGTGTGAA GTAGC		
		ACGTTT GTACACTT CGTCG		
		C TA		
GAM3758	PABPN1 3'	AGACGTGTCCATGGCGAA 84929	GAA A	
		AGACGTGT GT GCGAA		
		TCTGCACA TA CGCTT		
		GG_ C		
GAM3758	PITPNB 3'	TGCAGGACATGTGGGAAAAC 84930	A AAGT	
		TGCA GACGTGTG AGC		

ACGT CTGTACAC TTG
 C CCTT
 GAM3758 DKFZp761N1114 3' TGTCAGGCGTGTGAATCACAGC 84931 CA A G__
 TG AG CGTGTGAA TAGC
 || || ||||| ||||
 AC TC GCACACTT GTCG
 AG C AGT
 GAM3758 KIAA1128 3' TGCAAGACGTGTGTAAAGC 84932 AAGT
 TGCAAGACGTGTG AGC
 ||||| ||||| ||||
 ACGTTCTGCACAC TCG
 ATT_
 GAM3758 MGC14839 3' AAGGTGTGTGAAAAAGGA 84933 AC T C
 AAG GTGTGAAG AG GA
 ||| ||||| || ||
 TTC CACACTTT TC CT
 CA T _
 GAM3758 MGC26651 3' TGCAAAGTATACAAAGTAGTGA 84934 AC TG C
 A TGCAAG GTG AAGTAG GAA
 ||||| ||| ||||| ||||
 ACGTTT TAT TTCATC CTT
 CA GT A
 GAM3758 LOC112609 3' GCAAGACAGGTGGTGAAC 84935 T AA _
 GCAAGACG GTG GT AGC
 ||||| ||| || ||||
 CGTTCTGT CAC CA TTG
 C _ C
 GAM3758 LOC145547 5' TGCAGGATCGGTGGGTAGCGAA 84936 A _ T AA
 C TGCA GA CG GTG GTAGCGAAC
 |||| || || ||||| |||||
 ACGT CT GC CAC CATCGCTTG
 C A _ C_
 GAM3758 LOC149478 3' TGTGAGACGTGTCAGACAGGA 84937 CA GA _ C
 TG AGACGTGT AG TAG GA
 || ||||| || |||| ||
 AC TCTGCACA TC GTC CT
 AC G_ T _
 GAM3758 LOC91796 3' TGTA AACGTGTGTTTGAAC 84938 C AAGT
 TG AAGACGTGTG AGC
 || ||||| ||||| ||||
 AC TTTTGCACAC TTG
 A AAAC
 GAM3759 SNAP23 3' TATATGAATCACTAAGAG 84941 AGTTGC
 TATATGAATTAT AAGAG
 ||||| ||||| |||||
 ATATACTTAGTG TTCTC
 A_____
 GAM3759 SNAP23 3' TATATGAATCACTAAGAG 84941 AGTTGC
 TATATGAATTAT AAGAG
 ||||| ||||| |||||

			ATATACTTAGTG	TTCTC	
			A_____		
GAM3759	DNAM-1	3'	TATGAATTGCCAAGAG	84942	ATTATA _
			TATGA GTTGC AAGAG		
			ATACT TAACG TTCTC		
			_____ G		
GAM3760	ACHE	3'	TGGGGTGGGGATGGGCA	84945	AGAC C
			TGGGGTGG GG GTGGGCG		
			ACCCACCC CC TACCCGT		
			_____ -		
GAM3760	ACHE	3'	TGGGGTGGGGATGGGCA	84945	AGAC C
			TGGGGTGG GG GTGGGCG		
			ACCCACCC CC TACCCGT		
			_____ -		
GAM3760	CRAT	5'	TGGGGCGGGGGCGGGGCA	84946	AGAC T
			TGGGGTGG GGCG GGGCG		
			ACCCCGCC CCGC CCCGT		
			C_____		
GAM3760	FASN	3'	TGGGGTGGGGTGGGGA	84947	AGACG C C
			TGGGGTGG G GTGGG GA		
			ACCCACCC C CACCC CT		
			_____ -		
GAM3760	FASN	3'	TGGGGTGGGGATGGTGGA	84948	A C CG
			TGGGGTGG GA GG TGGG		
			ACCCACCC CT CC ACCT		
			C A _____		
GAM3760	GFRA2	5'	TGGGGTGAGAGGCGGGCGA	84949	G C GT
			TGGGGTG AGA GGC GGGCGA		
			ACCCCAC TCT CCG CCCGCT		
			_____ -		
GAM3760	GRP58	5'	TGGGGTGGGGACGGCCGGA	84950	A G
			TGGGGTGG GACGGC TGGG		
			ACCCACCC CTGCCG GCCT		
			C _____		
GAM3760	MEOX1	3'	TGGGGTGGGGAGGTGGG	84951	A CG C
			TGGGGTGG GA G GTGGG		
			ACCCACCC CT C CACCC		
			C _____		
GAM3760	MEOX1	3'	TGGGGTGGGGAGGTGGG	84951	A CG C
			TGGGGTGG GA G GTGGG		

			ACCCACC CT C CACCC		
			C _ _		
GAM3760 NCOR2	3'	TGGCGTGGAGGTGCGTGG	84952	G	ACG
		TGG GTGGAG GCGTGG			
		ACC CACCTC CGCACC			
		G CA_			
GAM3760 PAX2	3'	TGGGGTGAGGCTGGGGCG	84953	AGAC	GT
		TGGGGTGG GGC GGGCG			
		ACCCCACT CCG CCCGC			
		_ _ AC			
GAM3760 PAX2	3'	TGGGGTGAGGCTGGGGCG	84953	AGAC	GT
		TGGGGTGG GGC GGGCG			
		ACCCCACT CCG CCCGC			
		_ _ AC			
GAM3760 PDE4A	5'	GGGTGGAGGCGGTGGG	84954	A	CG
		GGGTGGAG CGG TGGG			
		CCCACCTC GCC ACCC			
		C _			
GAM3760 PSD	5'	TGGGGTGGGGGCTGGCG	84955	AGAC	GTG
		TGGGGTGG GGC GGCG			
		ACCCACC CCG CCGC			
		_ _ A_			
GAM3760 RANBP3	3'	TGGGGTGGGGGCGGGTGGGCG	84956	AGA	C
		TGGGGTGG CGG GTGGGCG			
		ACCCACC GCC CACCCGC			
		CCC _			
GAM3760 RANBP3	3'	TGGGGTGGGGGCGGGTGGGCG	84956	AGA	C
		TGGGGTGG CGG GTGGGCG			
		ACCCACC GCC CACCCGC			
		CCC _			
GAM3760 RANBP3	3'	TGGGGTGGGGGCGGGTGGGCG	84956	AGA	C
		TGGGGTGG CGG GTGGGCG			
		ACCCACC GCC CACCCGC			
		CCC _			
GAM3760 SPTBN4	3'	TGGGGTGGGGGTGGTGA	84957	AGAC	C GC
		TGGGGTGG GG GTGG GA			
		ACCCACC CC CACC CT			
		_ _ A_			
GAM3760 TNFSF12	3'	TGAGGTGGAGAGTGGGCG	84958	CGGC	
		TGGGGTGGAGA GTGGGCG			

ACTCCACCTCT CACCCGC

GAM3760 TTC3 3' TGGGGTGGGGAAGGAGAATGG 84959 A C C__
TGGGGTGG GA GG GTGG
||||||| || || ||||
ACCCACCTCT CC TACC
C T TCT

GAM3760 XYLB 3' TGGGGTGGGGGCGGCTATGGG 84960 AGA _
TGGGGTGG CGGC GTGGG
||||||| |||| |||||
ACCCACCTCT GCCG TACCC
CCC A

GAM3760 YWHA 3' TGGGGAGGAGGGGGTGG 84961 T AC C
TGGGG GGAG GG GTGG
||||| |||| || ||||
ACCC CCTC CC CACC
T C_ _

GAM3760 ZYX 3' TGAGGTGGGGGCAGGTGG 84962 AGA C
TGGGGTGG CGG GTGG
||||||| || ||||
ACTCCACCTCT GTC CACC
CCC _

GAM3760 ARHF 3' TGGGGTGGAGATGGGAGGG 84963 C CGT
TGGGGTGGAGA GG GGG
||||||| || |||
ACCCACCTCT CC CCC
A CT_

GAM3760 C11orf16 3' TGGGGTGGAGATACTGGTGG 84964 CG __
TGGGGTGGAGA GC GTGG
||||||| || ||||
ACCCACCTCT TG CACC
A_ AC

GAM3760 CARM1 3' TAGGGTGGGGACGGCGCAAC 84965 A GTG
TGGGGTGG GACGGC GGCGAT
||||||| ||||| |||||
ATCCACCTCTGCGG CCGTTG
C _

GAM3760 DKFZP434J1813 5' TGGGGTGGAGAGGGCGG 84966 C C
TGGGGTGGAGA GG GTGG
||||||| || ||||
ACCCACCTCT CC CGCC

GAM3760 DKFZp547O146 5' TGGGGTGGGGAGAGGGGCG 84967 A C CGT
TGGGGTGG GA GG GGGCG
||||||| || || ||||
ACCCACCTCT TC CCCGC
C C _

GAM3760 FAM3A 3' TGGGGATGGAGATGGCGTGAGG 84968 _ C C
A TGGGG TGGAGA GGCGTGGG GA
||||| ||||| ||||| ||

ACCCC ACCTCT CCGCACTC CT
 T A _
 GAM3760 FLJ10305 3' TGGGGTGGGGGTGGG 84969 AGAC C
 TGGGGTGG GG GTGGG
 ||||| || ||||
 ACCCCACC CC CACCC

 GAM3760 FLJ14810 3' GGGGTGGGGACGGCGAGAAGGC 84970 A T__
 GAT GGGGTGG GACGGCG GGGCGAT
 ||||| ||||| |||||
 CCCACC CTGCCGC TCCGCTA
 C TCT

GAM3760 FLJ14950 3' TGGGGTGGGGGTGGGTGTGGG 51873 AGAC_ C
 TGGGGTGG GG GTGGG
 ||||| || ||||
 ACCCCACC CC CACCC
 CCCAC A

GAM3760 FLJ25193 5' TGGGGTGGAGGGGCA 84971 ACGGCGT
 TGGGGTGGAG GGGCG
 ||||| ||||
 ACCCCACCTC CCCGT

 GAM3760 FRAG1 3' TGGGGTGGGGAAGGCCAGAATG 84972 A C ____
 G TGGGGTGG GA GGC GTGG
 ||||| || ||| ||||
 ACCCCACC CT CCG TACC
 C T GTCT

GAM3760 JM4 3' TGGCGTGGGGGTAGGGCG 84973 G AGAC C _
 TGG GTGG GG GT GGGCG
 || ||| || || |||||
 ACC CACC CC CA CCCGC
 G ____ _ T

GAM3760 KIAA0084 5' GGGTGGAGGCGTGGGCG 84974 GAC
 GGGTGA GGCGTGGGCG
 ||||| |||||
 CCCACCT CCGCACCCGC

 GAM3760 KIAA0461 3' TGGGGTGGGAGAAATGGGTGG 84975 _ C__ C
 TGGGGTGG AGA GG GTGG
 ||||| || || ||||
 ACCCCACC TCT CC CACC
 C TTA _

GAM3760 KIAA1111 3' TGGGGTGAAGTTGGAGTGGG 84976 AGAC C
 TGGGGTGG GG GTGGG
 ||||| || ||||
 ACCCCACT CC CACCC
 CCAA T

GAM3760 LGP1 3' TGGGGGGAGCTGGGCG 84977 T GACG G
 TGGGG GGA GC TGGGCG
 |||| || || |||||

ACCCC CCT CG ACCCGC

GAM3760	MAPKAPK3	3'	TGGGGTGGGGCTGGTAAGC	84978	AGAC	___
			TGGGGTGG GGC GTGGGC			
			ACCCACC CCG CATTCT			
			___ AC			
GAM3760	MESDC1	3'	TGGGGTAGGGGTGGGAGTGAT	84979	AGAC	C C__
			TGGGGTGG GG GTGGG GAT			
			ACCCCATC CC CACCC CTA			
			C___ _ TCA			
GAM3760	MGC3184	5'	TGGGGCGGAGGCGGCTCTGA	84980	A	G_
			TGGGGTGGAG CGGC TGG			
			ACCCCGCCTC GCCG ACT			
			C AG			
GAM3760	NPTXR	3'	TGGGGTGGGGATGCCAAGA	84981	A	CG GT
			TGGGGTGG GA GC GGG			
			ACCCACC CT CG TCT			
			C A_ GT			
GAM3760	NPTXR	3'	TGGGGTGGGGATGCCAAGA	84981	A	CG GT
			TGGGGTGG GA GC GGG			
			ACCCACC CT CG TCT			
			C A_ GT			
GAM3760	POLR2D	3'	TGGGGTGGAGGTGTTCTG	84982	ACGGC	GG
			TGGGGTGGAG GTG CG			
			ACCCACCTC CAC GC			
			___ AA			
GAM3760	PPP1R16B	3'	TGGGGTGGAGGTGGCCTGA	84983	AC	G
			TGGGGTGGAG GGC TGG			
			ACCCACCTC CCG ACT			
			CA G			
GAM3760	SEMA4G	3'	TGGGGTGGAGGTGGGAGA	84984	ACGGC	C
			TGGGGTGGAG GTGGG GA			
			ACCCACCTC CACCC CT			
			___ T			
GAM3760	SEMA4G	3'	TGGGGTGGAGGTGGGAGA	84984	ACGGC	C
			TGGGGTGGAG GTGGG GA			
			ACCCACCTC CACCC CT			
			___ T			
GAM3760	LOC126353	3'	TAGGGTGGGGGCTTGCGA	84985	AGAC	GTG
			TGGGGTGG GGC GGCGA			

	ATCCCACC CCG CCGCT		
	C__ AA_		
GAM3760 LOC126964 3'	GGGGTGGAGGCGCACACA 84986	GAC	G
	GGGGTGGG GCGGTG GCG		
	CCCCACCT CCGCGT TGT		
	__ G		
GAM3760 LOC132422 5'	TGGGGTGGGGGCGGCGGG 84987	AGA	T
	TGGGGTGG CCGCG GG		
	ACCCACCC GCCGC CC		
	CCC _		
GAM3760 LOC145693 5'	TGGGGTGGAGGTGGGCGTGCG 84988	AC_	
	TGGGGTGGAG GCGTGCG		
	ACCCACCTC CCGCACCC		
	CAC		
GAM3760 LOC147004 3'	TGGGGTGGGGGGGGGTGCG 84989	AGAC CGT	_
	TGGGGTGG GG GG GCG		
	ACCCACCC CC CC CGC		
	__ CC_ A		
GAM3760 LOC147111 3'	TGGGGTGGAGGTGGCACTGG 84990	G AC	_
	TGGGGTG AG GGCG TGG		
	ACCCAC TC CCGT ACC		
	_ CA G		
GAM3760 LOC149506 3'	TGGGCTGGGGATGGTGA 84991	G AGAC C	GC
	TGGG TGG GG GTGG GA		
	ACCC ACC CC TACC CT		
	G __ _ A_		
GAM3760 LOC150498 3'	TGGGGAGGAGGGGGTGG 84961	T AC C	
	TGGGG GGAG GG GTGG		
	ACCC CCTC CC CACC		
	T C_ _		
GAM3760 LOC151056 3'	TGGGGTGGGGGGAGGGGCG 84992	AGAC CGT	
	TGGGGTGG GG GGGCG		
	ACCCACCC CC CCCGC		
	C__ CTC		
GAM3760 LOC221424 5'	TGGGGCGGGGGCGGCCGCACG 84994	AGA G G	
	TGGGGTGG CCGC TG GCG		
	ACCCCGCC GCCG GC TGC		
	CCC G G		
GAM3760 LOC221424 5'	GGGGTGGAGGCGGCGGC 84993	A GTG	
	GGGGTGGAG CCGC GGC		

CCCCACCTC GCCG CCG
 C ____
 GAM3760 LOC254100 5' TGGGGTGGCGATGGTTGTGA 84995 A C C_
 TGGGGTGG GA GG GTGG
 ||||| || || ||||
 ACCCCACC CT CC CACT
 G A AA
 GAM3760 LOC256529 5' TGGGGTGAGGATAGACTGGGTG 84996 ____ _ C
 G TGGGGTGG AGAC GG GTGG
 ||||| |||| || ||||
 ACCCCACT TCTG CC CACC
 CCTA A _
 GAM3760 LOC256529 3' TGGGGTGAGGATAGACTGGGTG 84996 ____ _ C
 G TGGGGTGG AGAC GG GTGG
 ||||| |||| || ||||
 ACCCCACT TCTG CC CACC
 CCTA A _
 GAM3760 LOC92017 5' TGGGGTGGGGGGGCG 84997 AGAC CGT
 TGGGGTGG GG GGGCG
 ||||| || ||||
 ACCCCACC CC CCCGC
 ____ ____
 GAM3761 PCDHB16 5' TGAGATTAATGATTAAATAA 85000 A TT
 A GGATTAATGATTA TAA
 | ||||| ||||| |||
 A TCTAATTACTAAT ATT
 C TT
 GAM3761 TAP2 3' GGATAATGATTAAAAAC 85001 T TTT
 GGAT AATGATTA AAC
 ||| ||||| |||
 CCTA TTAATAAT TTG
 _ TT_
 GAM3761 FLJ22060 3' TAAGGATTAATATTAATTCAA 85002 ATT
 TAAGGATTAATG ATTTAA
 ||||| |||||
 ATTCCTAATTAT TAAGTT
 AAT
 GAM3761 FLJ25436 3' TAAGGATAATGATTACTT 85003 T
 TAAGGAT AATGATTATTT
 ||||| |||||
 ATTCCTA TTAATAATGAA
 _
 GAM3761 NFAT5 3' AGGGGTAAGGAACATTTAACAA 85004 AT T T
 AGG TAA GA TATTTAACAA
 ||| ||| || |||||
 TCC ATT CT GTAAATTGTT
 CC C T
 GAM3761 LOC146138 3' TAAGGATTAATGTATTAATC 85005 _ T
 TAAGGATTAATG ATTA TT
 ||||| ||||| ||| |||

ATTCCTAATTAC TAAT AG
 A T
 GAM3761 LOC257239 3' AGGGCATGATTATTTAA 85006 ATTA
 AGG ATGATTATTTAA
 ||| |||||
 TCC TACTAATAAATT
 CG__
 GAM3761 LOC51279 3' AGGATTAAGTGAAATAACA 85007 _ TTATT
 AGGATTA TGA TAACA
 ||||| ||| ||||
 TCCTAATT ACT ATTGT
 C TT__
 GAM3762 ARAF1 3' GAGGAGACAGGGGGCTCA 85010 A C A
 GAGGA AC GGGG CTCA
 ||||| || |||||
 CTCCT TG CCCC GAGT
 C T C
 GAM3762 CDC34 3' AGAGGAGACGGGGACCAG 85011 AAC CTCA
 AGAGGA CGGGGA CCGG
 ||||| ||||| ||||
 TCTCCT GCCCCT GGTC
 CT_ ____
 GAM3762 CIAS1 3' GAGGGACCGGAGAACACTGGC 85012 AA CT C
 GAGG ACCGGGGA CAC GGC
 ||||| ||||| ||| |||
 CTCC TGGCCTCT GTG CCG
 C_ T_ A
 GAM3762 COL2A1 5' GAGGAAGCGGGAGACCCGGC 85013 AC _ TCA
 GAGGAA CGGG GAC CCGGC
 ||||| ||||| ||| |||||
 CTCCTT GCCC CTG GGCCG
 C_ T ____
 GAM3762 COL2A1 5' GAGGAAGCGGGAGACCCGGC 85013 AC _ TCA
 GAGGAA CGGG GAC CCGGC
 ||||| ||||| ||| |||||
 CTCCTT GCCC CTG GGCCG
 C_ T ____
 GAM3762 FTL 5' AGAGGAAATCGGAGGGCGG 85014 C ACTCAC
 AGAGGAAA CGGGG CGG
 ||||| ||||| |||
 TCTCCTTT GCCTC GCC
 A CC____
 GAM3762 GDI2 5' AGAGGAAAATGGAGCTGG 85015 CC A CACC
 AGAGGAAA GGGG CT GG
 ||||| ||||| ||| ||
 TCTCCTTT CCTC GA CC
 TA _ ____
 GAM3762 GP1BB 3' AGGCGGGGACCGGTCCAG 85016 AAAC CA_
 AGG CGGGGACT CCGG
 ||| ||||| |||||

			TCC GCCCCTGG GGTC			
			_____ CCA			
GAM3762	GP1BB	3'	GAGGAGGCGGGGACCGG	85017	AAC	CTCA
			GAGGA CGGGGA CCGG			
			CTCCT GCCCCT GGCC			
			CC_ _____			
GAM3762	MYLK2	3'	GAGGGAACCGGGAGCGG	85018	A	ACTCAC
			GAGG AACCGGGG CGG			
			CTCC TTGGCCCT GCC			
			C C_____			
GAM3762	NRXN1	5'	AGGGAGGCCACTTCGCCGG	85019	A	AACC GG _A
			AG GGA GG ACT C CCGG			
			TC CCT CC TGA G GGCC			
			_ _____ GG A C			
GAM3762	RGS19IP1	3'	AGGGGGGCGGGGACCCCGGC	85020	A AAA	T A
			AG GG CCGGGGAC C CCGGC			
			TC CC GGCCCCTG G GGCCG			
			_ CCC _ _			
GAM3762	SLC19A2	5'	GGAGGGGACCCGGCCCGG	85021	AACC	A_
			GGA GGGGACTC CCGG			
			CCT CCCCTGGG GGCC			
			_____ CCG			
GAM3762	SLC30A3	5'	AGAGAGAGGCCGGGCCCGG	85022	_ AA	GACTCA
			AGAG GA CCGGG CCGG			
			TCTC CT GGCCC GGCC			
			T CC _____			
GAM3762	C17orf31	3'	AGAGGCCGGGGACCC	85023	AAA	
			AGAGG CCGGGGACTC			
			TCTCC GGCCCCTGGG			

GAM3762	C8orf13	5'	GGGCCCTGCTGGGGACTCGCCG	85024	AAA _____	A
	G		GG CC GGGGACTC CCGG			
			CC GG CCCCTGAG GGCC			
			CG_ ACGA C			
GAM3762	DGKZ	3'	AGCGGGGGCTGGGGACCCGGC	85025	A AAACC	TCA
			AG GG GGGGAC CCGGC			
			TC CC CCCCTG GGCCG			
			G CCCGA _____			
GAM3762	DKFZp434F054	5'	AGAGGGGCCCCGGGGACTCAGGC	85026	AAA	CC
			AGAGG CCGGGGACTCA GGC			

		TCTCC GGCCCCTGAGT CCG		
		CCG _		
GAM3762	DKFZP434P1750	3' AGAGGGAAGTGGGGCAGGAGC	85027	A C ACT CC
		AGAGG AAC GGGG CA GGC		
		TCTCC TTG CCCC GT TCG		
		C A _ CC		
GAM3762	FLJ10578	5' GGAAACCGCGGCCTCGGC	85028	G A ACC
		GGAAACCG GG CTC GGC		
		CCTTTGGC CC GAG CCG		
		G G _		
GAM3762	FLJ13224	3' AGAGGAAAGCGACTCGTTGGC	85029	ACC G ACC
		AGAGGAA GG GACTC GGC		
		TCTCCTT TC CTGAG CCG		
		_ G CAA		
GAM3762	FLJ20093	5' GAGAGCGCGGGGCTCGCTGGC	85030	AAAC A ACC
		GAGG CGGGG CTC GGC		
		CTCT GCCCC GAG CCG		
		CGC_ _ CGA		
GAM3762	FLJ20847	5' GAGGGGGCTGGAGACCCGGGGC	85031	AAACC ACC
		GAGG GGGGACTC GGC		
		CTCC CCTCTGGG CCG		
		CCCGA CC_		
GAM3762	FLJ32894	3' GAGGAAACCAGAGTTGG	85032	ACTCACC
		GAGGAAACCGGGG GG		
		CTCCTTTGGTCTC CC		
		AA_		
GAM3762	HEMK	3' AAAGGAAACACCCCTCACTGGC	85033	CGGGGA C
		AGAGGAAAC CTCAC GGC		
		TTTCCTTTG GAGTG CCG		
		TGGG_ A		
GAM3762	IMP13	5' GGAAACCGAGTCCCTGGC	85034	GA CACC
		GGAAACCGGG CT GGC		
		CCTTTGGCTC GG CCG		
		AG A_		
GAM3762	KIAA0527	3' AGAGGAAATGGTACTTACTGG	85035	CC GG C C
		AGAGGAAA GG ACT AC GG		
		TCTCCTTT CC TGA TG CC		
		A_ A_ A A		
GAM3762	KIAA0552	3' AGGGGACACTGGGGACTCTGGC	85036	A A C ACC
		AG GGA AC GGGGACTC GGC		

TC CCT TG CCCCTGAG CCG
 C G A A__
 GAM3762 KIAA1274 5' AGAGGGAGCCCGTGCTCACCGG 85037 _AA GGGA
 C AGAGG A CCG CTCACCGGC
 ||||| I ||| |||||
 TCTCC T GGC GAGTGGCCG
 C CG AC__
 GAM3762 LSM4 5' GGGGACCGGGCTCGCCGGC 85038 AA GA A
 GG ACCGGG CTC CCGGC
 || ||||| ||| |||||
 CC TGGCCC GAG GGCCG
 CC _ C
 GAM3762 MGC16025 5' AAGGAGCCTGGACTCACTGGC 85039 AA GG C
 GAGGA CC GGACTCAC GGC
 ||||| || ||||| |||
 TTCCT GG CCTGAGTG CCG
 C_ A_ A
 GAM3762 OR1F2 5' GAGGAACTCGGAGACACTCACT 85040 AC _ C
 GG GAGGAA CGGGGAC TCAC GG
 ||||| ||||| ||| ||
 CTCCTT GCCTCTG AGTG CC
 GA TG A
 GAM3762 P450RAI-2 3' GAGGATGCTGGGGAGACAGGGC 85041 AACC CT CC
 GAGGA GGGGA CA GGC
 ||||| ||||| || |||
 CTCCT CCCCT GT CCG
 ACGA CT C_
 GAM3762 SCLY 3' AAGGAAACTGGGGGTGCACACT 85042 C _ ACC |||
 CGCTGGCG AC GGGG ACTC GGC G
 || |||| ||| ||| I
 TGCCCC TGAG CCG C
 A CACGTG CGA |||
 GAM3762 SIAT8C 5' AGGGAAACCGGGGAAATCGG 85043 A CTCAC
 AG GGAAACCGGGGA CGG
 || ||||| ||| |||
 TC CCTTTGGCCCCT GCC
 _ TTA_
 GAM3762 SLAM 3' AGAGGAAACTTGGGCCTGTGGC 85044 CG A CACC
 AGAGGAAAC GGG CT GGC
 ||||| ||| || |||
 TCTCCTTTG CCC GG CCG
 AA _ ACA_
 GAM3762 ZDHC1 5' GGACGGAGACTGGGCCGG 85045 AAC CA_
 GGA CGGGGACT CCGG
 ||| ||||| ||| |||
 CCT GCCTCTGA GGCC
 _ CCC
 GAM3762 ZER6 3' GAGAAGCCAACCTACTGG 85046 AA GGG C C
 GAGGA CC GACT AC GG
 ||||| || ||| ||| |||

	CTCTT GG TTGA TG CC		
	C_ ____ A A		
GAM3762 LOC144455 3'	AGAAGAAACCGGGCCCGG 85047	GA	CTCA
	AGAGGAAACCGGG CCGG		
	TCTTCTTTGGCCC GGCC		
	G_____		
GAM3762 LOC151199 5'	AGAGGCAACCGGAGACCGG 85048	A	CTCA
	AGAGG AACCGGGGA CCGG		
	TCTCC TTGGCCTCT GGCC		
	G _____		
GAM3762 LOC157503 3'	AGAAGAAACCTCTGGCTCATTG 85049	GG_ A	CC
G	AGAGGAAACC GG CTCA GG		
	TCTTCTTTGG CC GAGT CC		
	AGA _ AA		
GAM3762 LOC196951 5'	GAGGAAACTGGGTGAAAGGC 85050	C _	CTCACC
	GAGGAAAC GGG GA GGC		
	CTCCTTTG CCC CT CCG		
	A A TT_____		
GAM3762 LOC219575 5'	AGAGGAAACTGGGAGAGG 85051	C _	CTCACC
	AGAGGAAAC GGG GA GG		
	TCTCCTTTG CCC CT CC		
	A T _____		
GAM3762 LOC253664 5'	AGAGGATCGGGGACCC 85052	AAC	
	AGAGGA CGGGGACTC		
	TCTCCT GCCCCTGGG		
	A_____		
GAM3762 LOC90141 3'	AAGGAAACTGGCACCATTTGGC 85053	CG G T	CC
	GAGGAAAC GG AC CA GGC		
	TTCCTTTG CC TG GT CCG		
	A_ G _ AA		
GAM3762 LOC92283 3'	AGAGGAAACCTGACTG 85054	GGG	CACC
	AGAGGAAACC GACT G		
	TCTCCTTTGG CTGA C		
	A_ _____		
GAM3763 FLJ31101 3'	TAAGTTAATAATAATGTATTGG 85057	A A	GA
	TAAGTTAATGA TAA GTA TGG		
	ATTCAATTATT ATT CAT ACC		
	_ A A_		
GAM3763 JAM1 3'	TAAGTTAATAAATAGACTGGTG 85058	AA_____ A	
GATGG	TAAGTTAATGAATA GT GATGG		

ATTCAATTATTTAT CA CTACC
 CTGAC C
 GAM3763 JAM1 3' TAAGTTAATAAATAGACTGGTG 85058 AA__ A
 GATGG TAAGTTAATGAATA GT GATGG
 ||||| || ||||
 ATTCAATTATTTAT CA CTACC
 CTGAC C
 GAM3763 JAM1 3' TAAGTTAATAAATAGACTGGTG 85058 AA__ A
 GATGG TAAGTTAATGAATA GT GATGG
 ||||| || ||||
 ATTCAATTATTTAT CA CTACC
 CTGAC C
 GAM3763 JAM1 3' TAAGTTAATAAATAGACTGGTG 85058 AA__ A
 GATGG TAAGTTAATGAATA GT GATGG
 ||||| || ||||
 ATTCAATTATTTAT CA CTACC
 CTGAC C
 GAM3763 KIAA0417 3' TTAATGAATTCAGCAGGTGG 85059 AA_ A
 TTAATGAAT AGTAG TGG
 ||||| |||||
 AATTACTTA TCGTC ACC
 AAG C
 GAM3763 KIAA1946 3' GTTAAGAAAAAGTAGATGG 85060 T T
 GTTAA GAA AAAGTAGATGG
 ||||| |||||
 CAATT CTT TTTTCATCTACC
 - -
 GAM3763 P15-2 3' TAAGTTATTGAATAAATG 85061 A AAGTA
 TAAGTTA TGAATA GATG
 ||||| |||||
 ATTCAAT ACTTAT TTAC
 A _____
 GAM3763 SETBP1 3' TAAGTTAATGAAAAGATATATG 85062 TA TAG_
 G TAAGTTAATGAA AAG ATGG
 ||||| |||||
 ATTCAATTACTT TTC TACC
 _ TATA
 GAM3763 LOC149117 3' GTTAATAAATAATTGATTGATG 85063 A__ A
 G GTTAATGAATAA GT GATGG
 ||||| |||||
 CAATTATTTATT TA CTACC
 AAC A
 GAM3763 LOC221830 3' GTTATACAAAGTAGATGG 85064 ATGA
 GTTA ATAAAGTAGATGG
 ||||| |||||
 CAAT TGTTTCATCTACC
 A____
 GAM3764 EPB72 3' TTTAAGGGTTAGAGTAAT 85067 T A
 TTT AGGGTTA AGTAAT
 ||||| |||||

		AAA TCCCAAT TCATTA			
		T C			
GAM3764	PON1	3' TTTTAGGGTAAGTACTTT	85068	TA	AAT
		TTTTAGGGT AAGT ACTTT			
		AAAATCCCA TTCA TGAAA			
		— —			
GAM3764	NDUFB5	3' TTTTAGAGTTGGTTCAATACTT	85069		AAAG
	TA	TTTTAGGGTT TAATACTTTA			
		AAAATCTCAA GTTATGAAAT			
		CCAA			
GAM3765	CD28	3' ACAGCATTAAATAGGAAC TACG	85072	A	GGG
		ACG CATTAAATAGGAA ACG			
		TGT GTAATTTATCCTT TGC			
		C GA_			
GAM3765	GPRK6	3' CGCACACAGGAAGGGGCG	85073	A TAA	A
		CG CAT ATAGGAAGGG CG			
		GC GTG TGCCTTCCC GC			
		— — C			
GAM3765	PPP2R4	3' ACGAACAGAGGGAGGGGATGG	85074	_ TTAAATA	A C
		ACGA CA GGA GGA GG			
		TGCT GT CCT CCCT CC			
		T CTC_ C A			
GAM3765	EREG	3' ATTAAATAGGAAACAG	85075		AGG
		ATTAAATAGGA GACGG			
		TAATTTATCCT TTGTC			
		—			
GAM3765	FLJ25467	3' GACATTAAGGGGAGAC	85076	AAT	AA
		GACATTA AGG GGGAC			
		CTGTAAT TCC CTCTG			
		_ C_			
GAM3765	HCA127	3' ACATTAAATAGGAGAC	85077		AGG
		ACATTAAATAGGA GAC			
		TGTAATTTATCCT CTG			
		—			
GAM3765	IL22R	3' GACACTGGGTAGGGACAG	85078	AAATA	A
		GACATT GG AGGGACGG			
		CTGTGA CC TCCCTGTC			
		C_ A			
GAM3765	KIAA0993	3' GACATTAAATGGTAAAGG	85079	A _	
		GACATTAAAT GG AAGGG			

CTGTAATTTA CC TTTCC
 _ A
 GAM3765 MGC13053 3' ATTAAGAAGGGGGGCGG 85080 T_ AA A
 ATTAAA AGG GGG CGG
 ||||| ||| ||| |||
 TAATTT TCC CCC GCC
 CT CC _
 GAM3765 NKX2B 3' ACGACATTACGCTGGGACGG 85081 ATAGGAA
 ACGACATTAA GGGACGG
 ||||| ||| |||||
 TGCTGTAATT CCCTGCC
 GCGA__
 GAM3765 RPS6KA4 3' CCAAAGAGGAAGGGGTGG 85082 T AC
 TTAAA AGGAAGGG GG
 ||||| ||||| ||
 GGTTT TCCTTCCC CC
 C CA
 GAM3765 LOC126364 3' CGGCATGAGGGACAGGGAGGGG 85083 A TAA__ A A_
 GCGG CG CAT ATAGG AGGG CGG
 || ||| ||||| ||| |||
 GC GTA TGTCC TCCC GCC
 C CTCCC C CC
 GAM3765 LOC254159 5' GACATCGGGAAGGGACGG 85084 AAATA
 GACATT GGAAGGGACGG
 ||||| ||||| |||||
 CTGTAG CCTTCCCTGCC
 C__
 GAM3766 KIAA1946 3' TATCTGCACATATTTTAT 85087 C
 TGTC GCACATATTTTAT
 ||||| ||||| |||||
 ATAG CGTGTATAAAATA
 A
 GAM3766 LOC51207 5' ATGCTGTTTGCATCTCCTAT 85088 CC CATA
 GTGCTGT GCA TTTTAT
 ||||| ||| |||||
 TACGACA CGT AGGATA
 AA AG__
 GAM3767 IL8 3' TGATGCTTCAAATATCACAT 85091 ATA TG
 TGATGC T AATATCACAT
 ||||| | ||||| |||||
 ACTACG A TTATAGTGTA
 A__ GT
 GAM3767 FLJ10895 3' TTCGATGCATATTGTGGCAGTC 85092 AATA__
 AC TTTGATGCATATTG TCAC
 ||||| ||||| |||||
 AAGCTACGTATAAC AGTG
 ACCGTC
 GAM3767 LOC203369 3' TTTGTGCATGGAGGTATCACAT 85093 A ATT A_
 TTTG TGCAT GA TATCACAT
 ||||| ||||| || |||||

AAAC ACGTA CT ATAGTGTA
 _ C_ CC
 GAM3768 FCGR2A 3' GAAACAATCACTTTTAATTT 85096 AT
 GAAACG GTTATTTTAAATTT
 ||||| |||||
 CTTTGT TAGTGAAAATTAAA

 GAM3769 ATP2B4 3' TGGGGTGATGCCAAGAGGATTG 85099 AAG ____ AAC
 TCA TGG GATGTT GGA TGTCA
 ||| ||||| ||| |||||
 ACC CTACGG CCT ACAGT
 CCA TTCT A_
 GAM3769 DPYD 3' AGGGCAATTTGGAAACTGTAC 85100 ATG_
 AGG TTGGAAACTGTAC
 ||| |||||
 TCC AACCTTTGACAGTG
 CGTTA
 GAM3769 GAD1 3' GGGAGGGTGTGACTTGTCA 85101 A A T AAAC
 GG AGG TGT GG TGTCA
 || ||| ||| |||
 CC TCC ACA CT ACAGT
 C C _ GA_
 GAM3769 GAD2 3' TGGGGGAATGTTGATGTCA 85102 AA AAAC
 TGG GGATGTTGG TGTCA
 ||| ||||| |||||
 ACC CTTACAACT ACAGT
 CC _
 GAM3769 MAPK4 3' GAAGGATGTTGGGTC 85103 AAAC
 GAAGGATGTTGG GTC
 ||||| |||
 CTTCTACAACC CAG

 GAM3769 NOTCH2 3' TAGAAGGAATGAGAAGTGTCA 85104 TGT GA
 TGGAAGGA TG AACTGTCA
 ||||| || |||||
 ATCTTCCT AC TTGACAGT
 T_ TC
 GAM3769 PXN 3' TGGAGTGTTTGGACTGTAC 85105 A GATG AA
 TGGA G TTGGA CTGTAC
 ||||| ||||| |||||
 ACCT C AACCT GACAGTG
 _ ACCA _
 GAM3769 STAT1 3' AGAAGGAAAAGTGTG 85106 TGTTGG
 GGAAGGA AAAGTGTG
 ||||| |||||
 TCTTCCT TTTGACAG

 GAM3769 ARHGEF9 3' TGAGAGGATGTTGGAAAC 85107 GA
 TG AGGATGTTGGAAAC
 || |||||

		AC TCCTACAACCTTTG		
		TC		
GAM3769	ARHU	3' GAAGGATGTATTTCACTGTCAC 85108	TGGAA	
		GAAGGATGT ACTGTCAC		
		CTTCCTACA TGACAGTG		
		TAAAG		
GAM3769	C20orf18	5' GGGGGGGCCGAAAAATTGTC 85109	AA AT	C__
		GG GG GTTGGAAA TGTC		
		CC CC CGGCCTTT ACAG		
		CC __ TTA		
GAM3769	C20orf18	5' GGGGGGGCCGAAAAATTGTC 85109	AA AT	C__
		GG GG GTTGGAAA TGTC		
		CC CC CGGCCTTT ACAG		
		CC __ TTA		
GAM3769	DKFZp434G179	3' GATTGTTGGAAGCTGTCA 85110	A	A
		GG TGTTGGAA CTGTCA		
		CT ACAACCTT GACAGT		
		A C		
GAM3769	FLJ14957	3' GGCATGCCTGGGGACTGTCAC 85111	_ _	AA
		GG ATGT TGG ACTGTCAC		
		CC TACG ACC TGACAGTG		
		G G CC		
GAM3769	GALNT11	3' GGGAGGACAGGGAAGTGTCA 85112	A	GTT A
		GG AGGAT GGAA CTGTCA		
		CC TCCTG CCTT GACAGT		
		C TC_ _		
GAM3769	KIAA0247	3' TGGAGGAAGAAGCTGTCA 85113	A	TGTT A
		TGGA GGA GGAA CTGTCA		
		ACCT CCT TCTT GACAGT		
		_ _ _ C		
GAM3769	KIAA0453	3' TGGAAGGATTTGGGTC 85114	G	AACT
		TGGAAGGAT TTGG GTC		
		ACCTTCCTA AACC CAG		
		_ _ _ _		
GAM3769	KIAA0563	5' TGGGAGGAGGCTGAACTGTCA 85115	A	T AA
		TGG AGGA GTTGG ACTGTCA		
		ACC TCCT CGACT TGACAGT		
		C C _		
GAM3769	KIAA1189	3' GGAAGGATTAAAGAAGTTGTCA 85116	GTT	AC
		GGAAGGAT GGAA TGTC		

			CCTTCCTA TCTT ACAGT		
			ATT CA		
GAM3769	KIAA1582	5'	TGGAAGGGTTGCCTGTC	85117	AT GAAA
			TGGAAGG GTTG CTGTC		
			ACCTTCC CAAC GACAG		
			__ G__		
GAM3769	NETO2	3'	TGGAATGAATGGGCTGTCA	85118	_ TT AAA
			TGGAA GGATG GG CTGTCA		
			ACCTT CTTAC CC GACAGT		
			A __ __		
GAM3769	LOC147071	5'	TGGGAGGAGGCTGAACTGTCA	85115	A T AA
			TGG AGGA GTTGG ACTGTCA		
			ACC TCCT CGACT TGACAGT		
			C C _		
GAM3769	LOC149832	3'	GGGAGGCTGTGGGGACTGTCAC	85119	A A T AA
			GG AGG TGT GG ACTGTCAC		
			CC TCC ACA CC TGACAGTG		
			C G _ CC		
GAM3769	LOC150299	3'	TGGAAGGAGGTTCTGCGGCTGT	85120	T GGAAA_
			TGGAAGGA GTT CTGT		
			ACCTTCCT CAA GACA		
			C GACGCC		
GAM3769	LOC152286	5'	GGAAGGCTGGTGGAACTGTCAC	85121	A T A
			GGAAGG TG TGGAA CTGTCAC		
			CCTTCC AC ACCTT GACAGTG		
			G C _		
GAM3769	LOC162461	3'	TGGGGGGTGGGCGGAACTGTC	85122	AA A T_
	AC		TGG GG TG TGGAACTGTCAC		
			ACC CC AC GCCTTTGACAGTG		
			CC _ CC		
GAM3769	LOC200681	5'	GAAGGATGACTAGGGCTGTCAC	85123	_ AAA
			GAAGGATG TTGG CTGTCAC		
			CTTCCTAC GATC GACAGTG		
			T CC_		
GAM3769	LOC201173	5'	TGGGAGGAGGCTGAACTGTCA	85115	A T AA
			TGG AGGA GTTGG ACTGTCA		
			ACC TCCT CGACT TGACAGT		
			C C _		
GAM3769	LOC201220	5'	TGGGAGGAGGCTGAACTGTCA	85115	A T AA
			TGG AGGA GTTGG ACTGTCA		

ACC TCCT CGACT TGACAGT
 C C _
 GAM3769 LOC92181 3' GAGGGAGGAAAATTGTCA 85124 A TGTT C_
 GA GGA GGAAA TGTCA
 || ||| |||| ||||
 CT CCT CCTTT ACAGT
 C _ _ TA
 GAM3770 FTSJ2 3' AACTGGAAATCTGTGCGTGG 85127 C T _ _
 AAC GGA ATCT GCG GG
 ||| ||| ||| ||| ||
 TTG CCT TAGA CGC CC
 A T CA A
 GAM3770 KCNA6 5' ACCTGGGCGCTGGGGATTT 85128 _ ATATC _
 ACC GG TGC GGGGATTT
 ||| || ||| |||||
 TGG CC GCG CCCCTAAA
 A C _ _ A
 GAM3770 BA108L7.2 3' GGATTGGAGGATTTA 85129 ATC C
 GGAT TG GGGGATTTA
 |||| || |||||
 CCTA AC CTCCTAAAT
 _ _
 GAM3770 FLJ31153 3' CAGATATTGCAGATTTAA 85130 C GG
 CGGATAT TGC GGATTTAA
 ||||| ||| |||||
 GTCTATA ACG TCTAAATT
 _ _
 GAM3770 MAP2K6 5' GGACATCTGCATATCTTAA 85131 GGGA
 GGATATCTGCG TTAA
 ||||| ||| ||||
 CCTGTAGACGT GAATT
 ATA_
 GAM3770 NRM 3' CCTGGATGTTAAGGATTTA 85132 _ ATCTGC
 CC GGAT GGGGATTTA
 || ||| |||||
 GG CCTA TTCCTAAAT
 A CAA_
 GAM3770 NRM 3' CCTGGATGTTAAGGATTTA 85132 _ ATCTGC
 CC GGAT GGGGATTTA
 || ||| |||||
 GG CCTA TTCCTAAAT
 A CAA_
 GAM3770 NRM 3' CCTGGATGTTAAGGATTTA 85132 _ ATCTGC
 CC GGAT GGGGATTTA
 || ||| |||||
 GG CCTA TTCCTAAAT
 A CAA_
 GAM3771 FLJ12598 5' CATGGTACCTGTAAATGACAT 85135 A AT C
 TATGGTGC CT GTAAA GACAT
 ||||| || |||| ||||

		GTACCATG GA CATT CTGTA	
		— — A	
GAM3771	FLJ13195	3' TATGATGCATTGAGGATGACAT 85136	CTA TAAAC
		TATGGTGCA TG GACAT	
		ATACTACGT AC CTGTA	
		A__ TCCTA	
GAM3771	LOC143146	3' TATGGTACCTTCGTAAGTGACA 85137	A A AC
	T	TATGGTGCTGTAAGTGACA 85137	
		ATACCATG GA GCATT CTGTA	
		— A CA	
GAM3772	ADAR	3' CACTTGGGGGAAAAAAGGGG 85140	TGA
		CACTTGG GAGAAAGGGG	
		GTGAACC TTTTTCCTCC	
		CCC	
GAM3772	ADAR	3' CACTTGGGGGAAAAAAGGGG 85140	TGA
		CACTTGG GAGAAAGGGG	
		GTGAACC TTTTTCCTCC	
		CCC	
GAM3772	ADAR	3' CACTTGGGGGAAAAAAGGGG 85140	TGA
		CACTTGG GAGAAAGGGG	
		GTGAACC TTTTTCCTCC	
		CCC	
GAM3772	BARHL1	3' CCTGGGGGAGAAAGGGG 85141	TGA
		CTTGG GAGAAAGGGG	
		GGACC CTCTTTCCTCC	
		C__	
GAM3772	BDNF	5' CACCTGGGTGGAAGTCTGGGG 85142	A AAA
		CACTTGGTG GAG GGGG	
		GTGGACCAC CTT CCCC	
		— GAG	
GAM3772	CMKLR1	3' CACTAGAAGAAAGGG 85143	T TGA
		CACT GG GAGAAAGGG	
		GTGA TC TTCTTTCCTCC	
		— —	
GAM3772	COL2A1	3' CTTAGAAAGAGAGGGG 85144	T AA
		CTTGG GAGAGA GGGG	
		GAATC TTCTCT CCCC	
		T —	
GAM3772	COL2A1	3' CTTAGAAAGAGAGGGG 85144	T AA
		CTTGG GAGAGA GGGG	

GAATC TTCTCT CCCC
T _

GAM3772 COL4A4 5' CCTGGTAAGTTGGGAGGGAGGG 85145 _ AA III
GC CTTGGTGA GAG AGGGG C
||||| III ||| I
GGACCATT CTC TCCCC G
CAACC CC III

GAM3772 COX10 3' TGGCAGCGGAGGGAAAGGGG 85146 _ A
TGGT GAG GAAAGGGG
||| III |||||
ACCG CTC CTTTCCCC
TCGC C

GAM3772 DMPK 5' CTGGGTGGGAGAAAGGGG 85147 T A
CT GGTG GAGAAAGGGG
|| ||| |||||
GA CCAC CTCTTTCCCC
C C

GAM3772 DPYSL2 3' CTTGGTGAGAGACGGGG 85148 AA
CTTGGTGAGAGA GGGG
||||||| |||
GAACCACTCTCT CCCC
G_

GAM3772 DRD5 3' CATTTGTTTAAAAAGGGAGGGG 85149 C GT_ AA
CA TTG GAGAG AGGGG
|| ||| ||| |||
GT AAC TTTTC TCCCC
A AAAT CC

GAM3772 F13A1 3' CCTGACCCCGAGAAAGGGG 85150 TGA_
CTTGG GAGAAAGGGG
|||| |||||
GGA CTCTTTCCCC
GGGG

GAM3772 FKBP1A 3' CACATACGAGGAGAAAGGGG 85151 TTG _
CAC GTGAG AGAAAGGGG
|| ||| |||||
GTG TGCTC TCTTTCCCC
TA_ C

GAM3772 GABRE 3' CTATCTGCAGAGAAAGGGG 85152 TGG _
CT TG AGAGAAAGGGG
|| || |||||
GA AC TCTCTTTCCCC
TAG G

GAM3772 GABRE 3' CTATCTGCAGAGAAAGGGG 85152 TGG _
CT TG AGAGAAAGGGG
|| || |||||
GA AC TCTCTTTCCCC
TAG G

GAM3772 GABRE 3' CTATCTGCAGAGAAAGGGG 85152 TGG _
CT TG AGAGAAAGGGG
|| || |||||

			GA AC TCTCTTTCCCC			
			TAG G			
GAM3772	GABRE	3'	CTATCTGCAGAGAAAGGGG	85152	TGG _	
			CT TG AGAGAAAGGGG			
			GA AC TCTCTTTCCCC			
			TAG G			
GAM3772	GGA3	3'	CATCTGGTGAGAGGAGAGGG	85153	C AA_	
			CA TTGGTGAGAG AGGG			
			GT GACCACTCTC TCCC			
			A CTC			
GAM3772	GGA3	3'	CATCTGGTGAGAGGAGAGGG	85153	C AA_	
			CA TTGGTGAGAG AGGG			
			GT GACCACTCTC TCCC			
			A CTC			
GAM3772	GRB7	5'	CTGAGCGAGAGAGGGG	85154	T AA	
			CT GGTGAGAGA GGGG			
			GA TCGCTCTCT CCCC			
			C _			
GAM3772	H1F0	3'	CACTTGTTTAAAAAAGGGG	85155	GTGA	
			CACTTG GAGAAAGGGG			
			GTGAAC TTTTTC CCC			
			AAA_			
GAM3772	INPP5A	3'	CACCTGGCAGAGGGG	85156	G AAA	
			CACTTGGT AGAG GGG			
			GTGGACCG TCTC CCC			
			_ _			
GAM3772	IVD	3'	CACTAGGTGCAGGAAAAGGGG	85157	T _ AG	
			CACT GGTG AG AAAGGGG			
			GTGA CCAC TC TTTCCCC			
			T G CT			
GAM3772	KIF5C	3'	CACTTCGAAAGAGGG	85158	GG AA	
			CACTT TGAGAGA GGG			
			GTGAA GCTTTCT CCC			
			_ _			
GAM3772	MECP2	3'	CACTGCGGGGAGAGGGG	85159	_ T AAA	
			CACT TGG GAGAG GGG			
			GTGA GCC CTCTC CCC			
			C C _			
GAM3772	MLLT2	3'	ACTTGATATCTGAGGGGG	85160	A_ AAA	
			ACTTGGTG GAG GGGG			

TGA ACTAT CTC CCCC
 AGA ____
 GAM3772 NAGA 3' CACTTTGGA AAAAGGAGGGG 85161 _ T AA
 CACTT GG GAGAG AGGGG
 ||||| || ||||| |||||
 GTGAA CC TTTTC TCCCC
 A _ C_
 GAM3772 NEDD4L 3' CAGTTGGTGAGGACAGG 85162 C A A
 CA TTGGTGAG GA AGG
 || ||||| || |||
 GT AACCACTC CT TCC
 C _ G
 GAM3772 NF2 5' CCTGAGCGGAAAGGGG 85163 _ AGA
 CTTG GTG GAAAGGGG
 |||| || |||||
 GGAC CGC CTTTCCCC
 T ____
 GAM3772 NGFR 3' CACCTAGCAGTGTGGGAGAAGG 85164 ____ A A |||
 GGGC CTTGGT G GAGAA GGGG C
 ||||| | ||||| ||| |
 GGATCG C CTCTT CCCC G
 TCACA C C |||
 GAM3772 PCDH11X 5' ACCGAGGGGGAGAAAGGGG 85165 T_ TGA
 ACT GG GAGAAAGGGG
 ||| || |||||
 TGG CC CTCTTTCCCC
 CT CC_
 GAM3772 PIM1 3' CATCTGACAAGAGAGGGG 85166 C TG AA
 CA TTGG AGAGA GGGG
 || |||| ||||| |||||
 GT GACT TCTCT CCCC
 A GT ____
 GAM3772 PXN 3' CACCTGTGAAAGGGG 85167 G AAA
 CACTTG TGAGAG GGG
 ||||| ||||| |||
 GTGGAC ACTTTC CCC
 _ _
 GAM3772 RAB5C 5' CACTTAGTGGGGAGGGGG 85168 A_ AAA
 CACTTGGTG GAG GGGG
 ||||| || |||
 GTGAATCAC CTC CCCC
 CC ____
 GAM3772 RARA 3' GGCAGAGGGAGAAAGGGG 85169 _ _
 GGT GA GAGAAAGGGG
 ||| || |||||
 CCG CT CTCTTTCCCC
 T CC
 GAM3772 RARG 3' CACCTGGCAGAGGAAGGGG 85170 G A
 CACTTGGT AGAG AAGGGG
 ||||| ||||| |||||

			GTGGACCG TCTC TTCCCC		
			— C		
GAM3772	RPL10	3'	TTGGTGAGTATTAAGAGGGGGG 85171	—	AA
			TTGGTGAG AGA GGGG		
			AACCACTC TCT CCCC		
			ATAAT CC		
GAM3772	RUNX3	3'	CACCTAGGGGAAAAGGGG 85172	TGAGA	
			CACTTG GAAAGGGG		
			GTGGATC CTTTCCCC		
			CC—		
GAM3772	SLC39A1	3'	TTGAGAAAGAGGAAGGGG 85173	_T A	
			TTG G GAGAG AAGGGG		
			AAC C TTCTC TTCCCC		
			TT C		
GAM3772	SLC7A8	3'	ACAAAAGCAGAGAGAGGGG 85174	TT_ G A	
			AC GGT AGAGA AGGGG		
			TG TCG TCTCT TCCCC		
			TTT _ C		
GAM3772	SLC9A3R1	3'	CATTTGTCAAGAAAGGGG 85175	C GTGA	
			CA TTG GAGAAAGGGG		
			GT AAC TTCTTTCCCC		
			A AG—		
GAM3772	SLN	3'	TGGTGAGACAGATCAGGGG 85176	— A_	
			TGGTGAGA GA AGGGG		
			ACCACTCT CT TCCCC		
			GT AG		
GAM3772	SNRPN	5'	CACTGGTAAAAGGGG 85177	T AAA	
			CACT GGTGAGAG GGG		
			GTGA CCATTTTC CCC		
			— —		
GAM3772	SNRPN	5'	CACTGGTAAAAGGGG 85177	T AAA	
			CACT GGTGAGAG GGG		
			GTGA CCATTTTC CCC		
			— —		
GAM3772	SNRPN	5'	CACTGGTAAAAGGGG 85177	T AAA	
			CACT GGTGAGAG GGG		
			GTGA CCATTTTC CCC		
			— —		
GAM3772	SNRPN	5'	CACTGGTAAAAGGGG 85177	T AAA	
			CACT GGTGAGAG GGG		

GTGA CCATTTTC CCC

GAM3772 TAL1 5' CACTCCGCCGGAAGGGG 85179 G GAGA
CACTT GT GAAAGGGG
||||| || |||||
GTGAG CG CTTTCCCC
G GC_

GAM3772 TAL1 3' ACTTAAAAGGAAGGGG 85178 TGG A
ACT TGAGAG AAGGGG
||| ||||| |||||
TGA ATTTTC TTCCCC

GAM3772 THRA 3' CCAGGCAGAGAAAGGGG 85180 T G
CT GGT AGAGAAAGGGG
|| ||| |||||
GG CCG TCTCTTTCCCC
T _

GAM3772 TIAM1 5' ACTAGGTGAGAGACTAGG 85181 T AA
ACT GGTGAGAGA GGG
||| ||||| |||
TGA CCACTCTCT TCC
T GA

GAM3772 TRPM1 5' CACTTGGCAGAGGGGGG 85182 G AAA
CACTTGGT AGAG GGGG
|||||| ||| |||
GTGAACCG TCTC CCCC
_ C_

GAM3772 BOP 5' TTGGTGAGAAATTTGGGG 85183 AA_
TTGGTGAGAGA GGGG
||||||| |||
AACCACTCTTT CCCC
AAA

GAM3772 C11orf23 3' CACCCGGGAAAGGGG 85184 TGAGA
CACTTGG GAAAGGGG
||||| |||||
GTGGGCC CTTTCCCC

GAM3772 CCNI 5' ACTGAGGAGGGAGAAAGGGG 85185 T_ TGA
ACT GG GAGAAAGGGG
||| || |||||
TGA CC CTCTTTCCCC
CT TCC

GAM3772 CNM2 3' CTCCTGAGGGAAAGGGG 85186 GG A
CTT TGAG GAAAGGGG
||| ||| |||||
GAA ACTC CTTTCCCC
GG C

GAM3772 DKFZp434K1210 3' ACTCTGAGGGAGAGGGG 85187 GG A A
ACTT TGAG GA AGGGG
|||| ||| || |||

		TGAG ACTC CT TCCCC			
		__ C C			
GAM3772	DKFZP547E1010	5' CATTGTGTAAGATAGGG	85188	C	GAA
		CA TTGGTGAGA AGGG			
		GT AACCATTCT TCCC			
		A A__			
GAM3772	DKFZP547E1010	5' CATTGTGTAAGATAGGG	85188	C	GAA
		CA TTGGTGAGA AGGG			
		GT AACCATTCT TCCC			
		A A__			
GAM3772	DKFZP564D0478	3' CTTGGTGACAACGTGAAGGGG	85189		G A__
		CTTGGTGA AG AAGGGG			
		GAACCACT TT TTCCCC			
		G GCAC			
GAM3772	DKFZP564O0823	3' CTTGTACCAGAAAGGGG	85190	G AG	
		CTTG TG AGAAAGGGG			
		GAAC AT TCTTTCCCC			
		_ GG			
GAM3772	DKFZP566I1024	3' CATCCAGGGAGAAAGGGG	85191	_ T TGA	
		CA CT GG GAGAAAGGGG			
		GT GG CC CTCTTTCCCC			
		A T __			
GAM3772	DKFZp586I021	3' ACCTGGCACCCAGAGAGGGG	85192	AG_ A	
		ACTTGGTG AGA AGGGG			
		TGGACCGT TCT TCCCC			
		GGG C			
GAM3772	DNCH1	3' CACTATTACAGAAAGGGG	85193	TGG AG	
		CACT TG AGAAAGGGG			
		GTGA AT TCTTTCCCC			
		TA_ G_			
GAM3772	ELF4	3' CTCGGAAGAGGGAAGGGG	85194	T A_	
		CTTGG GAGAG AAGGGG			
		GAGCC TTCTC TTCCCC			
		T CC			
GAM3772	FLJ00001	3' ACTTTCCAGAGAGAAAGGGG	85195	GGT_	
		ACTT GAGAGAAAGGGG			
		TGAA CTCTCTTTCCCC			
		AGGT			
GAM3772	FLJ10743	3' ACTTGGTGAGAACTGGG	85196	AAA	
		ACTTGGTGAGAG GGG			

		TGAACCACTCTT CCC	
		GA_	
GAM3772 FLJ11506	3'	TGGCTTTAAAGAGAAAGGGG 85197	_____
		TGGT GAGAGAAAGGGG	
		ACCG TTCTCTTTCCCC	
		AAAT	
GAM3772 FLJ12529	3'	TTGGAGGAAAGGGAAGGGG 85198	T_ A_
		TTGG GAGAG AAGGGG	
		AACC CTTTC TTCCCC	
		TC CC	
GAM3772 FLJ20308	3'	ACATCAGTGAGGGAAGGGG 85199	_TG A
		AC T GTGAG GAAAGGGG	
		TG A CACTC CTTTCCCC	
		T GT C	
GAM3772 FLJ20337	3'	CACCTGGTGAGAAAAGG 85200	A
		CACTTGGTGAGAGAA GG	
		GTGGACCACTCTTTT CC	
		—	
GAM3772 FLJ20452	3'	ACTTAGTGGGAGGAATAGGG 85201	A _ _
		ACTTGGTG GAG AA AGGG	
		TGAATCAC CTC TT TCCC	
		C C A	
GAM3772 FLJ21195	3'	CACTTCGCGCGGGAAGGGG 85202	G AGA
		CACTT GTG GAAAGGGG	
		GTGAA CGC CTTTCCCC	
		G GCC	
GAM3772 FLJ23309	3'	ACTTGTAAGATGGAGAGGGG 85203	_ A
		ACTTGGTGAGA GA AGGGG	
		TGAACCATTCT CT TCCCC	
		AC C	
GAM3772 GAL3ST-4	3'	CTTGGGGCAGGAAAGGGG 85204	TG_ A
		CTTGG AG GAAAGGGG	
		GAACC TC CTTTCCCC	
		CCG _	
GAM3772 HXCP2	3'	CACGTGGACACAGGGAAGGGG 85205	T TG_ A A
		CAC TGG AG GAA GGGG	
		GTG ACC TC CTT CCCC	
		C TGTG C _	
GAM3772 JAM1	3'	CACTTGGTGGAACAGG 85206	A AA
		CACTTGGTG GAG AGG	

			GTGAACCAC CTT TCC		
			_ G_		
GAM3772	JAM1	3'	CACTTGGTGGAACAGG	85206	A AA
			CACTTGGTG GAG AGG		
			GTGAACCAC CTT TCC		
			_ G_		
GAM3772	JAM1	3'	CACTTGGTGGAACAGG	85206	A AA
			CACTTGGTG GAG AGG		
			GTGAACCAC CTT TCC		
			_ G_		
GAM3772	JAM1	3'	CACTTGGTGGAACAGG	85206	A AA
			CACTTGGTG GAG AGG		
			GTGAACCAC CTT TCC		
			_ G_		
GAM3772	KCND1	5'	ACTAAATAAGAGGAAGGGG	85207	TG A
			ACT GTGAGAG AAGGGG		
			TGA TATTCTC TTCCCC		
			TT C		
GAM3772	KIAA0121	5'	TTGGAAAGAAAGAGAAAGGGG	85208	T_____
			TTGG GAGAGAAAGGGG		
			AACC TTCTCTTCCCC		
			TTTCT		
GAM3772	KIAA0189	3'	CTCTGCTTGAGAAAGGGG	85209	G GA
			CTT GT GAGAAAGGGG		
			GAG CG CTCTTTCCCC		
			A AA		
GAM3772	KIAA0280	3'	ACTTGGTGACCAAGGGG	85210	GAGA
			ACTTGGTGA AAGGGG		
			TGAACCACT TTCCCC		
			GG_		
GAM3772	KIAA0316	3'	ACTTGGAAGAAAGGGG	85211	TG
			ACTTGG AGAGAAAGGGG		
			TGAACC TTTCTTTCCCC		
			—		
GAM3772	KIAA0789	5'	TGGCTTTAAGGAAAGGGG	85212	___ A
			TGGT GAG GAAAGGGG		
			ACCG TTC CTTTCCCC		
			AAA _		
GAM3772	KIAA0864	3'	CACATGGTGAGACAGGG	85213	T GAA
			CAC TGGTGAGA AGGG		

GTG ACCACTCT TCCC
 T G__
 GAM3772 KIAA0939 3' CACCTGGTGACGAGGGGG 85214 _ AAA
 CACTTGGTGA GAG GGGG
 ||||| ||| |||
 GTGGACCACT CTC CCCC
 G ____
 GAM3772 KIAA0964 3' CACTTGGCGGGGGGAGGGAGGG 85215 A__ AA
 G CACTTGGTG GAG AGGGG
 ||||| ||| |||||
 GTGAACCGC CTC TCCCC
 CCCC CC
 GAM3772 KIAA1001 3' CTTAAAAGGAGAGGAAGGGG 85216 T__ A
 CTTGG GAGAG AAGGGG
 |||| |||| |||||
 GAATT CTCTC TTCCCC
 TTC C
 GAM3772 KIAA1246 5' CATTTAGCAAGAAGAAGGGG 85217 C TG GA
 CA TTGG AGA AAGGGG
 || ||| ||| |||||
 GT AATC TCT TTCCCC
 A GT TC
 GAM3772 KIAA1344 3' ACAAGAAGAGGAAGGGG 85218 TT T A
 AC GG GAGAG AAGGGG
 || || ||||| |||||
 TG TC TTCTC TTCCCC
 T_ _ C
 GAM3772 KIAA1399 5' CACTTGATGAGGCAAGG 85219 AGA
 CACTTGGTGAG AAGG
 ||||| ||| |||
 GTGAACTACTC TTCC
 CG_
 GAM3772 KIAA1805 3' CCTACTAAAAGGGGAGGGG 85220 G AA_
 CTTG TGAGAG AGGGG
 ||| ||||| |||||
 GGAT ATTTTC TCCCC
 G CCC
 GAM3772 KIAA1904 3' CACTCATGGAAAGGG 85221 G AGA
 CACTTG TG GAAAGGG
 ||||| || |||||
 GTGAGT AC CTTTCCC
 _ _
 GAM3772 KIAA1915 3' ACTGGTGAGGAGCATGGGG 85222 T _ AAA
 ACT GGTGAG AG GGGG
 ||| ||||| || |||
 TGA CCACTC TC CCCC
 _ C GTA
 GAM3772 MEP50 3' CACATCAAGAGAAAGGGG 85223 TTGG
 CAC TGAGAGAAAGGGG
 ||| ||||| |||||

			GTG GTTCTCTTTCCCC		
			TA__		
GAM3772	MGC10818	3'	CACTTGGTAAAGGAAAGG	85224	A
			CACTTGGTGAG GAAAGG		
			GTGAACCATTC CTTTCC		
			C		
GAM3772	MGC10981	3'	CACTTGGTGGAGCTGGG	85225	A AAA
			CACTTGGTG GAG GGG		
			GTGAACCAC CTC CCC		
			_ GA_		
GAM3772	MGC11266	3'	CACCTGGCAGGGGAGGGG	85226	G AGAA
			CACTTGGT AG AGGGG		
			GTGGACCG TC TCCCC		
			_ CCC_		
GAM3772	MGC4415	3'	TGGTTTGGAAGGAAGGGG	85227	___ A
			TGGT GAGAG AAGGGG		
			ACCA CTTTC TTCCCC		
			AAC C		
GAM3772	MGC4604	3'	CTCAGTAGAGAAAGGGG	85228	TG G
			CT GT AGAGAAAGGGG		
			GA CA TCTCTTTCCCC		
			GT _		
GAM3772	PAK6	3'	ACTTAGTGGGAGAGAGGGG	85229	A A
			ACTTGGTG GAGA AGGGG		
			TGAATCAC CTCT TCCCC		
			C C		
GAM3772	PDE8B	3'	CCTTTTACAGGAAAGGGG	85230	GG _ A
			CTT TG AG GAAAGGGG		
			GGA AT TC CTTTCCCC		
			AA G _		
GAM3772	PLSCR3	3'	ACATGGAGGAAAGGGG	85231	T TG A
			AC TGG AG GAAAGGGG		
			TG ACC TC CTTTCCCC		
			T _ _		
GAM3772	PLSCR3	3'	ACATGGAGGAAAGGGG	85231	T TG A
			AC TGG AG GAAAGGGG		
			TG ACC TC CTTTCCCC		
			T _ _		
GAM3772	PLUNC	3'	CCTGGTGGGAAAGGAGAGGGG	85232	A A__
			CTTGGTG GAGA AGGGG		

			GGACCAC CTTT TCCCC		
			C CCTC		
GAM3772	PLUNC	3'	CCTGGTGGGAAAGGAGAGGGG	85232	A A__
			CTTGGTG GAGA AGGGG		
			GGACCAC CTTT TCCCC		
			C CCTC		
GAM3772	PRDM10	3'	CACTTGGTAAGAACAAGG	85233	A
			CACTTGGTGAGAG AAGG		
			GTGAACCATTCTT TTCC		
			G		
GAM3772	PSMF1	5'	CTGGAGGAAAGAAGGGGG	85234	T_ A
			TTGG GAGAGAA GGGG		
			GACC CTTTCTT CCCC		
			TC C		
GAM3772	PV1	3'	CACTAGGTGAGAATTGGG	85235	T AAA
			CACT GGTGAGAG GGG		
			GTGA CCACTCTT CCC		
			T AA_		
GAM3772	REM	5'	CCTTCTGAAAGAAGGGGG	85236	GG A
			CTT TGAGAGAA GGGG		
			GGA ACTTTCTT CCCC		
			AG C		
GAM3772	RHO6	3'	CACTCTGCAAGAGAAGGGGG	85237	G TG A
			CACTT G AGAGAA GGGG		
			GTGAG C TCTCTT CCCC		
			A GT C		
GAM3772	SARM	3'	ACTGGTGAGGAAGGGG	85238	T A A
			ACT GGTGAG GAA GGGG		
			TGA CCACTC CTT CCCC		
			- - -		
GAM3772	SLC26A8	3'	CTCTTTGGAGAAAGGGG	85239	GG A
			CTT TG GAGAAAGGGG		
			GAG AC CTCTTTCCCC		
			AA _		
GAM3772	SLC26A8	3'	CTCTTTGGAGAAAGGGG	85239	GG A
			CTT TG GAGAAAGGGG		
			GAG AC CTCTTTCCCC		
			AA _		
GAM3772	SLC2A13	3'	TTGAATAAAAGAAAGGGG	85240	_
			TTGG TGAGAGAAAGGGG		

AACT ATTTTCTTTCCCC
 T
 GAM3772 SMT3H2 3' CACTAATGGAGAAAGGGG 85241 T A
 CACT GGTG GAGAAAGGGG
 |||| ||| |||||
 GTGA TTAC CTCTTTCCCC

 — —
 GAM3772 SPAG4L 5' CTGGTGAGGAGGAAGGGG 85242 _ A
 TTGGTGAG AG AAGGGG
 ||||| || |||||
 GACCACTC TC TTCCCC
 C C
 GAM3772 SPIN 3' CTTTAAAAAGAAAGGGG 85243 GG
 CTT TGAGAGAAAGGGG
 ||| |||||
 GAA ATTTTCTTTCCCC
 A_
 GAM3772 LOC129676 5' ACTGGTGAGGACAATGGGG 85244 T A AA_
 ACT GGTGAG GA GGGG
 ||| ||||| || |||
 TGA CCACTC CT CCCC
 — — GTTA
 GAM3772 LOC130644 3' CACTGGGAGAAAGGGG 85245 T TGA
 CACT GG GAGAAAGGGG
 |||| || |||||
 GTGA CC CTCTTTCCCC

 — —
 GAM3772 LOC142941 5' ACTTGATGGGAGGGGG 85246 A AAA
 ACTTGGTG GAG GGGG
 ||||| ||| |||
 TGA ACTAC CTC CCCC
 C —
 GAM3772 LOC143903 5' CACTCGGCCAGCCAGAGAGGGG 85247 G _ A
 CACTTGGT AG AGA AGGGG
 ||||| || ||| |||||
 GTGAGCCG TC TCT TCCCC
 G GG C
 GAM3772 LOC145622 5' CTCCATGTGGAGAAAGGGG 85248 G A_
 CTT GTG GAGAAAGGGG
 ||| ||| |||||
 GAG TAC CTCTTTCCCC
 G AC
 GAM3772 LOC145757 3' CACTTCAAGGAAAGGGG 85249 GG A
 CACTT TGAG GAAAGGGG
 |||| ||| |||||
 GTGAA GTTC CTTTCCCC

 — —
 GAM3772 LOC146237 3' TAGCAGAAGGAGAAAGGGG 71918 _ _
 TGGT GA GAGAAAGGGG
 |||| || |||||

	ATCG CT CTCTTTCCCC		
	T TC		
GAM3772 LOC147917 3'	CACTGGGAGAAAGGAGGGG 85250	T T	A_
	CACT GG GAGAGA AGGGG		
	GTGA CC CTCTTT TCCCC		
	_ _ CC		
GAM3772 LOC148114 5'	CACTTGGCTGAGGCTAAGGG 85251	_	AGA
	CACTTGG TGAG AAGGG		
	GTGAACC ACTC TTCCC		
	G CGA		
GAM3772 LOC148645 3'	CTGATGAAGAGGGAGGGG 85252	_	AA
	TTGGTGA GAG AGGGG		
	GACTACT CTC TCCCC		
	T CC		
GAM3772 LOC149448 3'	TGGTGGGAGGGAGGGGCC 85253	A AA	III
	TGGTG GAG AGGGG CC		
	ACCAC CTC TCCCC GG		
	C CC III		
GAM3772 LOC149711 3'	TGTGTGCAGAGAAAGGGG 85254	_ _	
	TG GTG AGAGAAAGGGG		
	AC CAC TCTCTTTCCCC		
	A G		
GAM3772 LOC150848 5'	ACCTGCAAGGAAAGGGG 85255	G TG	A
	ACTT G AG GAAAGGGG		
	TGGA C TC CTTTCCCC		
	_ GT _		
GAM3772 LOC151623 5'	CTTGGTGAGAACTGAGGGG 85256	AA_	
	CTTGGTGAGAG AGGGG		
	GAACCACTCTT TCCCC		
	GAC		
GAM3772 LOC152580 3'	CACTTGGTGAGTGATGG 85257	A AA	
	CACTTGGTGAG GA GG		
	GTGAACCACTC CT CC		
	A A_		
GAM3772 LOC152715 5'	TTGGTGAGAATCACAGGGG 85258	AA__	
	TTGGTGAGAG AGGGG		
	AACCACTCTT TCCCC		
	AGTG		
GAM3772 LOC153338 5'	TGCTTGAGAAAAGGAGGGG 85259	G_	_
	TG TGAGAGAA AGGGG		

	AC ACTCTTTT TCCCC		
	GA CC		
GAM3772 LOC154215 3'	CCTGGGAGAAAGGGG 85260	TGA	
	CTTGG GAGAAAGGGG		
	GGACC CTCTTTCCCC		
	—		
GAM3772 LOC154547 3'	CACTAATGGAGAAAGGGG 85241	T A	
	CACT GGTG GAGAAAGGGG		
	GTGA TTAC CTCTTTCCCC		
	— —		
GAM3772 LOC157247 5'	CACTTGAGTGGAAGGAGGGG 85261	_ A A_	
	CACTTG GTG GAGA AGGGG		
	GTGAAC CAC CTTT TCCCC		
	T _ CC		
GAM3772 LOC158997 3'	CACTAATGGAGAAAGGGG 85241	T A	
	CACT GGTG GAGAAAGGGG		
	GTGA TTAC CTCTTTCCCC		
	— —		
GAM3772 LOC163682 3'	CACTGGTGAGACCACAGGG 85262	T GAA_	
	CACT GGTGAGA AGGG		
	GTGA CCACTCT TCCC		
	_ GGTG		
GAM3772 LOC166341 3'	CATTCGGCAAGGAAAGGGG 85263	C TG A	
	CA TTGG AG GAAAGGGG		
	GT AGCC TC CTTTCCCC		
	A GT _		
GAM3772 LOC199678 3'	CACATGGAAATAAAAGGGG 85264	T T A	
	CAC TGG GAG GAAAGGGG		
	GTG ACC TTT TTTTCCCC		
	T _ A		
GAM3772 LOC199906 5'	CACTGTCCCAGAGAAAGGGG 85265	TGGTG	
	CACT AGAGAAAGGGG		
	GTGA TCTCTTTCCCC		
	CAGGG		
GAM3772 LOC201669 5'	CTTAGTGAGAACCCAAGG 85266	AA_	
	CTTGGTGAGAG AGGG		
	GAATCACTCTT TTCC		
	GGG		
GAM3772 LOC201799 3'	ACCTAAAGAGAGAAAGGGG 85267	T	
	ACTTGG GAGAGAAAGGGG		

TGGATT CTCTCTTTCCCC
 T
 GAM3772 LOC221561 3' CACTAATGGAGAAAGGGG 85241 T A
 CACT GGTG GAGAAAGGGG
 |||| ||| |||||
 GTGA TTAC CTCTTTCCCC

— —
 GAM3772 LOC221962 3' CTTGGTGAGAACTGAGGGG 85256 AA_
 CTTGGTGAGAG AGGGG
 ||||| |||
 GAACCACTCTT TCCCC
 GAC

GAM3772 LOC253289 3' CTTGGGAGAAAGGGG 85268 TGA
 CTTGG GAGAAAGGGG
 |||| |||||
 GAACC CTCTTTCCCC

—
 GAM3772 LOC253782 3' ACTACAGCAAGAGAAAGGGG 85269 _ TG
 ACT TGG AGAGAAAGGGG
 ||| ||| |||||
 TGA GTC TCTCTTTCCCC
 T GT

GAM3772 LOC253943 3' TTGGTGAAGAGTATAAGGG 85270 _ A__
 TTGGTGA GAG AAGGG
 ||||| ||| |||
 AACCACT CTC TTCCC
 T ATA

GAM3772 LOC255461 5' CTTGGTGAGAACTGAGGGG 85256 AA_
 CTTGGTGAGAG AGGGG
 ||||| |||
 GAACCACTCTT TCCCC
 GAC

GAM3772 LOC255516 5' CTTGGTGAGAACTGAGGGG 85256 AA_
 CTTGGTGAGAG AGGGG
 ||||| |||
 GAACCACTCTT TCCCC
 GAC

GAM3772 LOC256273 3' ACATAGCCAAGAAAGGGG 85271 T GA
 AC TGGT GAGAAAGGGG
 || ||| |||||
 TG ATCG TTCTTTCCCC
 T G_

GAM3772 LOC256306 5' CTTGGAGAATGAGGAAGGGG 85272 T _ A
 CTTGG GA GAG AAGGGG
 |||| || ||| |||||
 GAACC CT CTC TTCCCC
 T TA C

GAM3772 LOC257591 3' CACTAATGGAGAAAGGGG 85241 T A
 CACT GGTG GAGAAAGGGG
 |||| ||| |||||

GTGA TTAC CTCTTTCCCC

GAM3772 LOC51093 3' TGGAAGGAGAGAAAGGGG 85273 T__

TGG GAGAGAAAGGGG

||| |||||

ACC CTCTCTTTCCCC

TTC

GAM3772 LOC57086 3' CACTTGACACAGGAAGGGG 85274 TGAG A

CACTTGG AG AAGGGG

||||| || |||||

GTGAACC TC TTCCCC

TGTG C

GAM3772 LOC58525 5' CAGTTGGTGAGTGGCCCAGGGG 85275 C AGAA__

CA TTGGTGAG AGGGG

|| ||||| ||||

GT AACCCTC TCCCC

C ACCGGG

GAM3772 LOC90317 3' CACATGGTGAGAATGAGGG 85276 T AA

CAC TGGTGAGAG AGGG

||| ||||| ||||

GTG ACCACTCTT TCCC

T AC

GAM3772 LOC90538 3' CACCTGGTAGAAGGG 85277 G GAA

CACTTGGT AGA AGGG

||||| || ||||

GTGGACCA TCT TCCC

GAM3772 LOC91397 5' CATTTGGCAAGAGGAAGGGG 85278 C TG A

CA TTGG AGAG AAGGGG

|| |||| |||| |||||

GT AACC TCTC TTCCCC

A GT C

GAM3772 LOC91445 3' CACTGGGATTTGAAAGGGG 85279 T T GA_

CACT GG GA GAAAGGGG

|||| || || |||||

GTGA CC CT CTTTCCCC

_ _ AAA

GAM3773 CALB1 5' TGTGTCCGCGCGAAGGG 85282 A _ CCAC

TGTGTCCG GC AAG GG

||||| || ||| ||

ACACAGGC CG TTC CC

G C _

GAM3773 CBFA2T3 3' TGTGTCCGGCAGGCCAGGG 85283 A A C

TGTGTCCG GCA GCCA GG

||||| || |||| ||

ACACAGGC CGT CGGT CC

_ C C

GAM3773 CDC34 3' TGTCGTCTAAGGAGCCACGG 85284 _ CG CA

TGT GTC AG AGCCACGG

||| || || |||||

		ACA CAG TC TCGGTGCC	
		G AT C_	
GAM3773 ENG	5'	TGTGTCCAGTGGCAGGGCTGCG 85285	A__ A_ CA
G		TGTGTCCG GCA GC CGG	
		ACACAGGT CGT CG GCC	
		CAC CC AC	
GAM3773 HSF4	5'	TGTGTCCAGGACCGAGCGG 85286	G CAA A__
		TGTGTCC AG GCC CGG	
		ACACAGG TC TGG GCC	
		_ C_ CTC	
GAM3773 JAG2	3'	TGCGTCAACAGCCACGG 85287	CG A
		TGTGTC AGCA GCCACGG	
		ACGCAG TTGT CGGTGCC	
		— —	
GAM3773 LOH11CR2A	5'	TGTGTCCAGCAGCCAGGG 85288	G A C
		TGTGTCC AGCA GCCA GG	
		ACACAGG TCGT CGGT CC	
		_ _ C	
GAM3773 MUC3B	3'	TGTGTCCGGGGCAGGGCGGA 85289	A_ A CCA
		TGTGTCCG GCA G CGGA	
		ACACAGGC CGT C GCCT	
		CC _ CC_	
GAM3773 NKX2E	5'	TGTGTCCGGGCAGCAGG 85290	A A CAC
		TGTGTCCG GCA GC GG	
		ACACAGGC CGT CG CC	
		C _ T_	
GAM3773 PAM	3'	TGTGTTCAAGCAAAGAATGG 85291	C CCAC
		TGTGT CGAGCAAG GG	
		ACACA GTTCGTTT CC	
		A CTTA	
GAM3773 PAM	3'	TGTGTTCAAGCAAAGAATGG 85291	C CCAC
		TGTGT CGAGCAAG GG	
		ACACA GTTCGTTT CC	
		A CTTA	
GAM3773 PAM	3'	TGTGTTCAAGCAAAGAATGG 85291	C CCAC
		TGTGT CGAGCAAG GG	
		ACACA GTTCGTTT CC	
		A CTTA	
GAM3773 PINX1	3'	TGTGTCTGAGAGCCACGA 85292	C CA
		TGTGTC GAG AGCCACGG	

		ACACAG CTC TCGGTGCT		
		A _		
GAM3773	SAG	5' TGTTCCTGAGCAAGCTGG 85293	G C	CAC
		TGT TC GAGCAAGC GG		
		ACA AG CTCGTTCG CC		
		_ A A_		
GAM3773	UCP2	5' TGTGTCCGAGCCGCAGG 85294	AA	CAC
		TGTGTCCGAGC GC GG		
		ACACAGGCTCG CG CC		
		G_ T_		
GAM3773	AP1G2	5' TGCGTCCGCACCCCACGG 85295	GA	AG
		TGTGTCC GCA CCACGG		
		ACGCAGG CGT GGTGCC		
		_ GG		
GAM3773	AP3D1	3' TGTGCCCACGCTGGCCGTGG 85296	A AA	AC
		TGTGTCCG GC GCC GG		
		ACACGGGT CG CGG CC		
		G AC CA		
GAM3773	BSPECV	3' TGGGTTGAAGCAGCCACGG 85297	T CC	A
		TG GT GAGCA GCCACGG		
		AC CA TTCGT CGGTGCC		
		C AC _		
GAM3773	FLJ21934	3' TGTGTTTGGGCGCACACCAGGA 85298	CCGA_	A C
		TGTGT GCA GCCA GGA		
		ACACA CGT TGGT CCT		
		AACCCG G _		
GAM3773	FLJ30681	3' TGTGTCCAGTGAGAAAGTGGA 85299	_ C	CCAC
		TGTGTCC GAG AAG GGA		
		ACACAGG CTC TTC CCT		
		TCA T A_		
GAM3773	GIT2	3' TGTGTCCGGGGAAGCCAGG 85300	AGC	C
		TGTGTCCG AAGCCA GG		
		ACACAGGC TTCGGT CC		
		CCC _		
GAM3773	GIT2	3' TGTGTCCGGGGAAGCCAGG 85300	AGC	C
		TGTGTCCG AAGCCA GG		
		ACACAGGC TTCGGT CC		
		CCC _		
GAM3773	GIT2	3' TGTGTCCGGGGAAGCCAGG 85300	AGC	C
		TGTGTCCG AAGCCA GG		

ACACAGGC TTCGGT CC
 CCC _
 GAM3773 GTPBP5 3' TCCGTAGCAAGCCATGGA 85301 _ C
 TCCG AGCAAGCCA GGA
 |||| ||||| |||
 AGGC TCGTTCGGT CCT
 A A
 GAM3773 HSPC072 5' TGTGTCCACAATACGG 85302 GA GCC
 TGTGTCC GCAA ACGG
 ||||| ||| |||
 ACACAGG TGTT TGCC
 _ A_
 GAM3773 IL-17RC 3' GTGAAACCAAGCCACGG 85303 TCC G
 GTG GA CAAGCCACGG
 ||| || |||||
 CAC TT GTTCGGTGCC
 T_ G
 GAM3773 KIAA0252 5' TGTGTCCGAGTCGATCACGA 85304 CAAGC
 TGTGTCCGAG CACGG
 ||||| |||
 ACACAGGCTC GTGCT
 AGCTA
 GAM3773 KIAA1145 3' TGTGTCCGAAGTGCTTGGA 85305 CAA_ CAC
 TGTGTCCGAG GC GGA
 ||||| || |||
 ACACAGGCTT CG CCT
 CACCA AA_
 GAM3773 KIAA1922 5' TGTGTCCGACAGGACGGA 85306 G AGCC
 TGTGTCCGA CA ACGGA
 ||||| || |||
 ACACAGGCT GT TGCCT
 _ CC_
 GAM3773 MGC35558 3' TGTCTCCGAGCAAAACGA 85307 G CC
 TGT TCCGAGCAAG ACGG
 ||| ||||| |||
 ACA AGGCTCGTTT TGCT
 G _
 GAM3773 RNF8 3' TATGTCCAGCAGCTGTGG 85308 G A CAC
 TGTGTCC AGCA GC GG
 ||||| ||| || ||
 ATACAGG TCGT CG CC
 _ _ ACA
 GAM3773 LOC144519 3' TGAGTTCCAGGCCACGGA 85309 TG_ G CAA
 TG TCC AG GCCACGGA
 || ||| || |||||
 AC AGG TC CGGTGCCT
 TCA G _
 GAM3773 LOC147353 3' TGTGTCCAGTAATCAGGA 85310 G C GC C
 TGTGTCC AG AA CA GGA
 ||||| || || |||

ACACAGG TC TT GT CCT
 _ A A _
 GAM3773 LOC148114 5' TGTGCCCCGGCACCTGCGG 85311 A AA A_
 TGTGTCCG GC GCC CGG
 ||||| || ||
 ACACGGGC CG TGG GCC
 _ _ AC
 GAM3773 LOC164397 3' TGAGTCCGAGCAGCAGGA 85312 T A CAC
 TG GTCCGAGCA GC GGA
 || ||||| || ||
 AC CAGGCTCGT CG CCT
 T _ T_
 GAM3773 LOC165476 5' GTGTCCACAGCCAGGCCGCGG 85313 _ AA_ A
 GTGTCCG AGC GCC CGG
 ||||| || ||
 CACAGGT TCG CGG GCC
 G GTC C
 GAM3773 LOC199958 3' TGGTCCACAGCAAGCCACGGA 85314 T _
 TG GTCCG AGCAAGCCACGGA
 || |||| |||||
 AC CAGGT TCGTTCGGTGCCT
 _ G
 GAM3773 LOC201617 5' TGTGTCCGACACACTGGA 85315 G AGC _
 TGTGTCCG CA CAC GGA
 ||||| || ||
 ACACAGGCT GT GTG CCT
 _ _ A
 GAM3773 LOC253767 3' TGTGTCCAGGACCGAGCGG 85286 G CAA A_
 TGTGTCC AG GCC CGG
 ||||| || ||
 ACACAGG TC TGG GCC
 _ C_ CTC
 GAM3773 LOC254707 5' TGTGCCCCGGGCACCCCGGA 85316 A AG A
 TGTGTCCG GCA CC CGGA
 ||||| || ||
 ACACGGGC CGT GG GCCT
 C G_ _
 GAM3773 LOC64744 3' TGGTCCTCCAGCCACGGA 85317 T GAGCA
 TG GTCC AGCCACGGA
 || |||| |||||
 AC CAGG TCGGTGCCT
 _ AGG_
 GAM3773 LOC89231 5' TGTGTCCACATCACACGG 85318 AG_ AGC
 TGTGTCCG CA CACGG
 ||||| || ||
 ACACAGGT GT GTGCC
 GTA _
 GAM3774 TAZ 3' AAAATGAAAATAGAATATTT 85321 A
 AGAATGAAAATA AATATTT
 ||||| |||||

		TTTTACTTTTAT TTATAAA	
		C	
GAM3774	ZNF216	3' TTTAAGAATAAAAGTAAAA 85322	A
		TTTAAGAATGAAA TAAAA	
		AAATTCTTATTTT ATTTT	
		C	
GAM3774	PORIMIN	3' TCTAAGAATTTATTCTAAAATA 85323	GAAAA_
		TTT TTTAAGAAT TAAAATATTT	
		AGATTCTTA ATTTTATAAA	
		AATAAG	
GAM3774	RGS20	3' AAGAATGAAAATGCCCATATTT 85324	AAA_
		AAGAATGAAAAT ATATTT	
		TTCTTACTTTTA TATAAA	
		CGGG	
GAM3774	TRAF3	5' TTTAAAAATGAAAATGAAAAC 85325	_
		TTTAAGAATGAAAAT AAAAT	
		AAATTTTACTTTTA TTTTG	
		C	
GAM3774	TRAF3	3' TTTAAAAATGAAAATGAAAAC 85325	_
		TTTAAGAATGAAAAT AAAAT	
		AAATTTTACTTTTA TTTTG	
		C	
GAM3774	LOC145098	5' TTTAGAAATGAAAATAAAA 85326	AG
		TTTA AATGAAAATAAAA	
		AAAT TTACTTTTATTTT	
		CT	
GAM3775	E2F1	3' CACACATTCACCCCGGTACAC 85329	AATTA _
		CACACGTTCCG CCG ACAC	
		GTGTGTAAGT GGC TGTG	
		GGG_ CA	
GAM3775	TACSTD1	3' CACACATTTGAATGTTACACA 85330	C TACCG
		CACACGTT GAAT ACACA	
		GTGTGTAA CTTA TGTGT	
		A CAA_	
GAM3775	DKFZp547l014	5' ACATGTTTGAATTACCTCAC 85331	C C GA
		ACA GTT GAATTACC CAC	
		TGT CAA CTTAATGG GTG	
		A A A_	
GAM3775	KIAA0444	3' CAGGTTCGAATCTTCCATAC 85332	C A_ _
		CA GTTCGAATT CCG AC	

GT CAAGCTTAG GGT TG
 C AA A
 GAM3775 KIAA1000 3' ACATGTTCAAATTGCCTAAC 85333 C A _
 ACA GTTCGAATT CC GAC
 ||| ||||| || |||
 TGT CAAGTTTAA GG TTG
 A C A
 GAM3775 LOC157869 3' TTCCATAACCGACACAC 85334 GA T
 TTC AT ACCGACACAC
 ||| || |||||
 AAG TA TGGCTGTGTG
 G_ T
 GAM3776 FBXL7 3' TCGGTGCTTACATACGCTGCTT 85337 CGTA CTT
 TCGGTGC AC CGCTGCTT
 ||||| || |||||
 AGCCACG TG GCGACGAA
 AA_ TAT
 GAM3776 LOC153579 3' TCGGTGCCTGACCGCCGCT 85338 GTAACCT
 TCGGTGCC TCGCTGCT
 ||||| |||||
 AGCCACGG GGCGGCGA
 ACT____
 GAM3776 LOC254659 5' TCGGTCTCGCTCGCTGCT 85339 GC AACCT
 TCGGT CGT TCGCTGCT
 |||| ||| |||||
 AGCCA GCG AGCGACGA
 GA _____
 GAM3777 FOXI1 3' CTTAACCTCCTTGAGC 85342 TTTA
 CTTAACC TCTTTGAGC
 ||||| |||||
 GAATTGG AGGAACTCG

 GAM3777 MAB21L1 5' TCCCTTCCTTTTATCTTTGAGC 85343 AA _
 C TCTT CCTTT ATCTTTGAGCC
 ||| |||| |||||
 AGGG GGAAA TAGAACTCGG
 AA A
 GAM3777 EFA6R 3' TATCTTAGCCTTGGAAGC 85344 A TATCTTT
 TATCTTA CCTT GAGC
 ||||| ||| |||
 ATAGAAT GGAA TTCG
 C CCT____
 GAM3777 FLJ11722 3' CTTAACCTTTCTGAGC 85345 TATC
 CTTAACCTT TTTGAGC
 ||||| |||||
 GAATTGGAA AGACTCG

 GAM3777 HSA011916 3' CTTGGCTTCTCTTTGAGCC 85346 AAC A
 CTT CTTT TCTTTGAGCC
 || ||| |||||

	GAA GAAG AGAAACTCGG		
	CC_ _		
GAM3777 HSA011916 3'	CTTGGCTTCTCTTTGAGCC 85346	AAC	A
	CTT CTTT TCTTTGAGCC		
	GAA GAAG AGAAACTCGG		
	CC_ _		
GAM3777 KIAA1033 3'	TCTTAACCTTTGAAAGTAGAGC 85347	ATCTTT_	
C	TCTTAACCTTT GAGCC		
	AGAATTGGAAA CTCGG		
	CTTTCAT		
GAM3777 KIAA1257 3'	CTTAACCTCTTTGAG 85348	TTTA	
	CTTAACC TCTTTGAG		
	GAATTGG AGAAACTC		
GAM3777 KIAA1946 3'	TATCCTGAAGGTATTTTGTAGC 85349	AACCTT C	
C	TATCTT TAT TTTGAGCC		
	ATAGGA ATA AAACTCGG		
	CTTCC_ A		
GAM3777 PRO0899 5'	CTTAACCTTTCTGAGC 85345	TATC	
	CTTAACCTT TTTGAGC		
	GAATTGGAA AGACTCG		
GAM3777 PXR2b 3'	TCTTAATTCTTCTTTTGTAGCC 85350	CC A _	
	TCTTAA TTT TCTTT GAGCC		
	AGAATT AAG AGAAA CTCGG		
	_ A A		
GAM3777 LOC138255 5'	TATCATAACCTTTGGGAAAAGC 85351	T ATCTTT	
	TATC TAACCTTT GAGC		
	ATAG ATTGGAAA TTCG		
	T CCCTT_		
GAM3777 LOC145453 3'	TATCTTTGTTTTTCATGAGCC 85352	AACC A TT	
	TATCTT TTT TC TGAGCC		
	ATAGAA AAA AG ACTCGG		
	AC_ A T_		
GAM3777 LOC202025 5'	TATCTTCAGTTTAACCCTTTGA 85353	AACCTTTA_	
GC	TATCTT TCTTTGAGC		
	ATAGAA GGAAACTCG		
	GTCAAATTG		
GAM3778 AVPR2 3'	AAGCTCTCCTCATACAGCTG 85356	AATG A	
	AAG TTTCATACA CTG		

		TTC GGAGTATGT GAC		
		GAGA C		
GAM3778 COIL	3'	AAAAATGTGTACAGCTGAAG 85357	TTCA	A
		AAGAATGT TACA CTGAAG		
		TTTTTACA ATGT GACTTC		
		C__ C		
GAM3778 DVL3	3'	AAATGTTTCAGGCCTGGAG 85358	TACAA	A
		GAATGTTTCA CTG AG		
		TTTACAAAGT GAC TC		
		CCG__ C		
GAM3778 GPC4	3'	AGAATTACTCTTACAACCTGAAG 85359	GT	A
A		AGAAT TTC TACAACCTGAAGA		
		TCTTA GAG ATGTTGACTTCT		
		AT A		
GAM3778 ITK	3'	AAGAATGTACACATGTACAGTT 85360	TT_ _	AC A
GAGGA		AAGAATGT CA TACA TGA GA		
		TTCTTACA GT ATGT ACT CT		
		TGT AC CA C		
GAM3778 P23	3'	GAATGTTTCATTCTGA 85361	ACAA	
		GAATGTTTCAT CTGA		
		CTTACAAAGTA GACT		
		A__		
GAM3778 PCSK2	3'	AAGAGGCTCCATACAACCTGGAG 85362	AT	A
A		AAGA GTTTCATACAACCTG AGA		
		TTCT CGAGGTATGTTGAC TCT		
		C_ C		
GAM3778 PPARGC1	3'	GAATTTTCATACAATGA 85363	G	C
		GAAT TTTCATACAA TGA		
		CTTA AAAGTATGTT ACT		
		- -		
GAM3778 REQ	3'	GAATGCTTCAGTCACTGGAGA 85364	TACA	A
		GAATGTTTCA ACTG AGA		
		CTTACGAAGT TGAC TCT		
		CAG_ C		
GAM3778 TRPS1	3'	AAATGTTTCATATGAAA 85365	CAAC	
		GAATGTTTCATA TGAAG		
		TTTACAAAGTAT ACTTT		

GAM3778 TYRP1	3'	AAGATTGTTTCATAGCACAAGA 85366	A	_ ACT
		AAGA TGTTTCATA CA GA		

TTCT ACAAAGTAT GT CT
 A C GTT
 GAM3778 UBB 3' GAATGCCATGACTGAAG 85367 TT ACA
 GAATGT CAT ACTGAAG
 ||||| || |||||
 CTTACG GTA TGA CTTC
 _ C_
 GAM3778 XK 3' AAGGGTGTCTCAGAGGATACAACT 85368 AA TC_ A
 GGAGA AAG TGTT ATACAACTG AGA
 || ||| ||||| |||
 TTC ACAG TATGTTGAC TCT
 CC TCTCC C
 GAM3778 BET3 3' AAGAATGTGTCTTTATTGAAGA 85369 T ATACAAC
 AAGAATGT TC TGAAGA
 ||||| || |||||
 TTCTTACA AG ACTTCT
 C AAATA_
 GAM3778 C20orf150 3' AAAAATGGGACATACTGAAG 85370 TTT CA
 AAGAATG CATA ACTGAAG
 ||||| ||| |||||
 TTTTAC GTAT TGA CTTC
 CCT _
 GAM3778 ESPL1 3' GGAAATGTTTCATATAAAACAC 85371 A CA_
 TG A GAATGTTTCATA ACTG
 | ||||| |||
 C TTTACAAAGTAT TGAC
 C ATTTTG
 GAM3778 FER1L4 3' AGACTGTTTCATAAAAAAAGA 85372 A CAACT
 AGA TGTTTCATA GAAGA
 || ||||| |||
 TCT ACAAAGTAT TTTCT
 G TTT_
 GAM3778 FLJ10853 3' AGAGTGTTGAACTGAAG 85373 A TCATAC
 AGA TGTT AACTGAAG
 || ||| |||||
 TCT ACAA TTGA CTTC
 C CT_
 GAM3778 FLJ11016 3' AGATGTTTCATATGCACTCGAG 85374 A CA_ GA
 A AGA TGTTTCATA ACT AGA
 || ||||| || |||
 TCT ACAAAGTAT TGA TCT
 _ ACG GC
 GAM3778 FLJ12934 3' AAGAGAGTTTACA ACTGAAGA 85375 AT TCA
 AAGA GTT TACA ACTGAAGA
 ||| || ||||| |||
 TTCT CAA ATGTTGA CTTC
 CT _
 GAM3778 GIOT-2 3' AAGACTGCAGATACTGAAG 85376 A TTCATAC
 AAGA TGT AACTGAAG
 ||| || |||||

		TTCT ACG TTGACTTC	
		G TCTA__	
GAM3778	GPX5	3' GAGTGCTTCAAGAACTGAAGA 85377	A TAC
		GA TGTTTCA AACTGAAGA	
		CT ACGAAGT TTGACTTCT	
		C TCT	
GAM3778	KIAA0321	5' AAGGGTGCTGCAGTAACTGAAG 85378	AA T TAC
	A	AAG TGTT CA AACTGAAGA	
		TTC ACGA GT TTGACTTCT	
		CC C CA_	
GAM3778	KIAA1354	3' AAGAAGATACAACTGAAG 85379	TGTTTC
		AAGAA ATACAACTGAAG	
		TTCTT TATGTTGACTTC	
		C__	
GAM3778	MGC26778	3' GAATGTTTCCCTCTGAAG 85380	ATACAA
		GAATGTTTC CTGAAG	
		CTTACAAAG GACTTC	
		GGA__	
GAM3778	LOC122773	3' AATGGAGAGACAACTGAAGA 85381	TTTCAT
		AATG ACAACTGAAGA	
		TTAC TGTTGACTTCT	
		CTCTC_	
GAM3778	LOC148823	3' GAATGTTTCATGCACTG 85382	ACA
		GAATGTTTCAT ACTG	
		CTTACAAAGTA TGAC	
		CG_	
GAM3778	LOC149132	5' AGAATGTTTCAGGGCCTGGAGA 85383	T TACAA A
		AGAATGTT CA CTG AGA	
		TCTTACAA GT GAC TCT	
		_ CCCG_ C	
GAM3778	LOC203292	3' GAATGTTTCATTCTGA 85361	ACAA
		GAATGTTTCAT CTGA	
		CTTACAAAGTA GACT	
		A__	
GAM3778	LOC221876	5' AGAATGTTTCATTGTTACTGA 85384	ACA_
		AGAATGTTTCAT ACTGA	
		TCTTACAAAGTA TGACT	
		ACAA	
GAM3778	LOC90499	3' GAATGTTTCATTCTGA 85361	ACAA
		GAATGTTTCAT CTGA	

CTTACAAAGTA GACT
A____

GAM3779 ANKH 3' CTGACAGCCACAGCCCATGTA 85387 CAA _ C
CTGAC CCAT GTTCA GTA
||||| ||| ||||| |||
GACTG GGTG CGGGT CAT
TC_ T A

GAM3779 ARNT2 3' GAACTGACCTACCCATGT 74242 AA_
GAACTGACC CCATGT
||||||| |||||
CTTGACTGG GGTACA
ATG

GAM3779 MIP 3' CTGGCTAAACCCCTCCACGTA 85388 ACC_ ATG
CTG AACC TTCACGTA
||| ||| |||||
GAC TTGG AGGTGCAT
CGAT GG_

GAM3779 C20orf21 3' GAGCTGACCAAGCACACGT 85389 A CCAT T
GA CTGACCAA GT CACGT
|| ||||| || |||||
CT GACTGGTT CG GTGCA
C _ T

GAM3779 FLJ21817 3' GACTGACCAATCACAACACGT 85390 A C TT
GA CTGACCAA CATG CACGT
|| ||||| ||| |||||
CT GACTGGTT GTGT GTGCA
_ A T_

GAM3779 FLJ22671 5' GAGCTGGCCACCATGCC 74248 A A A
GA CTG CCA CCATGTT
|| ||| ||| |||||
CT GAC GGT GGTACGG
C C _

GAM3779 HIC2 3' GAACTGACGGCCATCCCCGCGT 85391 CAA G A
A GAACTGAC CCAT TTC CGTA
||||||| ||| ||| |||||
CTTGACTG GGTA GGG GCAT
CC_ G C

GAM3779 KIAA0826 3' CTGACTGCATGTTTCATGT 85392 CAAC C
CTGAC CATGTTCA GT
||||| ||||| |||
GACTG GTACAAGT CA
AC_ A

GAM3779 LOC253461 3' GAACTGCCATCATGTTTCACGTA 85393 A AC
GAACTG CCA CATGTTTCACGTA
||||| ||| |||||
CTTGAC GGT GTACAAGTGCAT
_ A_

GAM3779 LOC91263 5' GAACTGACTGCTTGCTTGGCAC 85394 CAACCA _
GT GAACTGAC TGTT CACGT
||||||| ||| |||||

		CTTGACTG	ACGA	GTGCA		
		ACGA__	ACC			
GAM3780	RFX2	3'	TCCGTAACTGTGAGCTTCA	85397	___	AA
			TCC ATTGT AGCTTCA			
			AGG TGACA TCGAAGT			
			CAAT C_			
GAM3780	KIAA1085	3'	TCCATTGCTAAAGCCTCA	85398	_	
			TCCATTGT AAAGCTTCA			
			AGGTAACG TTTCGGAGT			
			A			
GAM3780	KIAA1157	3'	TCCACTGCTTAAGGCTTCA	85399	__	A
			TCCATTGT AA GCTTCA			
			AGGTGACG TT CGAAGT			
			AA C			
GAM3780	LOC146272	5'	CCCATTGTGTCCCAGCTTCA	85400	AA__	
			TCCATTGT AGCTTCA			
			GGGTAACA TCGAAGT			
			CAGGG			
GAM3780	LOC149460	3'	CCATTGCACTATAGCTTCA	85401	A__	
			CCATTGTA AGCTTCA			
			GGTAACGT TCGAAGT			
			GATA			
GAM3781	GCNT2	5'	TCGATTCCGTTTCATCCCGAGA	85404	_____	A
			TCGATTCCGT CC AGA			
			AGCTAAGGCA GG TCT			
			AAGTAG C			
GAM3781	BLP1	3'	TCATTCCGTCTGCAAGGTAA	85405	G __	A
			TC ATTCCGTC CAAG TGA			
			AG TAAGGCAG GTTC ATT			
			_ AC C			
GAM3781	BLP1	3'	TCATTCCGTCTGCAAGGTAA	85405	G __	A
			TC ATTCCGTC CAAG TGA			
			AG TAAGGCAG GTTC ATT			
			_ AC C			
GAM3781	LOC143914	5'	TCGATTCCGTTTGAGTGA	85406	CCA	A
			TCGATTCCGT AG TGA			
			AGCTAAGGCA TC ACT			
			AAC _			
GAM3781	LOC253891	5'	CCGATTCCGTCCCAGTG	85407	A	A
			TCGATTCCGTCC AG TG			

GGCTAAGGCAGG TC AC
G _
GAM3782 STAM 3' CTATAATTGCACCAAAAATTTA 85410 CGGAT
G CTAT TACCAAAAATTTAG
||||| |||||||||
GATA GTGGTTTTTTAAATC
TTAAC
GAM3783 AOC2 3' GCCTAACCACGCCGCCCG 85413 CT
GCCTA CGCGCCGCCCG
||||| |||||||||
CGGAT GTGCGGCGGGC
TG
GAM3783 ARRB2 5' CGCGCGCCCGCCGCC 85414 _ TACTCG
CG GCGCC CGCCGCC
|| ||||| |||||||
GC CGCGG GCGGCGGG
G _
GAM3783 BRF1 5' CGGAGCAGCCCGCGCCGCCG 85416 C CTA
CGG GC CTCGCGCCGCCG
||| || |||||||||
GCC CG GGGCGCGGCGGGC
T TC_
GAM3783 BRF1 5' GCGCCCGGGCGCGCCGCCG 85415 AC_
GCGCCT TCGCGCCGCCG
||||| |||||||||
CGCGGG GGGCGGCGGGC
CCC
GAM3783 C7orf2 5' CGCCGCCCGCGCCGCC 85417 TAC
CGCC TCGCGCCGCC
||||| |||||||||
GCGG GGGCGGCGGG
C_
GAM3783 CACNA1A 3' CGCCGCCCGCTGCC 85418 G TA GCC
CG CGCC CTCGC GCC
|| ||||| |||||
GC GCGG GGGCG CGGG
G _ A_
GAM3783 CALM1 5' CGCCGCCTGCGCCGCC 85419 G ACTC
CG CGCCT GCGCCGCC
|| ||||| |||||||
GC GCGGA CGCGGCGG
G _
GAM3783 CDC34 5' GCGCCGCCCGCGCCGCCG 85420 TAC _
GCGCC TCGC GCCGCCG
||||| ||||| |||||||
CGCGG GGGCG GGGCGGGC
C_ G
GAM3783 CDKN2A 5' GCTGCTCCCCGCCGCCG 85421 GC A G
GC CT CTC CGCCGCCG
|| || ||||| |||||||

		CG GA GGG GCGGCGGGC	
		AC _ _	
GAM3783 CHN1	5'	GGCGCTCGCCGCCCGCCCG 85422	CTAC _
		GGCGC TCGC GCCGCCCG	
		CCGCG AGCG CGGCGGGC	
		_____ G	
GAM3783 CORO2A	5'	GCGCTCCTCGCCGCCCG 85423	CTA GC
		GCGC CTC GCCGCCCG	
		CGCG GAG CGGCGGGC	
		AG_ _	
GAM3783 DSCAM	5'	CGCCGCCCGCCCGCCGCCCG 85424	G T A T G
		CG CGCC C C CGCCGCCCG	
		GC GCGG G G GCGGCGGGC	
		G GC _ _	
GAM3783 DTNB	5'	CAGCGCCTACTCAGGCCCC 85425	C G
		CGGCGCCTACTCG GCC CC	
		GTCGCGGATGAGT CGG GG	
		C _	
GAM3783 DTNB	5'	CAGCGCCTACTCAGGCCCC 85425	C G
		CGGCGCCTACTCG GCC CC	
		GTCGCGGATGAGT CGG GG	
		C _	
GAM3783 DTNB	5'	CAGCGCCTACTCAGGCCCC 85425	C G
		CGGCGCCTACTCG GCC CC	
		GTCGCGGATGAGT CGG GG	
		C _	
GAM3783 DVL3	5'	CGGGTCCCAGCGCCGCCCG 85426	CG CTC
		CGG CCTA GCGCCGCCCG	
		GCC GGGT CGCGGCGGGC	
		CA _ _	
GAM3783 EN2	5'	CGGCGCTCACGCCCGCCCG 85427	CTAC _
		CGGCGC TCGCGCC GCCCG	
		GCCGCG AGTGCGG CGGGC	
		_____ G	
GAM3783 EN2	5'	CGGCCGCCGCCGCCGCCCG 85428	_ TACTCG
		CGGC GCC CGCCGCCCG	
		GCCG CGG GCGGCGGGC	
		G CG_ _ _	
GAM3783 EP300	5'	CGGGCCGAGCAGCGCCGCCCG 85429	C TACTC
		CGG GCC GCGCCGCCCG	

GCC CGG CGCGGCGGGC
 _ CTCGT
 GAM3783 F2R 5' CGGTCCCTCAGCCGCC 85430 CG TA C
 CGG CC CTCG GCCGCC
 ||| || ||| |||||
 GCC GG GAGT CGGCGG
 A_ _ _
 GAM3783 HAGH 5' AGCGCCACGCCGCC 85431 TACTC
 GGCGCC GCGCCGCC
 ||||| |||||
 TCGCGG TGCGGCGGG

 GAM3783 HCN4 5' GGCGCGGCGCGCCGCCCG 85432 CTACT
 GGCGC CGCGCCGCCCG
 |||| | |||||
 CCGCG GCGCGGCGGGC
 CC____
 GAM3783 HNF3G 5' CGGCGCCCGCCCGTCC 85433 TACT G C
 CGGCGCC CGC CCG CC
 ||||| ||| ||| ||
 GCCGCGG GCG GGC GG
 _____ _ A
 GAM3783 JAG2 5' CGGCCCGCCGCGCCGCCCG 85434 G TA T _
 CGGC CC C CGC GCCGCCCG
 ||| || | ||| |||||
 GCCG GG G GCG CGGCGGGC
 _ GC _ G
 GAM3783 KCNA7 5' CGCCGCCGCGCCGCCGCC 85435 TAC _
 CGCC TCGC GCCGCC
 ||| ||| |||||
 GCGG GGCG CGGCGGG
 C_ G
 GAM3783 KCNK1 5' GGCTCCCGCCCGCCGCCCG 85436 G TA T G
 GGC CC C C CGCCGCCCG
 ||| || | |||||
 CCG GG G G GCGGCGGGC
 A GC _ _
 GAM3783 LASS2 5' CGGCGCCGCGCGCCGCCCG 85437 TAC _
 CGGCGCC TCGC GCCGCCCG
 ||||| ||| |||||
 GCCGCGG GGCG CGGCGGGC
 C_ G
 GAM3783 LIG1 5' GGTCCCGCGCGCCGCTGCCCG 85438 CG ACT ____
 GG CCT CGCGCC GCCCG
 || ||| ||||| |||||
 CC GGG GCGCGG CGGGC
 A_ C_ CGA
 GAM3783 LMO2 5' CGCCGGCTCCGCGCCGCCCG 85439 TA _
 CGCC CTC GCGCCGCCCG
 ||| ||| |||||

GCGG GAG CGCGGCGGGC
 CC G
 GAM3783 LRP8 5' CGCCGCCGCGCTGCCGCCCG 85440 G TAC _
 CG CGCC TCGC GCCGCCCG
 || ||| ||| |||||
 GC GCGG GGCG CGGCGGGC
 G C_ A
 GAM3783 LRP8 5' CGCCGCCGCGCTGCCGCCCG 85440 G TAC _
 CG CGCC TCGC GCCGCCCG
 || ||| ||| |||||
 GC GCGG GGCG CGGCGGGC
 G C_ A
 GAM3783 LRP8 5' CGCCGCCGCGCTGCCGCCCG 85440 G TAC _
 CG CGCC TCGC GCCGCCCG
 || ||| ||| |||||
 GC GCGG GGCG CGGCGGGC
 G C_ A
 GAM3783 MAP3K5 5' CGGCGCCTCCGTGGCCGCGCCG 85441 AC____ C
 CTCG CGGCGCCT TCGCGCCGC CG
 ||||| ||||| ||
 GCCGCGGA GGCGCGGCG GC
 GGCACC A
 GAM3783 MAPK12 5' CGGGCCGGCTCCGCGCCGCTCG 85442 C TA _ C
 CGG GCC CTC GCGCCGC CG
 ||| ||| ||| ||||| ||
 GCC CGG GAG CGCGGCG GC
 _ CC G A
 GAM3783 MYO1D 5' CGGCGCCTTCTCGGCCG 85443 A C
 CGGCGCCT CTCG GCCG
 ||||| ||| |||
 GCCGCGGA GAGC CGGC
 A _
 GAM3783 NAB2 5' CGGCGCCTGCTGCGTGC 85444 A C CC
 CGGCGCCT CT GCG GC
 ||||| || ||| ||
 GCCGCGGA GA CGC CG
 C _ A_
 GAM3783 NFKBIL2 5' GCCTCTTCGCGCCGCTGCCCG 85445 AC ____
 GCCT TCGCGCC GCCCG
 ||| ||||| |||
 CGGA AGCGCGG CGGGC
 GA CGA
 GAM3783 ODC1 5' CAGCGCCTGGCTCCCGCCCG 85446 A_ GCG
 CGGCGCCT CTC CCGCCCG
 ||||| ||| |||||
 GTCGCGGA GAG GGCGGGC
 CC ____
 GAM3783 OLFM1 5' CGGCGCCTGGCTCGTGTCCCA 85447 A_ CG____ _
 CGCC CGGCGCCT CTCG CCGC CC
 ||||| ||| ||| ||

GCCGCGGA GAGC GGTG GG
 CC ACAGG C
 GAM3783 OLFM1 5' CGGCGCCTGGCTCGTGTCCCA 85447 A_ CG__ _
 CGCC CGGCGCCT CTCG CCGC CC
 ||||| ||| ||| ||
 GCCGCGGA GAGC GGTG GG
 CC ACAGG C
 GAM3783 OLFM1 5' CGGCGCCTGGCTCGTGTCCCA 85447 A_ CG__ _
 CGCC CGGCGCCT CTCG CCGC CC
 ||||| ||| ||| ||
 GCCGCGGA GAGC GGTG GG
 CC ACAGG C
 GAM3783 PCOLCE2 5' CGGCGCTCGGCTGCCC 85448 CTAC C C
 CGGCGC TCG GC GCCC
 ||||| ||| ||| |||
 GCCGCG AGC CG CGGG
 _ _ A
 GAM3783 PITPN 5' CGCCGCTGCCGACGCCGCCG 85449 G CTA C
 CG CGC CT GCGCCGCCCG
 || ||| |||||
 GC GCG GG TGCGGCGGGC
 G AC_ C
 GAM3783 RELN 5' CGCGCGCCCTACGCGCCGCTCG 85450 _ ACT C
 CG GCGCCT CGCGCCGC CG
 || ||||| ||||| ||
 GC CGCGGG GCGCGGCG GC
 G AT_ A
 GAM3783 SDC2 5' GCGCCTGCTCCCGCCGCCG 85451 A G
 GCGCCT CTC CGCCGCCCG
 ||||| ||| |||||
 CGCGGA GAG GCGGCGGGC
 C G
 GAM3783 SGT 5' GCGCACCGCGGTGCCGCCG 85452 CT T _
 GCGC AC CGC GCCGCCCG
 ||| || ||| |||||
 CGCG TG GCG CGGCGGGC
 _ _ CCA
 GAM3783 SMARCC2 5' CGGGCCCCGCCGCCGCCG 85453 C ACT _
 CGG GCCT CGC GCCGCCCG
 ||| ||| ||| |||||
 GCC CGGG GCG CGGCGGGC
 _ _ G
 GAM3783 SMARCC2 5' CGGGCCCCGCCGCCGCCG 85453 C ACT _
 CGG GCCT CGC GCCGCCCG
 ||| ||| ||| |||||
 GCC CGGG GCG CGGCGGGC
 _ _ G
 GAM3783 TJP1 5' CGGCGTCTCCTCGGAAGCCG 85454 C A C_
 CGGCG CT CTCG GCCG
 ||||| || ||| |||

GCCGC GA GAGC CGGC
 A G CTT
 GAM3783 TMEM1 5' GCGCCGCAGCTGCCGCCCG 85455 TACTC _
 GCGCC GC GCCGCCCG
 |||| || |||||
 CGCGG CG CGGCGGGC
 CGT__ A
 GAM3783 TRIM8 3' CAGCGCCCCGCGCC 85456 ACTCG
 CGGCGCCT CGCCGCC
 ||||| |||||
 GTCGCGGG GCGGCGG

 GAM3783 WEE1 5' CGGCCCGGCGCCGCC 85457 G TACTC
 CGGC CC GCGCCGCC
 ||| || |||||
 GCCG GG CGCGGCGGG
 _ C__
 GAM3783 5T4 5' CGGCGCCCGCTCCGAAGGCTCG 85458 TA G CC_ C
 CGGCGCC CTC CG GC CG
 ||||| ||| || ||
 GCCGCGG GAG GC CG GC
 GC _ TTC A
 GAM3783 A2BP1 5' CGGCCCTGGGCTCCGTCCG 85459 G ACTC G C
 CGGC CCT GC CCG CCG
 ||| ||| || ||| |||
 GCCG GGA CG GGC GGC
 G CC_ A A
 GAM3783 ABHD3 5' GCTGCCTACTCCCCCTCG 85460 _ GCG G _
 GC GCCTACTC CC CC CG
 || ||||| || ||
 CG CGGATGAG GG GG GC
 A _ _ A
 GAM3783 ALTE 5' CGGCGCCTACCGCGTAGACCCG 85461 T CC_
 CGGCGCCTAC CGCG GCCCG
 ||||| ||| ||||
 GCCGCGGATG GCGC TGGGC
 _ ATC
 GAM3783 ALTE 5' CGCCGCTTCCGCGCCGCCCG 85462 G CTAC
 CG CGC TCGCGCCGCCCG
 || ||| |||||
 GC GCG GGCGCGGCGGGC
 G AA_
 GAM3783 ARHGEF9 5' CGGCGCCTGCTCAGTCTGTCCG 85463 A CGCCGC
 CGGCGCCT CTCG CCG
 ||||| ||| ||
 GCCGCGGA GAGT GGC
 C CAGACA
 GAM3783 BPES 3' GCCTCCCTCGCGCCGCCCG 85464 A_
 GCCT CTCGCGCCGCCCG
 ||| |||||

CGGA GAGCGCGGCGGGC
GG
GAM3783 C2orf178 5' CGGCGCCCGCTCCCAGTCCCG 85465 TA G CCG
CGGCGCC CTC CG CCG
||||| ||| || |||
GCCGCGG GAG GT GGGC
GC G CA_
GAM3783 C2orf6 5' CGGCGCCCGCCTTGCCC 85466 TACTCG _
CGGCGCC CGCC GCCC
||||| ||| |||
GCCGCGG GCGG CGGG
____ AA
GAM3783 C2orf7 5' CGCGGCCCGCGCGCGTCGCT 85467 G AC _ C
CG CGCCT TCGCGC CGC CG
|| ||| ||||| ||| ||
GC GCGGG GGCGCG GCG GC
G GC CA A
GAM3783 CASP9 5' CGGGCCTCGGCCGCCC 85468 C TAC C
CGG GCC TCG GCCGCCC
||| ||| ||| |||||
GCC CGG AGC CGGCGGG
- - -
GAM3783 CDC42BPB 5' CGGCGCCTCCTCGCCGCCC 85469 A CG
CGGCGCCT CT CGCCGCCC
||||||| || |||||
GCCGCGGA GG GCGGCGGG
_ A_
GAM3783 CENTG2 5' GCTGCGTACTGCGCCGCCCG 85470 _ C C
GC GC TACT GCGCCGCCCG
|| ||| |||||
CG CG ATGA CGCGGCGGGC
A C _
GAM3783 CLLD8 5' GCGTTTTCTACGCCGCCCG 85471 CCTA C
GCG CT GCGCCGCCCG
||| || |||||
CGC GA TGCGGCGGGC
AAAA _
GAM3783 CSR1 5' CGCCGTCTAGGCGCCGCCCG 85472 G _ CTC
CG CG CCTA GCGCCGCCCG
|| ||| |||||
GC GC GGAT CGCGGCGGGC
G A C_
GAM3783 CTSO 5' CGGCTCCTCTGCCGCC 85473 G A CGC
CGGC CCT CT GCCGCC
||| ||| || |||||
GCCG GGA GA CGGCGGG
A _ _
GAM3783 DKFZP434H0820 5' CGACGCCGCCGCTGTTGCCCG 85475 TAC GCC_
CGGCGCC TCGC GCCCG
||||| ||| |||||

GCTGCGG GGCG CGGGC
 C__ ACAA
 GAM3783 DKFZP434H0820 5' CGCCGCTCCCGCCGCC 85474 TA G
 CGCC CTC CGCCGCC
 |||| ||| |||||
 GCGG GAG GCGGCGGG
 C_ G
 GAM3783 DKFZP434N014 5' GCGCCTCTGCGCCGCCG 85476 A C
 GCGCCT CT GCGCCGCCG
 ||||| || |||||
 CGCGGA GA CGCGGCGGGC
 - -
 GAM3783 DKFZP566K1924 5' GCGCCGTGCGCCGCGTCCG 85477 TAC _ C
 GCGCC TCGC GCCG CCG
 |||| ||| ||| |||
 CGCGG AGCG CGGC GGC
 C__ G A
 GAM3783 Dlc2 5' GCTCCGCCTCGCGCCGCCG 85478 G TA
 GC CC CTCGCGCCGCCG
 || || |||||
 CG GG GAGCGCGGCGGGC
 A CG
 GAM3783 DRAP1 5' CGGGCCTGCTCGCCGCCG 85479 C A GC
 CGG GCCT CTC GCCGCCG
 ||| ||| ||| |||||
 GCC CGGA GAG CGGCGGGC
 _ C _
 GAM3783 EHM2 5' GCCGCTGCGCCGCCGCCG 85480 TA _ _
 GCC CT CGC GCCGCCG
 ||| || ||| |||||
 CGG GA GCG CGGCGGGC
 C_ C G
 GAM3783 EIF3S9 5' GCTGCCTACTCGCAGGGCTCCG 85481 _ CC _
 GC GCCTACTCGCG GC CCG
 || ||||| || |||
 CG CGGATGAGCGT CG GGC
 A CC A
 GAM3783 EMILIN-2 5' CGGCGGCCAGGGCGCCGCCG 85482 _ TACTC
 CGGCG CC GCGCCGCCG
 |||| || |||||
 GCCGC GG CGCGGCGGGC
 C TCC__
 GAM3783 FADS3 5' CGCCGCCTCCGCCGCCGCCG 85483 G A T _
 CG CGCCT C CGC GCCGCCG
 || |||| | ||| |||||
 GC GCGGA G GCG CGGCGGGC
 G _ _ G
 GAM3783 FHOD2 5' CGGCGGTGCGGCTGCCGCCG 85484 CCTAC _ _
 CGGCG TCG C GCCGCCG
 |||| ||| | |||||

GCCGC AGC G CGGCGGGC
 C___ C A
 GAM3783 FLJ10350 5' GCGCCGTCCGCGCCGTTTCG 85485 TAC CC
 GCGCC TCGCGCCG CG
 |||| ||||| ||
 CGCGG GGCGCGGC GC
 CA_ AA
 GAM3783 FLJ13639 3' GGCGTCCACTCACACGCC 85486 C C
 GGCG CTACTCGCGC GCC
 ||| ||||| |||
 CCGC GGTGAGTGTG CGG
 A _
 GAM3783 FLJ20539 5' CGCCGCCGCCGCCGCCGCCG 85487 G TAC _
 CG CGCC TCGC GCCGCCCG
 || ||| ||| |||||
 GC GCGG GGCG CGGCGGGC
 G C_ G
 GAM3783 FOXO3A 5' GGCGCCGCCGCCGCCGCC 85488 TAC _
 GGCGCC TCGC GCCGCC
 |||| ||| |||||
 CCGCGG GGCG CGGCGG
 C_ G
 GAM3783 GPR 5' CGGCTCCGCGCGCCGCCCG 85489 G TACT
 CGGC CC CGCGCCGCCCG
 ||| || |||||
 GCCG GG GCGCGGCGGGC
 A C_
 GAM3783 GRIN3A 5' CGGCGCCTGTACCCG 85490 AC G
 CGGCGCCT TCGC CCG
 ||||| ||| |||
 GCCGCGGA AGTG GGC
 C_ _
 GAM3783 H2AFY2 5' CGCCGCCTGCTCCCGGCGCCCG 85491 G A G C
 CG CGCCT CTC CG CGCCCG
 || |||| ||| || |||||
 GC GCGGA GAG GC GCGGGC
 G C G C
 GAM3783 HCNGP 3' CAGCGCCTGGCTCCCGTGCTGC 85492 A___ C C
 C CGGCGCCT CTCG GC GCC
 ||||| ||| || |||
 GTCGCGGA GGGC CG CGG
 CCGA A A
 GAM3783 HERPUD1 5' CGGCGTCTCAGCCGCCCG 85493 CCTA C
 CGGCG CTCG GCCGCCCG
 |||| ||| |||||
 GCCGC GAGT CGGCGGGC
 A___ _
 GAM3783 HIC 5' CGCCTAGCTCGCCGCCCG 85494 _ GC
 CGCCTA CTC GCCGCCCG
 ||||| ||| |||||

GCGGAT GAG CGGCGGGC
 C _
 GAM3783 HSF1 5' CGGGCCGCGCCGCGCCCG 85495 C TACT _
 CGG GCC CGC GCCGCCCCG
 ||| ||| ||| |||||
 GCC CGG GCG CGGCGGGC
 _ C_ G
 GAM3783 ICSBP1 5' CGCCGTCTCGCCGCCCCG 85496 TAC G
 CGCC TC CGCCGCCCCG
 |||| || |||||
 GCGG AG GCGGCGGGC
 C_ A
 GAM3783 IL-17RE 3' CGCCGCCAGCGCTGCCCG 85497 G CTC C
 CG CGCCTA GCGC GCCCG
 || ||||| |||||
 GC GCGGGT CGCG CGGGC
 G _ A
 GAM3783 IMAGE:4907098 5' CGGCGCACTGGCCGCC 85498 CT CGC
 CGGCGC ACT GCCGCC
 ||||| ||| |||||
 GCCGCG TGA CGGCGGG
 _ C_
 GAM3783 KIAA0010 5' CGGCGCCCCGCCGCC 85499 TACT G
 CGGCGCC CGC CCGCCC
 ||||| ||| |||||
 GCCGCGG GCG GGCGGG
 _ _
 GAM3783 KIAA0014 3' CGCCGCCTCCGGCCGCCCG 85500 G A T C
 CG CGCCT C CG GCCGCCCCG
 || ||||| || |||||
 GC GCGGA G GC CGGCGGGC
 G _ _ _
 GAM3783 KIAA0247 5' CGCCGCTTGCGCGCGCCCG 85501 TA C _
 CGCC CT GCGC CGCCCG
 |||| || |||||
 GCGG GA CGCG GCGGGC
 C_ A C
 GAM3783 KIAA0543 3' GGCGCCCACTTCCTGCC 85502 CGCG _
 GGCGCCTACT CC GCC
 ||||| ||||| |||
 CCGCGGGTGA GG CGG
 A_ A
 GAM3783 KIAA0672 5' CGCCGCCTACTCCTCCC 85503 G CGCG G
 CG CGCCTACT CC CCC
 || ||||| || |||
 GC GCGGATGA GG GGG
 G _ A
 GAM3783 KIAA0930 5' CGGCCTCGGCGCCGCC 85504 GCCTA _
 CGGC CTCG CGCCGCC
 |||| ||||| |||||

GCGG GAGC GCGGCGGG
 _____ C
 GAM3783 KIAA1028 5' CGCGCGCCGCCCGCCCG 85505 _ TAC G
 CG GCGCC TC CGCCGCCCG
 || |||| || |||||
 GC CGCGG GG GCGGCGGGC
 G C__ _
 GAM3783 KIAA1028 5' GCGCGCGCGCGCGCCCG 85506 CTACT
 GCGC CGCGCCGCCCG
 ||| |||||
 CGCG GCGCGGCGGGC
 CGCGC
 GAM3783 KIAA1280 5' GGCCCTCACAGCTGTCCG 85507 G TA _ CGC
 GGC CC CTCGC GC CCG
 ||| || |||| || |||
 CCG GG GAGTG CG GGC
 _ _ T ACA
 GAM3783 KIAA1458 5' CGCCGCTCCGCCGCC 85508 TA G
 CGCC CTC CGCCGCC
 ||| || |||||
 GCGG GAG GCGGCGGG
 CG _
 GAM3783 KIAA1893 5' CGCCGCCGCCGCCGCCCG 85487 G TAC _
 CG CGCC TCGC GCCGCCCG
 || |||| || |||||
 GC GCGG GGCG CGGCGGGC
 G C__ G
 GAM3783 MAN1C1 5' GGCGTCCGGAGCGCCGCCCG 85509 _ TACTC
 GGCG CC GCGCCGCCCG
 ||| || |||||
 CCGC GG CGCGGCGGGC
 A CCT__
 GAM3783 MAP-1 5' CGTGCCGCCACCCGCGCCGCC 85510 _ _ T
 G CG GC GCC ACTCGCGCCGCCCG
 || || || |||||
 GC CG CGG TGGGCGCGGCGGGC
 A G _
 GAM3783 MCF2L 3' CGGCGCCTGCCGCC 85511 ACTCGC
 CGGCGCCT GCCGCC
 ||||| |||||
 GCCGCGGA CGGCGGG

 GAM3783 MGC14425 3' GCGCGCCGCCGCTGCCCG 85512 CTAC _ C
 GCGC TCGC GC GCCCG
 ||| |||| || |||||
 CGCG GGCG CG CGGGC
 C__ G A
 GAM3783 MGC2647 5' GCGCCGCCCGCCGCCCG 85513 TAC G
 GCGCC TC CGCCGCCCG
 |||| || |||||

CGCGG GG GCGGCGGGC
 C__ _
 GAM3783 MGC2865 5' CGGCGCCTTGCCTCACGTCCG 85514 AC__ _
 CGGCGCCT TCGCG CCG
 ||||| |||||
 GCCGCGGA AGTGC GGC
 ACGC A
 GAM3783 MGC4172 5' GGGCCCACGCCGCC 85515 C TACT
 GG GCC CGCGCCGCC
 || ||| |||||
 CC CGG GTGCGGCGGG
 - -
 GAM3783 MICAL 5' GGCGCGGGGCGCCGCCCG 85516 CTACTC
 GGCGC GCGCCGCCCG
 ||||| |||||
 CCGCG CGCGGCGGGC
 CCC__
 GAM3783 MIP-T3 5' CGGCGTCCGCCGCC 85517 CCTAC G
 CGGCG TC CGCCGCC
 ||||| || |||||
 GCCGC AG GCGGCGGG
 - -
 GAM3783 MOT8 5' CGGCGCCCGCGCCCGCTCG 85519 TACT _ C
 CGGCGCC CGCGCC GC CG
 ||||| ||||| |||||
 GCCGCGG GCGCGG CG GC
 G A
 GAM3783 MOT8 5' CGCCGCCTCCCGCCGCCCG 85518 TA G
 CGCC CTC CGCCGCCCG
 ||||| ||| |||||
 GCGG GAG GCGGCGGGC
 CG G
 GAM3783 MSRA 5' CGGGCCTGGAGGCCGCCCG 85520 C ACTCGC
 CGG GCCT GCCGCCCG
 ||| ||||| |||||
 GCC CGGA CGGCGGGC
 - CTC__
 GAM3783 PCCX2 5' CGGCGCCGCCCGCCGCCCG 85437 TAC _
 CGGCGCC TCGC GCCGCCCG
 ||||| ||||| |||||
 GCCGCGG GGCG CGGCGGGC
 C__ G
 GAM3783 PD6D6IP 5' CAGCGCCTCCGCCGCC 85521 TAC G
 CGGCGCC TC CGCCGCC
 ||||| || |||||
 GTCGCGG AG GCGGCGG
 - -
 GAM3783 PTR4 5' CGGCGCCCGCTCGCCCG 85522 TA G
 CGGCGCC CTCGC CCG
 ||||| ||||| |||||

			GCCGCGG GAGCG GGC		
			GC _		
GAM3783	QSCN6	5'	CGGCGCCGCGGCACCGCC 85523	TACTC	
			CGGCGCC GCGCGCC		
			GCCGCGG CGTGGCGG		
			CGC_		
GAM3783	RAB21	5'	CGTCGCTTCCCGGCCGCCG 85524	G CTA C	
			CG CGC CTCG GCCGCCCG		
			GC GCG GGGC CGGCGGGC		
			A AA_ _		
GAM3783	RHOBTB1	5'	GCGCGCGGCGCGCCGCCG 85525	CTACT	
			GCGC CGCGCCGCCCG		
			CGCG GCGCGGCGGGC		
			CGCC_		
GAM3783	RINZF	5'	CGCCGCCGCCGCCGCCGCCG 85487	G TAC _	
			CG CGCC TCGC GCCGCCCG		
			GC GCGG GGCG CGGCGGGC		
			G C_ G		
GAM3783	RPC32	5'	CGGCGCTTGACTGCCGCCCG 85526	CT_ CGC	
			CGGCGC ACT GCCGCCCG		
			GCCGCG TGA CGGCGGGC		
			AAC _		
GAM3783	RTCD1	5'	CGGCGCCTCTCGGGACAC 85527	A CGC	
			CGGCGCCT CTCG CGC		
			GCCGCGGA GAGC GTG		
			_ CCT		
GAM3783	SLC21A11	5'	CGCCGCTCCGGCCGCCGCCG 85528	G CTA C _	
			CG CGC CT GC GCCGCCCG		
			GC GCG GG CG CGGCGGGC		
			G A_ C G		
GAM3783	SOX17	5'	CGGCCCGAAGCCGCCGCCG 85529	G TACTCG	
			CGGC CC CGCCGCCCG		
			GCCG GG GCGGCGGGC		
			_ CTTCG_		
GAM3783	TMEM8	5'	CGGCCCGCGCCGCCGCCG 85530	G TA TCG	
			CGGC CC C CGCCGCCCG		
			GCCG GG G GCGGCGGGC		
			G GC _		
GAM3783	TOMM40	5'	CGGCGCCTGCTCCCGGCC 85531	A G CC	
			CGGCGCCT CTC CG GCC		

GCCGCGGA GAG GC CGG
 C G _
 GAM3783 ZDHC2 5' CGCCGTTCCCCGCGCCCG 85532 TA_ G
 CGCC CTC CGCCGCCCG
 ||| ||| |||||
 GCGG GGG GCGGCGGGC
 CAA _
 GAM3783 LOC124402 5' GGCGCCGCGCGCTGCCCG 85533 TAC C
 GGCGCC TCGCGC GCCCG
 |||| |||| ||||
 CCGCGG GGCGCG CGGGC
 C_ A
 GAM3783 LOC125704 5' CGCGCGCCCGCCGCC 85414 _ TACTCG
 CG GCGCC CGCCGCC
 || ||| |||||
 GC CGCGG GCGGCGGG
 G _
 GAM3783 LOC126526 5' GCGCCCACTCGCGCCGCCCG 85534
 GCGCCTACTCGCGCCGCCCG
 ||||| |||||
 CGCGGGTGAGCGGCGGGC
 GAM3783 LOC129642 5' CGGCGCTCCGCGCGCC 85535 CTAC C
 CGGCGC TCG GCCGCC
 |||| ||| |||||
 GCCGCG GGC CGGCGGG
 A_ _
 GAM3783 LOC129642 5' CGGCCGCCCGCGCCGCTCG 85536 _ TACT C
 CGGC GCC CGCGCCGC CG
 ||| ||| ||||| ||
 GCCG CGG GCGCGGCG GC
 G _ A
 GAM3783 LOC146223 5' CGCCGCCGCCGCCGCCGCCCG 85487 G TAC _
 CG CGCC TCGC GCCGCCCG
 || ||| ||| |||||
 GC GCGG GGCG CGGCGGGC
 G C_ G
 GAM3783 LOC146562 3' CGGCGCCCTACTGTGCTGCC 85537 _ CGC C
 CGGCGCC TACT GC GCC
 ||||| ||| |||
 GCCGCGG ATGA CG CGG
 G CA_ A
 GAM3783 LOC147463 5' GCGCGTCCCGCCGCCCG 85538 CTA G
 GCGC CTC CGCCGCCCG
 ||| ||| |||||
 CGCG GAG GCGGCGGGC
 C_ G
 GAM3783 LOC148534 5' GGCGCTGGCCAGTGCCGCCCG 85539 CTA CGC
 GGCGC CT GCCGCCCG
 |||| || |||||

CCGCG GG CGGCGGGC
 ACC TCA
 GAM3783 LOC149297 5' CGGCATGGCGACGCGCCGCTCG 85540 CCTACT C
 CGGCG CGCGCCGC CG
 |||| ||||| ||
 GCCGT GCGCGGCG GC
 ACCGCT A
 GAM3783 LOC149576 3' GCGTTAGCCCGCCGCCG 85541 CC CT G
 GCG TA C CGCCGCCG
 ||| || |||||
 CGC AT G GCGGCGGGC
 A_ CG_
 GAM3783 LOC150275 5' CGGCGGCCTCGGCCGCCG 85542 CCTA C
 CGGCG CTCG GCCGCCG
 |||| ||| |||||
 GCCGC GAGC CGGCGGGC
 CG__ _
 GAM3783 LOC151009 5' GGTGCCTACCCCTCACTGTCCG 85543 C G_ CGC
 GG GCCTACTC CGC CCG
 || ||||| ||| |||
 CC CGGATGGG GTG GGC
 A GA ACA
 GAM3783 LOC151534 5' CGGGCTCCGCGCCGCTCG 85544 C CTAC C
 CGG GC TCGCGCCGC CG
 ||| || ||||| ||
 GCC CG GCGCGGCG GC
 _ A__ A
 GAM3783 LOC153571 3' CAGCGCCCCCTCGCCGCCG 85545 TA G
 CGGCGCC CTC CGCCGCCG
 ||||| ||| |||||
 GTCGCGG GGG GCGGCGGGC
 _ A
 GAM3783 LOC155382 5' CGGCCCCGCGCCGCCGCCG 32642 G TA
 CGGC CC CTCGCGCCGCCG
 |||| || |||||
 GCCG GG GGGCGCGGCGGGC
 _ GC
 GAM3783 LOC160932 5' GCGCGCTCGGGCCGCTGCCG 85546 CTA C ____
 GCGC CTCG GCC GCCG
 |||| ||| ||| ||||
 CGCG GAGC CGG CGGGC
 C__ C CGA
 GAM3783 LOC160932 5' CGGCGCCCGCGCGCTCG 85547 ACT _
 CGGCGCCT CGCGC CG
 ||||| |||| ||
 GCCGCGGG GCGCG GC
 C__ A
 GAM3783 LOC162022 5' CAGCGCCTGTGCCCGCTCG 85548 ACTC G C
 CGGCGCCT GC CCGC CG
 ||||| || ||| ||

GTCGCGGA CG GGCG GC
 CA__ _ A
 GAM3783 LOC162417 5' GGTGCCCTCGCCGCCCG 85549 C ACTCG
 GG GCCT CGCCGCCCG
 || ||| |||||
 CC CGGG GCGGCGGGC
 A GA__
 GAM3783 LOC165257 5' CGGCGCCTCGGGGCGCCGCC 85550 ACTC
 CGGCGCCT GCGCCGCC
 ||||| |||||
 GCCGCGGA CGCGGCGG
 GCCC
 GAM3783 LOC167026 5' CGCCGCTCCGCCGCC 85551 TA G
 CGCC CTC CGCCGCC
 ||| ||| |||||
 GCGG GAG GCGGCGGG
 C_ _
 GAM3783 LOC201161 5' GCGCGCCCCCGCCGCCCG 85552 CTA G
 GCGC CTC CGCCGCCCG
 ||| ||| |||||
 CGCG GGG GCGGCGGGC
 C_ _ G
 GAM3783 LOC201514 5' CGGCGCCTGTCCGCGAGC 85553 AC CC
 CGGCGCCT TCGCG GC
 ||||| ||| ||
 GCCGCGGA GGCGC CG
 CA T_
 GAM3783 LOC201780 5' CGGTCGCCGCACTCGCCGCCCG 85554 _ TACTCG
 CGG CGCC CGCCGCCCG
 ||| ||| |||||
 GCC GCGG GCGGCGGGC
 A CGTCA_
 GAM3783 LOC219654 5' GCGCCCCGCGCGCTGCCCG 85555 ACT C
 GCGCCT CGCGC GCCCG
 ||||| ||||| |||||
 CGCGGG GCGCG CGGGC
 GC_ A
 GAM3783 LOC221501 3' GGCGCGCCCGCCGCC 85556 _ ACTCG
 GGCGC CT CGCCGCC
 ||||| || |||||
 CCGCG GG GCGGCGGG
 C ____
 GAM3783 LOC221882 5' GCGCCCGCCCGCCGCCCG 85557 TA T G
 GCGCC C C CGCCGCCCG
 ||||| || |||||
 CGCGG G G GCGGCGGGC
 GC__
 GAM3783 LOC254102 5' GCCTGTCCGCGCCGCCCG 85558 AC
 GCCT TCGCGCCGCCCG
 ||| |||||

CGGA GGCGCGGCGGGC
CA
GAM3783 LOC254124 3' CGGCTGTCCGCGCCGCCCG 85559 GCCTAC
CGGC TCGCGCCGCCCG
|||| ||||||||
GCCG GGCGCGGCGGGC
ACA__
GAM3783 LOC255426 5' CGCCGCCGCCGCCGCCCG 85487 G TAC _
CG CGCC TCGC GCCGCCCG
|| ||| ||| ||||||
GC GCGG GGCG CGGCGGGC
G C_ G
GAM3783 LOC255838 5' CAGCGCTACCGCCGCC 85560 C TCG
CGGCGC TAC CGCCGCC
||||| ||| ||||||
GTCGCG ATG GCGGCGGG
_ _
GAM3783 LOC256160 5' CGGTCGCCGAGTCGCCGCCCG 85554 _ TACTCG
CGG CGCC CGCCGCCCG
||| ||| |||||||
GCC GCGG GCGGCGGGC
A CGTCA_
GAM3783 LOC90024 5' CAGCGCCCCGCCGCC 85456 ACTCG C
CGGCGCCT CGCCGC C
|||||| ||||| |
GTCGCGGG GCGGCG G
_ _ A
GAM3783 LOC90133 5' CGTCGCCTTGCCGCCGCCCG 85561 G ACTCG
CG CGCCT CGCCGCCCG
|| |||| |||||||
GC GCGGA GCGGCGGGC
A ACG_
GAM3783 LOC90379 5' CGCCGCCGCCCTGCTGCCCG 85562 G TA GC C
CG CGCC CTC GC GCCCG
|| |||| ||| ||||||
GC GCGG GGG CG CGGGC
G C_ A_ A
GAM3783 LOC91300 5' CGCCGCCGCCGCCGCCCG 85563 TAC _
CGCC TCGC GCCGCCCG
|||| ||| |||||||
GCGG GGCG CGGCGGGC
C_ G
GAM3783 LOC91300 5' CGCCGCCGCCGCCGCCCG 85563 TAC _
CGCC TCGC GCCGCCCG
|||| ||| |||||||
GCGG GGCG CGGCGGGC
C_ G
GAM3783 LOC91547 5' GCGCACCCGCGCCGCC 85564 CT
GCGC ACTCGCGCCGCC
|||| |||||||||

CGCG TGGGCGCGGCGG

GAM3783 LOC91978 5' CGGCCGCCCCGCGCCCG 85565 _ TACT G
CGGC GCC C CGCCGCCCCG
||||| ||| | |||||
GCCG CGG G GCGGCGGGC
G _ _ G

GAM3784 CDC2L2 5' CTGGCTTCTGCGCACGCGCCGG 85568 C G T
CTGGCT CTG TGT GCGCGCCGG
||||| ||| ||| |||||
GACCGA GAC GCG TGCGCGGCC

A _ _
GAM3784 IRS1 5' CTGGCTCTGCGCGCC 85569 CTGGTGT
CTGGCTC TGCGCGCC
||||| |||||
GACCGAG ACGCGCGG

GAM3784 LIF 3' CTGGCCCTGGCGCTTGTGTCTGG 85570 T GCGCGC
CTGGC CCTGGTGTT CGG
||||| ||||| |||
GACCG GGACCGCGA GCC

_ ACACA_
GAM3784 MGAT5 5' CTGGCTCCTGTGTCTAGC 85571 G C
CTGGCTCCTG TGTTG GC
||||||| ||||| ||
GACCGAGGAC ACAGT CG

GAM3784 MYO1D 3' CTGGCTCCTGGCTGAGGGGCTG 85572 GTTGCGC C
G CTGGCTCCTGGT GC GG
||||||| || ||
GACCGAGGACCG CG CC

ACTCCC_ A
GAM3784 ASE-1 3' GGCTCCTGCTGGCTGCGC 85573 G _
GGCTCCTG TG TTGCGC
||||||| || |||||
CCGAGGAC AC GACGCG
G C

GAM3784 HSA404617 3' CTGGCTCCTGTGTGCTCAAGGT 85574 _ G C_ C
GCTGG TGGCTCCTG GTGTT CG GC GG
||||||| ||||| || || ||
ACCGAGGAC CACGA GT CG CC

A _ TCCA A
GAM3784 KIAA0820 5' CTGGCTGCTGCTGCTGCGCCGG 85575 CCT G _
CTGGCT G TGTTGC GCGCCGG
||||| | ||||| |||||
GACCGA C ACGACG CGCGGCC

_ G A
GAM3784 KR18 3' CGTTCCTGGTGCCAGGCTGG 85576 GC G C C
TG TCCTGGTGTT CG GC GG
|| ||||| || || ||

		GC AGGACCACGG GT CG CC		
		A_ _ C A		
GAM3784	LOC152195 5'	TGGCCCCTGTTGCGC	85577	GGT
		TGGCTCCT GTTGCGC		
		ACCGGGGA CAACGCG		
		—		
GAM3784	LOC196047 5'	CTGGCTGCTGGTGCTTTGCTGG	85578	C GCGC C
		CTGGCT CTGGTGTT GC GG		
		GACCGA GACCACGA CG CC		
		C AA_ A		
GAM3784	LOC200205 3'	CTGGCTCCTGAGCCCTGCGC	85579	_ G
		CTGGCTCCTG GT TTGCGC		
		GACCGAGGAC CG GACGCG		
		T G		
GAM3784	LOC221935 3'	CTGGCTCCTGGGTGGCACTGG	85580	T T C C
		CTGGCTCCTGG GT G GCGC GG		
		GACCGAGGACC CA C CGTG CC		
		_ _ _ A		
GAM3785	BAIAP3 3'	CCTGCCCTTTGCATCCCCTC	85583	C GAG GCA_
		CC GC CC CATCCCCTC		
		GG CG GG GTAGGGGAG		
		A _ AAAC		
GAM3785	CELSR3 5'	CCCCGGGCCCGCCCTCCG	85585	G A GCACAT
		CCC CG GCC CCCCTCCG		
		GGG GC CGG GGGGAGGC		
		_ C GGGC_		
GAM3785	CELSR3 5'	CCGCGGCCGGAGCCCCTCCG	85584	A CACAT
		CCGCG GCCG CCCCTCCG		
		GGCGC CGGC GGGGAGGC		
		_ CTC_		
GAM3785	COL18A1 3'	CCTCCGAGCCGCCGGTCCTCTC	85586	G_ ACA C
	CG	CC CGAGCCGC TCC CTCCG		
		GG GCTCGGCG AGG GAGGC		
		AG GCC A		
GAM3785	COL18A1 3'	CCTCCGAGCCGCCGGTCCTCTC	85586	G_ ACA C
	CG	CC CGAGCCGC TCC CTCCG		
		GG GCTCGGCG AGG GAGGC		
		AG GCC A		
GAM3785	COL18A1 3'	CCTCCGAGCCGCCGGTCCTCTC	85586	G_ ACA C
	CG	CC CGAGCCGC TCC CTCCG		

		GG GCTCGGCG AGG GAGGC	
		AG GCC A	
GAM3785 CPNE7	5'	CCCGCGAGTCGCGCCGCC 85587	C ACATCC T
		CCCGCGAG CGC CC CC	
		GGGCGCTC GCG GG GG	
		A C_____ C	
GAM3785 DAPK1	5'	GCGAGTTGCCGAGTCCCCTCCG 85588	CC ACA_
		GCGAG GC TCCCCTCCG	
		CGCTC CG AGGGGAGGC	
		AA GCTC	
GAM3785 EPS8	5'	CCGCGAGCCGCGGAGCCGCCT 85589	ACAT _
		CCGCGAGCCGC CC CCT	
		GGCGCTCGGCG GG GGA	
		CCTC C	
GAM3785 HCN4	5'	CCCGCGAGCTCGCCTCGCCTCC 85590	_ ACA C
		CCCGCGAGC CGC TC CCTCC	
		GGGCGCTCG GCG AG GGAGG	
		A G__ C	
GAM3785 IRS1	5'	GCGCGCCGCCCCCTCCG 85591	A CACA
		GCG GCCG TCCCCTCCG	
		CGC CGGC GGGGGAGGC	
		G C__	
GAM3785 KCNJ6	5'	CCGCGGGTCTCCACCCCTCCG 85592	AGCCGCA T
		CCGCG CA CCCCTCCG	
		GGCGC GT GGGGAGGC	
		CCAGAG_ _	
GAM3785 LDB1	5'	CCGCCGGCCGCACAAAGACTC 85593	GA TCCC
		CCGC GCCGCACA CTC	
		GGCG CGGCGTGT GAG	
		GC TTCT	
GAM3785 LMO2	5'	CCGGCGAGCTCGCCCCTCC 85594	C _ ACATC
		CC GCGAGC CGC CCCTCC	
		GG CGCTCG GCG GGGAGG	
		C A _____	
GAM3785 NGB	5'	CCGCGACGCGGTCCCCTCCG 85595	GC ACA
		CCGCGA CGC TCCCCTCCG	
		GGCGCT GCG AGGGGAGGC	
		_ CC_	
GAM3785 NRXN2	5'	CCCGCGAAGCCCCCTCC 85596	_ GCACAT
		CCCGCGA GCC CCCCTCC	

GGGCGCT CGG GGGGAGG
T _____
GAM3785 PPT2 3' CCCCGGGCCCTACCCCTC 85597 G A GCAC
CCC CG GCC ATCCCTC
||| || ||| |||||
GGG GC CGG TGGGGGAG
_ C GA_
GAM3785 RAD17 5' CCCGGAGCTGCATCCCCT 85598 C C CA
CCCG GAGC GCA TCCCCT
|||| ||| ||| |||||
GGGC CTCG CGT AGGGGA
_ A _
GAM3785 RAD17 5' CCCGGAGCTGCATCCCCT 85598 C C CA
CCCG GAGC GCA TCCCCT
|||| ||| ||| |||||
GGGC CTCG CGT AGGGGA
_ A _
GAM3785 RAD17 5' CCCGGAGCTGCATCCCCT 85598 C C CA
CCCG GAGC GCA TCCCCT
|||| ||| ||| |||||
GGGC CTCG CGT AGGGGA
_ A _
GAM3785 SIGLEC6 5' CGGAGCTCCACTCCCTCT 85599 C CG A _
CG GAGC CAC TCCC CT
|| ||| || ||| ||
GC CTCG GTG AGGG GA
_ AG _ A
GAM3785 SMURF1 5' CCCGAGCCGCCGCCGCTCCG 85600 G ACAT _
CC CGAGCCGC CC CCTCCG
|| ||||| || |||||
GG GCTCGGCG GG GGAGGC
_ GC_ C
GAM3785 WW45 5' CCCGAGCCGCCGCCCTCC 85601 G ACATCC
CC CGAGCCGC CCTCC
|| ||||| |||
GG GCTCGGCG GGAGG
_ GC_
GAM3785 CBLN1 5' CCGGGACTAGCGTCCCCTCCG 85602 C GCC ACA
CCG GA GC TCCCCTCCG
||| || || |||||
GGC CT CG AGGGGAGGC
C GAT C_
GAM3785 CBLN1 5' CCGCGACTAGCGTCCCCTCCG 85603 GCC ACA
CCGCGA GC TCCCCTCCG
||||| || |||||
GGCGCT CG AGGGGAGGC
GAT C_
GAM3785 DKFZp547A023 5' CCGGGCTCCGCTCCCCTCCG 85604 CGAG ACA
CCG CCGC TCCCCTCCG
||| ||| |||||

			GGC GGCG AGGGGAGGC		
			CCGA ____		
GAM3785	EMILIN-2	5'	CCGCGGCCGCCCCCTCC	85605	A ACAT
			CCGCG GCCGC CCCCTCC		
			GGCGC CGGCG GGGGAGG		
			— ———		
GAM3785	FLJ10761	3'	CCCTTGGCCACGTCCCCTCCG	85606	GCGA ACA
			CCC GCCGC TCCCCTCCG		
			GGG CGGTG AGGGGAGGC		
			AAC_ C_		
GAM3785	FLJ14721	3'	CCTGCGAGCCGCCACCC	85607	C A
			CC GCGAGCCGC CATCC		
			GG CGCTCGGCG GTGGG		
			A G		
GAM3785	FLJ20288	5'	CCAGCGCCGCGTCCCCTCCG	85608	C GA ACA
			CC GC GCCGC TCCCCTCCG		
			GG CG CGGCG AGGGGAGGC		
			T _ C_		
GAM3785	FLJ21135	5'	CCGCGAGCCACCCCTCC	85609	ACAT
			CCGCGAGCCGC CCCCTCC		
			GGCGCTCGGTG GGGGAGG		
			—		
GAM3785	KIAA0116	5'	CCCACGAGCCGCACGTCATCT	85610	A CC
			CCCGCGAGCCGCAC TC CT		
			GGGTGCTCGGCGTG AG GA		
			C TA		
GAM3785	KIAA1649	5'	CCCGCGAGCCCGCCCCTC	85611	GCACAT C
			CCCGCGAGCC CCCCT C		
			GGGCGCTCGG GGGGA G		
			GC_ A		
GAM3785	MAPKAPK2	5'	CCCGCGGCCGCCCTCC	85612	A ACAT
			CCCGCG GCCGC CCCCTCC		
			GGGCGC CGGCG GGGGAGG		
			— ———		
GAM3785	MAPKAPK2	5'	CCCGCGGCCGCCCTCC	85612	A ACAT
			CCCGCG GCCGC CCCCTCC		
			GGGCGC CGGCG GGGGAGG		
			— ———		
GAM3785	MGC11303	5'	CCCGCGAGGTGCGCTCACTCCG	85613	C_ A TCCC
			CCCGCGAG CGC CA CTCCG		

GGGCGCTC GCG GT GAGGC
CAC A ____
GAM3785 MGC7036 3' CCCACCCTGCACATCCCTTC 85614 GAG _ C
CCCGC CC GCACATCCC TC
|||| || |||||||| ||
GGGTG GG CGTGTAGGG AG
__ A A
GAM3785 OATPRP4 5' CCCGGGCTCATCCCCTCC 85615 CGAGCC A
CCCG GC CATCCCCTCC
|||| || ||||||||
GGGC CG GTAGGGGAGG
C__ A
GAM3785 SEC15B 5' CCCGCAGCGCGTCCCCTCCG 85616 G C ACA
CCCGC AGC GC TCCCCTCCG
|||| || || ||||||||
GGGCG TCG CG AGGGGAGGC
_ _ C__
GAM3785 SLK 5' CCGCGAGCCTAGGGTCTCCTCC 85617 GCACA C
G CCGCGAGCC TC CCTCCG
|||||| || |||||
GGCGCTCGG AG GGAGGC
ATCCC A
GAM3785 VDU1 5' CCTGCAGCCGCACCTC 85618 C G CATCC
CC GC AGCCGCA CCTC
|| || ||||| |||
GG CG TCGGCGT GGAG
A _ ____
GAM3785 LOC120772 5' CCTGCTAGCCCCTTCCCCTCCG 85619 C G GCACA
CC GC AGCC TCCCCTCCG
|| || ||| ||||||||
GG CG TCGG AGGGGAGGC
A A GGA__
GAM3785 LOC138046 5' CCTGGAGCCAGCCCCTCC 85620 GC CACAT
CC GAGCCG CCCCTCC
|| |||| |||||||
GG CTCGGT GGGGAGG
AC C__
GAM3785 LOC145438 5' CGGAGTGGCCTCCCCTCCG 85621 C CC ACA
CG GAG GC TCCCCTCCG
|| || || ||||||||
GC CTC CG AGGGGAGGC
_ AC G__
GAM3785 LOC148530 5' GCTTCGCTCCCCTCCG 85622 GAG ACA
GC CCGC TCCCCTCCG
|| ||| ||||||||
CG GGCG AGGGGAGGC
AA_ ____
GAM3785 LOC221496 3' CCTGCGAGCCGAACCTCT 85623 C C A C
CC GCGAGCCG AC TCC CT
|| |||||| || ||| ||

		GG CGCTCGGC TG AGG GA		
		A T _ A		
GAM3785	LOC252995 3'	CCCCGAGCTGACCCCCTC	85624	G CGCAC
		CCC CGAGC ATCCCCTC		
		GGG GCTCG TGGGGGAG		
		_ AC__		
GAM3785	LOC254381 5'	CCGGTCCTGCGTGTCCCCTCCG	85625	CGAG _ ACA
		CCG CC GC TCCCCTCCG		
		GGC GG CG AGGGGAGGC		
		CA__ A CAC		
GAM3785	LOC256451 3'	CCCACGAGCCGCGCGTGCCTT	85626	ACA C C
	CG	CCCGCGAGCCGC TC CCT CG		
		GGGTGCTCGGCG AG GGA GC		
		CGC C A		
GAM3785	LOC256867 5'	CCTGCTAGCCCCCTTCCCCTCCG	85619	C G GCACA
		CC GC AGCC TCCCCTCCG		
		GG CG TCGG AGGGGAGGC		
		A A GGA__		
GAM3785	LOC56996 5'	CCCGCGAGCCGGGGGGCTCCG	85627	CACATCCC
		CCCGCGAGCCG CTCCG		
		GGGCGCTCGGC GAGGC		
		CCCCC__		
GAM3786	CCNT2 3'	AGGTTTAATTTCATTTTAT	85630	GGCT
		AGGTTTAATT TTTTAT		
		TCCAAATTAA AAAAATA		
		AGT_		
GAM3786	GHRHR 3'	TACAGGTTTATTGGCTCCT	85631	A
		TACAGGTTTA TTGGCTTTT		
		ATGTCCAAAT AACCGAGGA		
		_		
GAM3786	PTPRB 3'	TACAGGTTGAATTAGTTTT	85632	T C
		TACAGGTT AATTGG TTTT		
		ATGTCCAA TTAATC AAAA		
		C _		
GAM3786	TSGA10 5'	AGATTTAAGCCTTTTAT	85633	ATT
		AGGTTTA GGCTTTTAT		
		TCTAAAT TCGGAAAAATA		
		_		
GAM3786	MGC20533 3'	ACAGGTTTACTTTTTTA	85634	AATTG
		ACAGGTTT GCTTTTTTA		

TGTCCAAA TGAAAAAAT

GAM3786 TOB2 3' TACAGATTTGATCAATCTTTTT 85635 A TG _
TACAGGTTT AT G CTTTTT
||||||| || | |||||
ATGTCTAAA TA T GAAAAA
C GT A

GAM3786 LOC147671 3' TACAGATTTGATCAATCTTTTT 85635 A TG _
TACAGGTTT AT G CTTTTT
||||||| || | |||||
ATGTCTAAA TA T GAAAAA
C GT A

GAM3786 LOC150225 3' CAGATTTATGGACTTTTTT 85636 AT _
CAGGTTTA TGG CTTTTT
||||||| ||| |||||
GTCTAAAT ACC GAAAAA
_ T

GAM3786 LOC196807 5' GGCCTCTTGGCTTTTTT 85637 AA
GGTTT TTGGCTTTTTT
||||| |||||
CCGGA AACCGAAAAA
G_

GAM3787 ADCY6 5' TCCCGCGGTCTCCGAGCCCGC 85640 GC TC
TCCCGCGGTCC CCGG CCCGC
||||||| ||| |||||
AGGGCGCCAGG GGCT GGGCG
A_ C_

GAM3787 ATP6V0B 5' TCCCGCAGTCTGTCCGCCCG 85641 _
TCCCGCG GTCCGCCCG
||||||| |||||
AGGGCGT CAGGCGGGC
CAGA

GAM3787 BDNF 5' TCCAGCGCCCAGCCCCGGTCCC 85642 C G _ _
CG TCC GCG TCC GCCC GGTCCCCG
||| ||| ||| ||| |||||
AGG CGC GGG CGGG CCAGGGGC
T _ T G

GAM3787 CDKN2C 5' TCTCGCGGTCCCCGGCC 85643 C GC
TC CGCGGTCC CCGGTC
|| ||||| |||||
AG GCGCCAGG GGCCGG
A _

GAM3787 COL4A1 3' TCCTGCGGTCCATGCGATGCC 85644 C CC _ C
TGC TCC GCGGTCCG CGGT CCC GC
||| ||||| ||| ||| ||
AGG CGCCAGGT GCTA GGG CG
A AC C A

GAM3787 DBN1 5' CCGCTAGCTCGGTCCCCGC 85645 GGTCC C
CCGC GC CGGTCCCCGC
||| || |||||

GGCG CG GCCAGGGGCG
AT__ A
GAM3787 DNAJB1 5' TCCTGCGGCCCCGCGACCCGC 85646 C C TC
TCC GCGGTCCGCC GG CCCGC
||| ||||| || |||||
AGG CGCCGGGCGG CT GGGCG
A _ _
GAM3787 FANCC 5' TCCCGCGGTCGCCCCGC 85647 C
TCCCGCGGTC GCCCGGT
||||||| |||||
AGGGCGCCAG CGGGCCG
_ _
GAM3787 IER5 3' CCCGCGGTCTCTGGGCGTCCTC 85648 CGCCCG_ C
GC CCCGCGGTC GTCC CGC
||||||| ||| |||
GGGCGCCAG CAGG GCG
AGACCCG A
GAM3787 IGF2R 3' TCCCGCGGCTCCGTGCTCCCT 85649 _ CCCGG _
GC TCCCGCGG TCCG TCCCC GC
||||||| ||| ||||| ||
AGGGCGCC AGGC AGGGG CG
G ACG__ A
GAM3787 NMI 5' TCCCCCGGTCCGCCCGCCGAGC 85650 G G CC_
GC TCCC CGGTCCGCCCG TC CGC
||||| ||||| ||| |||
AGGG GCCAGGCGGGC GG GCG
G _ CTC
GAM3787 NOTCH4 5' TCTCCAAGCCCCGGTCCC 85651 _ C CCG
TC CCG GGT CCCGGTCCC
|| ||| ||| |||||
AG GGT TCG GGGCCAGGG
A _ _
GAM3787 TBX6 5' CGGCCAGCTGGTCCCCG 85652 C CC
CGGTC GC GGTCCCCG
||||| || |||||
GCCGG CG CCAGGGGC
T A_
GAM3787 TBX6 5' CGGCCAGCTGGTCCCCG 85652 C CC
CGGTC GC GGTCCCCG
||||| || |||||
GCCGG CG CCAGGGGC
T A_
GAM3787 WBSCR14 5' CCGCAACCGCCTGGTCCCTGC 85653 T C C
CCGCGG CCGCC GGTCCC GC
||||| ||||| ||||| ||
GGCGTT GGCGG CCAGGG CG
_ A A
GAM3787 WBSCR14 5' CCGCAACCGCCTGGTCCCTGC 85653 T C C
CCGCGG CCGCC GGTCCC GC
||||| ||||| ||||| ||

GGCGTT GGCGG CCAGGG CG
_ A A
GAM3787 CACNA1H 3' TCTGGCGGGTGCCCGGTCTTCG 85654 CC TCC CC
TC GCGG GCCCGGTC CG
|| ||| ||||| ||
AG CGCC CGGGCCAG GC
AC CA_ AA
GAM3787 CENTG1 3' TCCAGCGGTCCGCCCCGT 85655 C
TCC GCGGTCCGCCCCGT
||| |||||
AGG CGCCAGGCGGGCCA
T
GAM3787 Dlc2 5' CCGCGGTCCGCCCTTGGAGTTT 85656 _ TCCC_
CGC CCGCGGTCCGCC CG CGC
||||||| || |||
GGCGCCAGGCGGG CC GCG
AA TCAA
GAM3787 FLJ11526 5' TCCCGCGGCTCGCAGGGCCCCG 85657 TC CC T
C TCCCGCGG CGC GG CCCC
||||| ||| || |||||
AGGGCGCC GCG CC GGGGCG
GA TC _
GAM3787 FLJ11856 5' CGGGAGCCGTCCGGTCCCTGC 85658 C T_ C C
CG GG CCG CCGGTCCC GC
|| || ||| ||||| ||
GC CC GGC GGCCAGGG CG
_ TC A A
GAM3787 FLJ12697 3' TCCCGGGCGTGTCCTCCG 85659 C CCGCCC
TCCCG GGT GGTCCCG
||||| ||| |||||
AGGGC CCG CCAGGGGC
_ CA_
GAM3787 FLJ20694 3' TCCCGCAGTCTTCGAATGTC 85660 _ CCCG
TCCCGCGGTC CG GTC
||||||| || |||
AGGGCGTCAG GC CAG
AA TTA_
GAM3787 FLJ23441 5' TCCCGCGTCCGCCAGGCCCTC 85661 G _ _
CGC TCCCGCG TCCGCC GTCC CCGC
||||| ||||| ||||| |||||
AGGGCGC AGGCGGG CCGGG GGCG
_ T A
GAM3787 FUBP3 5' TCCCGGTCCGGCCTCCCG 85662 G GCCC _
TCCC CGGTCC GGTC CCG
||| ||||| ||| |||||
AGGG GCCAGG CCGG GGGC
_ _ A
GAM3787 HSPC003 5' TCCCGCGGGCCGCTGCCCG 85663 T CCGGTC
TCCCGCGG CCGC CCG
||||| ||| |||

AGGGCGCC GGCG GGGC
 C AC____
 GAM3787 KIAA0984 5' ACCGTCCGTCTCGGTCCCCGC 85664 G CC_
 GC GTCCG CGGTCCCCGC
 || |||| |||||
 TG CAGGC GCCAGGGGCG
 G AGA
 GAM3787 KIAA1623 5' CCCGCGCCGGCCTCGGTCTCG 85665 G C _ C
 C CCCGCG TC GCC CGGTCC CGC
 ||||| || ||| ||||| |||
 GGGCGC GG CGG GCCAGG GCG
 _ C A A
 GAM3787 KIAA1754 5' TCCCCGGTCCCGGTCCCCG 85666 G CCG
 TCCC CGGT CCCGGTCCCCG
 ||| ||| |||||
 AGGG GCCA GGGCCAGGGGC
 _ _
 GAM3787 LGI3 5' TCCCGCGGCTGGGCCACCCCGC 85667 CC_ CGGT
 TCCCGCGGT GCC CCCCCG
 ||||| ||| |||||
 AGGGCGCCG CGG GGGGCG
 ACC T____
 GAM3787 MGC14425 3' TCCCGCGGCTGCTGCCCGC 85668 CC CCG T
 TCCCGCGGT GC G CCCCCG
 ||||| || | |||||
 AGGGCGCCG CG C GGGGC
 A_ A____
 GAM3787 MGC2615 5' TCCCGCGGCCCGCCGGCTCCGC 85669 T C CC
 TCCCGCGG CCGCC GGT CCGC
 ||||| |||| ||| |||
 AGGGCGCC GGCGG CCG GGCG
 _ _ A_
 GAM3787 MGC3165 3' CCCAGGGTCTCGGTTCCTCG 85670 C CGCC C
 TCCCG GTTC CGGT CCCG
 |||| ||| ||| |||
 GGGGT CCAG GCCA GGGC
 C A_ A
 GAM3787 MGC4607 5' TCCCGCGGCCCGCCCGGCCCGC 85671 TC
 TCCCGCGGTCCGCCCCG CCGC
 ||||| ||||| |||||
 AGGGCGCCGGGCGGGCC GGGCG
 _
 GAM3787 MO25 5' TCCCGCGGCTGCCGCCGCGCGG 85672 _ _ TCC
 GGACC CGCGGT CCGCC CGG CC
 |||| ||| ||| ||
 GCGCCG GGCGG GCC GG
 AC CGIIC CCT
 GAM3787 NPEPL1 3' CCCGGTCCCCTCCCCG 85673 G G CGG
 CC CGGTCC CC TCCCCG
 || ||||| || |||||

GG GCCAGG GG AGGGGC

GAM3787 ODC-p 5' TCCCGCGGCCTGCGCCCCG 85674 C CCG T
TCCCGCGGTC GC G CCCC
||||||| || | ||||
AGGGCGCCGG CG C GGGGC
A ____
GAM3787 PLXNC1 5' TCCCGCGGCCGCCCATCCCCG 85675 T G
C TCCCGCGG CCGCCC GTCCCCGC
||||||| ||||| |||||
AGGGCGCC GGCGGG TAGGGGCG
G
GAM3787 SEMA4B 5' CCCC GCGGTCCGCCCCCGAGTC 85676 ____
TCCCGCGGTCCGCC GGTC
||||||| |||||
GGGGCGCCAGGCGGG TCAG
GGC
GAM3787 TRAF3 5' TCTCGCGGTCCGTCCCG 85677 C GCCCG C
TC CGCGGTCC GTC CCG
|| ||||| || |||
AG GCGCCAGG CAG GGC
A ____ C
GAM3787 UBAP 5' TCCCAGGCTCGGTCCCCG 85678 C CCGCC
TCCCG GGT CGGTCCCCG
||||| || |||||
AGGGT CCG GCCAGGGGC
A ____
GAM3787 VPS4A 5' TCCTGGGTCCGCCCCACACCCC 85679 CGC GGT_
GC TCC GGTCCGCC CCCC
||| ||||| |||||
AGG CCAGGCGGG GGGGCG
AC_ GTGT
GAM3787 LOC145644 5' TCCACGGTCTGGGCTCCTGC 85680 CGCCC TC C
TCCCGCGGTC GG CC GC
||||||| || |||
AGGGTGCCAG CC GG CG
AC_ GA A
GAM3787 LOC148753 5' TCCCGCGGCTGAGCAGCTCCGC 85681 CCGCC CC
TCCCGCGGT CGGT CCGC
||||||| ||| |||||
AGGGCGCCG GTCG GGCG
ACTC_ A_
GAM3787 LOC158301 3' TCCCCGGTCCGGCCTCCCG 85662 G GCCC _
TCCC CGGTCC GGTC CCGC
||| ||||| ||| |||||
AGGG GCCAGG CCGG GGGC
A
GAM3787 LOC170127 3' TCCCTGGTCTTCCTCCCG 85682 GC CG CGG C
TCCC GGTC CC TCCC G
||| ||||| || ||| |

AGGG CCAG GG AGGG C
 A_ AA _ A
 GAM3787 LOC197202 5' TCCAGCGGTCCAGGCTTTTCGC 85683 C CCC CCC_
 TCC GCGGTCCG GGT CGC
 ||| ||||| ||| |||
 AGG CGCCAGGT CCG GCG
 T _ AAAA
 GAM3787 LOC201780 5' TCCCGCGGTGCGCCGAGTC 85684 C _
 TCCCGCGGTC GCC CGGTC
 ||||| ||| |||||
 AGGGCGCCAG CGG GTCAG
 _ C
 GAM3787 LOC201931 5' TCCTGCGTCCGCCCCGC 85685 C G G
 TCC GCG TCCGCC GT
 ||| ||| ||||| ||
 AGG CGC AGGCGGG CG
 A _ G
 GAM3787 LOC253367 3' CCCGCGGTTGCTGCGCACTCT 85686 C C_ G C
 CCGC CCCGCGGT CGC CG TC CCGC
 ||||| ||| ||| |||||
 GGGCGCCA GCG GT AG GGCG
 A ACGC G A
 GAM3787 LOC254122 5' TCCCGCAGGTGTCCTCCCG 85687 _ CGCCCG
 TCCCGC GGTC GTCCCG
 ||||| ||| |||||
 AGGGCG CCAG CAGGGGC
 T _
 GAM3787 LOC256160 5' TCCCGCGGTGCGCCGAGTC 85684 C _
 TCCCGCGGTC GCC CGGTC
 ||||| ||| |||||
 AGGGCGCCAG CGG GTCAG
 _ C
 GAM3787 LOC90768 5' TCCCGCGATCTGGCCCTTCTCG 85688 C_ GG CC
 C TCCCGCGGTC GCC TC CGC
 ||||| ||| ||| |||
 AGGGCGCTAG CGGG AG GCG
 AC A_ A_
 GAM3788 ALS2 3' CTTGCAAACGGATCGGGGT 85691 A C_
 CTT GT ACGGATCGGGGT
 ||| ||| ||||| |||||
 GAA CG TGCCTAGCCCCA
 _ TT
 GAM3788 HLA-DQA1 3' TGCCTTAATTGAGGGG 85692 CACG TC
 TGCCTTAGT GA GGGG
 ||||| ||| |||
 ACGGAATTA CT CCCC
 A_ _
 GAM3788 PACE4 3' TGCTTGGCCATCGGGG 85693 C A CGGA
 TGC TT GTCA TCGGGG
 ||| ||| |||||

			ACG AA CGGT AGCCCC		
			_ C _		
GAM3788	PACE4	3'	TGCTTGGCCATCGGGG	85693	C A CGGA
			TGC TT GTCA TCGGGG		
			ACG AA CGGT AGCCCC		
			_ C _		
GAM3788	PDE4B	5'	TGCCTTAGTCATCCCAGGGT	85694	CGGA
			TGCCTTAGTCA TCGGGGT		
			ACGGAATCAGT GGTCCCA		
			AG_		
GAM3788	STK6	3'	CCTTAAGTATCGGGG	85695	GTC G
			CCTTA AC GATCGGGG		
			GGAAT TG CTAGCCCC		
			_ A		
GAM3788	TCF19	3'	TGTCTTGGCCACCAGGG	85696	C A GGAT
			TG CTT GTCAC CGGGG		
			AC GAA CGGTG GTCCC		
			A C _		
GAM3788	TCF19	3'	TGTCTTGGCCACCAGGG	85696	C A GGAT
			TG CTT GTCAC CGGGG		
			AC GAA CGGTG GTCCC		
			A C _		
GAM3788	KIAA0376	3'	TGCCTTGGCCACGGAGGGC	85697	A TCG
			TGCCTT GTCACGGA GGGT		
			ACGGAA CGGTGCCT CCCG		
			C _		
GAM3788	PRO0038	3'	TGCCTTAGTCTCCCAGGGT	85698	ACGGA
			TGCCTTAGTC TCGGGGT		
			ACGGAATCAG GGTCCCA		
			AG_		
GAM3788	LOC129198	3'	TGCCTTAGTCTGGCTCAG	85699	AC A
			TGCCTTAGTC GG TCGG		
			ACGGAATCAG CC AGTC		
			A_ G		
GAM3789	MTMR3	3'	TTTATATATTTAACAATTCT	85702	
			TTTATATATTTAATAATTTT		
			AAATATATAAATTGTTAAGA		
GAM3789	EDG2	3'	TTTATACATTTCTGCATTTTTC	85703	AATA
	AA		TTTATATATTT ATTTTCAA		

			AAATATGTAAA TAAAAAGTT	
			GACG	
GAM3789	EDG2	3'	TTTATACATTTCTGCATTTTTC 85703	AATA
	AA		TTTATATATTT ATTTTTC	
			AAATATGTAAA TAAAAAGTT	
			GACG	
GAM3789	KIAA0660	3'	TTTATACATTTTCGATGATTTTT 85704	AATA_
	CAA		TTTATATATTT ATTTTTC	
			AAATATGTAAA TAAAAAGTT	
			GCTAC	
GAM3789	MAPKAPK5	3'	TTTATACATTAAAGAATAATTT 85705	T__
	TTCAA		TTTATATATT AATAATTTTTC	
			AAATATGTAA TTATTA AAAAGTT	
			TTTC	
GAM3789	MAPKAPK5	3'	TTTATACATTAAAGAATAATTT 85705	T__
	TTCAA		TTTATATATT AATAATTTTTC	
			AAATATGTAA TTATTA AAAAGTT	
			TTTC	
GAM3790	CUGBP2	3'	TGCTATAAGAAGGAAACGT 85708	CC
			TGCTATAAGAAGG ATGT	
			ACGATATTCTTCC TGCA	
			TT	
GAM3790	FLJ14547	5'	CGTTGGATCAAGGAGGCCATGT 85709	C CTA A
			CG TG TAAG AGGCCATGT	
			GC AC GTTC TCCGGTACA	
			A CTA C	
GAM3790	FLJ20647	5'	TACCAAGGGAAGGCCATGTC 85710	TAA
			TGCTA GAAGGCCATGTC	
			ATGGT CTTCCGGTACAG	
			TCC	
GAM3790	KIAA1136	3'	ACTGCTATAATTCTTATGTC 85711	GAAGGCC
			GCTGCTATAA ATGTC	
			TGACGATATT TACAG	
			AAGAA__	
GAM3790	NSE1	3'	ACTCGCGGGGAAGGCCATGTC 85712	_ TATAA
			GCT GC GAAGGCCATGTC	
			TGA CG CTTCCGGTACAG	
			G CCC__	
GAM3790	LOC123242	5'	CATTGCTGAAGGCCATGT 85713	C ATAA
			CG TGCT GAAGGCCATGT	

	GT ACGA CTTCCGGTACA		
	A ____		
GAM3790 LOC148394 3'	GCTGCTATGAGAACGGGC 85714	A	__
	GCTGCTAT AGAA GGC		
	CGACGATA TCTT CCG		
	C GC		
GAM3790 LOC155060 3'	GCTGCTGGCAGGCCATGT 85715	ATAAGA	
	GCTGCT AGGCCATGT		
	CGACGA TCCGGTACA		
	CCG__		
GAM3790 LOC196955 3'	CATTGCTGAAGGCCATGT 85713	C	ATAA
	CG TGCT GAAGGCCATGT		
	GT ACGA CTTCCGGTACA		
	A ____		
GAM3790 LOC253001 5'	CATTGCTGAAGGCCATGT 85713	C	ATAA
	CG TGCT GAAGGCCATGT		
	GT ACGA CTTCCGGTACA		
	A ____		
GAM3790 LOC254196 3'	GCTGCTATGAGAACGGGC 85714	A	__
	GCTGCTAT AGAA GGC		
	CGACGATA TCTT CCG		
	C GC		
GAM3791 CHAC 3'	TTCTGGTTTTGTTTTTTTGTT 85718	CT	
	TTCTGGTTTTGTTTTT TTGTT		
	AAGACCAAAACAAAAA AACAA		
	—		
GAM3791 INHBA 3'	TACTTTTGTTTTTTTGTGTT 85719	G	C
	TG TTTTGTTTTT TTTGTT		
	AT AAAACAAAAA AAACAA		
	G A		
GAM3791 PCDH11X 3'	TGGTTTTGTTTTTTGTTTGTT 85720	C_	
	TGGTTTTGTTTTT TTTGTT		
	ACCAAAACAAAAA AAACAA		
	AC		
GAM3791 PCDH11Y 3'	TGGTTTTGTTTTTTGTTTGTT 85720	C_	
	TGGTTTTGTTTTT TTTGTT		
	ACCAAAACAAAAA AAACAA		
	AC		
GAM3791 PCDH11Y 3'	TGGTTTTGTTTTTTGTTTGTT 85720	C_	
	TGGTTTTGTTTTT TTTGTT		

			ACCAAAACAAAAA AAACAA		
			AC		
GAM3791	RUNX3	3'	GTTTTGTTTTTTTTTGT	85721	C_
			GTTTTGTTTTT TTTGT		
			CAAAACAAAAA AAACA		
			AA		
GAM3791	SLC2A8	3'	TGGTTTGTTTTTTTTGCT	85722	T C
			TGGTTT GTTTTT TTTGTT		
			ACCAAA CAAAAA AAACGA		
			_ A		
GAM3791	FLJ12960	3'	TGGTTTGTATTGCTGTT	85723	TTTCT
			TGGTTTGT TTTGTT		
			ACCAAACAA GACAA		
			TAAC_		
GAM3791	FLJ20507	3'	TTTTTGGTTTTGTTTTCCCTT	85724	C
			TTT TGGTTTTGTTTTCTTT		
			AAA ACCAAAACAAAAGGGAA		
			A		
GAM3791	FLJ20507	3'	TTTTTGGTTTTGTTTTCCCTT	85724	C
			TTT TGGTTTTGTTTTCTTT		
			AAA ACCAAAACAAAAGGGAA		
			A		
GAM3791	FLJ20507	3'	TTTCTGGTTTTTTGGTTTTGT	85725	GTTTTTC
	T		TTTCTGGTTTT TTTGTT		
			AAAGACCAAAA AAACAA		
			AAACCA_		
GAM3791	FLJ20507	3'	TTTCTGGTTTTTTGGTTTTGT	85725	GTTTTTC
	T		TTTCTGGTTTT TTTGTT		
			AAAGACCAAAA AAACAA		
			AAACCA_		
GAM3791	FLJ21616	3'	TGGTTTTTGTCTTTGTT	85726	GTTTT
			TGGTTTT TCTTTGTT		
			ACCAAAA AGAAACAA		
			AC__		
GAM3791	HMP19	3'	TTTGTTCATGTTCTTTGTT	85727	__
			TTTGT TTCTTTGTT		
			AAAACAAG AAGAAACAA		
			TAC		
GAM3791	ILF3	3'	TAGTTTTGTTTTCTTTATT	85728	
			TGGTTTTGTTTTCTTTGTT		

ATCAAAACAAAAAGAAATAA

GAM3791 KIAA1595 3' TTTCTGTTTTCTCTCTTTG 85729 G G
TT TTTCTG TTTT TTTTCTTTGTT

||||| ||| |||||||||
AAAGAC AAAG GAGAAGAAACAA
A A

GAM3791 MKRN4 3' TTTCCGTTTTGTTTTTTTTTG 85730 G C
TT TTTCTG TTTTGTTTT TTTGTT

||||| ||||||| |||||
AAAGGC AAAACAAAAA AAACAA
A A

GAM3791 MOT8 3' GGTTTTGTCTTTTTTGTT 85731 C
GGTTTTGTTTT TTTGTT

||||||||| |||||
CCAAAACAGAAA AAACAA

GAM3791 PP3501 3' TGGTTTTGTTTTGTTTTGTT 85732 TC
TGGTTTTGTTTT TTTGTT

||||||||| |||||
ACCAAAACAAAA AAACAA
CA

GAM3791 SPRY4 3' TTTCTGTTTTGTTTTTTTT 85733 G C
TTTCTG TTTTGTTTT TTT

||||| ||||||| |||
AAAGAC AAAACAAAAA AAA
A

GAM3791 LOC151446 3' TTCTGGTTTTGTTGTGTGCTTT 85734 TTT__
GTT TTCTGGTTTTGTT CTTTGTT

||||||||| |||||
AAGACCAAAACAA GAAACAA
CACAC

GAM3791 LOC153320 3' GTTTTGTTTTTTTTGCT 85735 C
GTTTTGTTTT TTTGTT

||||||||| |||||
CAAAACAAAAA AAACGA

GAM3791 LOC157562 5' TTCCTGGTGATGTTTTTTTGTT 85736 TT CT
TTTCTGGT TGTTTT TTTGTT

||||| ||||| |||||
AAGGACCA ACAAAAA AACAA
CT _

GAM3791 LOC161823 3' TTTCCGTTTTTTGTTTTTTTG 85737 _ CT
TT TTTCTGGTTT TGTTTT TTTGTT

||||||||| ||||| |||||
AAAGGCCAAA ACAAAAA AACAA
AA _

GAM3791 LOC51133 5' GTTTTGTTTTTTTTTGTT 85738 C_
GTTTTGTTTT TTTGTT

||||||||| |||||

		CAAAACAAAA AAACAA		
		AA		
GAM3791	LOC90410	3' TGGTTTTGAGAGGCTTTTTTTT 85739	_____	C III
		GTTA GTTTT GTTTT TTTGTT A		
		CAAAA CGAAAA AAACAA T		
		CTCTC A III		
GAM3792	FGFRL1	3' TGTCTGGAAGTGTGTGTCCA 85742		CGCG CGA
		TGTCTGGAG GTG CCA		
		ACAGACCTT CAC GGT		
		CA__ ACA		
GAM3792	H1F0	5' GTCTGGAGTGCGGCTCCC 85743	C	GCGA
		GTCTGGAG GCGGT CC		
		CAGACCTC CGCCG GG		
		A AG__		
GAM3792	HNF4A	3' TGTCTGGACACCATGACC 85744	G G GC	
		TGTCTGGA CGC GT GACC		
		ACAGACCT GTG TA CTGG		
		- G -		
GAM3792	LANCL1	3' TGCTTGGAGAACTGTGATCAAG 85745	TC C G CGAC	
		TG TGGAG GC GTG CAAG		
		AC ACCTC TG CAC GTTC		
		GA T A TA__		
GAM3792	SH3BP2	3' TGTCTGGAATGGGACCA 85746	GCGCG C	
		TGTCTGGA GTG GACCA		
		ACAGACCT TAC CTGGT		
		_____ C		
GAM3792	CYYR1	3' TCTGGAGCGTGTCTCTACCAAG 85747	CG GCG_	
		TCTGGAGCG GT ACCAAG		
		AGACCTCGC CA TGGTTC		
		A_ GAGA		
GAM3792	HSD17B12	3' TGCTGGAGCATCTGGCCAA 85748	T C__ TGCGA	
		TG CTGGAGCG GG CCAA		
		AC GACCTCGT CC GGTT		
		- AGA -		
GAM3792	KIAA1128	3' TGTCTGCGGTGCGGTGGAACA 85749	GAGC C C	
		TGTCTG GCGGTG GA CA		
		ACAGAC CGCCAC CT GT		
		GCCA _ T		
GAM3792	LIG-1	5' TGTCTGGAGCGCGCTGCGAACT 85750	G _____	
	CC	TGTCTGGAGCGCG TGCGA CC		

		ACAGACCTCGCGC ACGCT GG	
		G TGA	
GAM3792 PL6	3'	TGTCTGGAGTTGGAACCA 85751	CGC TGC
		TGTCTGGAG GG GACCA	
		ACAGACCTC CC TTGGT	
		AA_ _	
GAM3792 LOC115219	5'	TGTCTGGACTGTGGTTCACC 85752	G GC_ GCG
		TGTCTGGA C GGT ACC	
		ACAGACCT G CCA TGG	
		ACA AG	
GAM3792 LOC151996	5'	TGTCTGGAGGGGTATGGGCC 85753	CGC CGA_
		TGTCTGGAG GGTG CC	
		ACAGACCTC CCAT GG	
		C_ ACCC	
GAM3792 LOC167040	5'	TGTCTGGAGCAGTGGCCA 85754	GC CGA
		TGTCTGGAGC GGTG CCA	
		ACAGACCTCG TCAC GGT	
		_ C_	
GAM3792 LOC253150	5'	TGCCTGGAGCACCCCTTGGC 85755	_____
		TGTCTGGAGCGC GGT	
		ACGGACCTCGTG CCG	
		GGAA	
GAM3793 TRPM6	3'	TATAATATATATATTCCATATA 85758	CG AT_
		TATT TATAA TATATATTC TATATT	
		ATATT ATATATAAG ATATAA	
		AT GTAT	
GAM3793 LOC138399	3'	TATAAAGTATATATCCAT 85759	C
		TATAA GTATATATTCAT	
		ATATT CATATATAGGTA	
		T	
GAM3793 LOC145868	5'	TATAACATATATATCTCATATT 85760	CA
		TATAACGTATATATT TTATATT	
		ATATTGTATATATAG AGTATAA	
		_	
GAM3794 ACCN2	3'	TGTCTGGTGGAGGGAGGGGGG 85763	C AAA AC_
		C TG CTGGTGGG GA GGGGC	
		AC GACCACCT CT CCCCC	
		A CC_ CCC	
GAM3794 ACP1	5'	TACCTATAGGGGACGGGGC 85764	GT_ AAGAA
		TGCCTG GGGA CGGGGC	

			ATGGAT CCCT GCCCCG		
			ATC _____		
GAM3794	ACP1	5'	TACCTATAGGGGACGGGGC 85764	GT_	AAGAA
			TGCCTG GGA CGGGGC		
			ATGGAT CCCT GCCCCG		
			ATC _____		
GAM3794	ALX3	3'	TGCTGGTGGGGAGGGGAAGCAG 85765	C	AAA_ _
			GGC TGC TGGTGGG GAA CGGGGC		
			ACG ACCACCC CTT GTCCCG		
			_ CTCCC C		
GAM3794	BCL2A1	5'	TGCCTGGTGGAGAGCAAAG 85766	GAA	A
			TGCCTGGTGG AGA CGGGG		
			ACGGACCACC TCT GTTTC		
			_ C		
GAM3794	CDY1	5'	TGCCTGGTGGGACAGCTTGGGC 85767	A	AACG
			TGCCTGGTGGGA AG GGGC		
			ACGGACCACCCT TC CCCG		
			G GAA_		
GAM3794	CDY1	5'	TGCCTGGTGGGACAGCTTGGGC 85767	A	AACG
			TGCCTGGTGGGA AG GGGC		
			ACGGACCACCCT TC CCCG		
			G GAA_		
GAM3794	CDY2	5'	TGCCTGGTGGGACAGCTTGGGC 85767	A	AACG
			TGCCTGGTGGGA AG GGGC		
			ACGGACCACCCT TC CCCG		
			G GAA_		
GAM3794	DVL3	3'	TGCCTGATGGGGTGGGG 85768	AAAGAAC	
			TGCCTGGTGGG GGGG		
			ACGGACTIONC CCCC		
			CA_____		
GAM3794	EFNA3	3'	GCCTGGTGGGGAAGGGG 85769	AAA	C
			GCCTGGTGGG GAA GGGG		
			CGGACCACCC CTT CCCC		

GAM3794	FGF23	3'	CTGCTTGGGAACAGAGTGGGGC 85770	G_	_ AC
			C CTG TGGGAA AGA GGGGCC		
			GAC ACCCTT TCT CCCC GG		
			GA G CA		
GAM3794	FGFR1	3'	TGCCTGGTGGCAGGGAGGGG 85771	GAAA	AC
			TGCCTGGTGG GA GGGG		

		ACGGACCACC CT CCCC			
		GTCC _			
GAM3794 FGFR1	3'	TGCCTGGTGGCAGGGAGGGG 85771		GAAA AC	
		TGCCTGGTGG GA GGGG			
		ACGGACCACC CT CCCC			
		GTCC _			
GAM3794 FLRT2	3'	CCTGGTGGGGAAGGAA 85772		AAA C	
		CCTGGTGGG GAA GGGG			
		GGACCACCC CTT CCTT			
		— —			
GAM3794 GBF1	3'	GCCTGGTGGGAAGCACTGG 85773		AGA G	
		GCCTGGTGGGAA AC GG			
		CGGACCACCCTT TG CC			
		CG_ A			
GAM3794 HD	3'	TGTCTGCTGGGAAGGATGC 85774	C G	AGAAC _	
		TG CTG TGGGAA GGG GC			
		AC GAC ACCCTT CCT CG			
		A G _ A			
GAM3794 HMGCL	3'	TGCTAAGTAGGGAACGGGG 85775	CT	AAA	
		TGC GGTGGG GAACGGGG			
		ACG TCATCC CTTGCCCC			
		AT _			
GAM3794 IL1R1	3'	TGCTGGTGGGAAAGCATGGGC 85776	C	AACG	
		TGC TGGTGGGAAAG GGGC			
		ACG ACCACCCTTTC CCGG			
		_ GTA_			
GAM3794 PACE	5'	TGACTGGTGGGGGCATGGGGCC 85777	C	AAAGAAC	
		TG CTGGTGGG GGGGCC			
		AC GACCACCC CCCCCG			
		T CCGTA_			
GAM3794 PELO	5'	TGCCTGGCGGGAAGGAAACACG 85778		A_ GG	
C		TGCCTGGTGGGAA GAACG GC			
		ACGGACCGCCCTT TTTGT CG			
		CC G_			
GAM3794 PSEN1	3'	TGCTTGTGTGGGAGAGAAGAA 85779	C _	A C	
		TGC TG GTGGGA AGAA GGG			
		ACG AC CACCCT TCTT CTT			
		A A C _			
GAM3794 PSEN1	3'	TGCTTGTGTGGGAGAGAAGAA 85779	C _	A C	
		TGC TG GTGGGA AGAA GGG			

		ACG AC CACCCT TCTT CTT		
		A A C _		
GAM3794	RFX1	3' TGGTGGGAGGACGGGG	85780	AA A
		TGGTGGGA G ACGGGG		
		ACCACCCT C TGCCCC		
		_ C		
GAM3794	SHC1	3' GCCTGGCCGGGAGTGGGGC	85781	_ AAGAAC
		GCCTGGT GGA GGGGC		
		CGGACCG CCCT CCCC		
		G CA_____		
GAM3794	SORBS1	3' TGTCTGGTGGGGGATGGGA	85782	C AAA AC
		TG CTGGTGGG GA GGGG		
		AC GACCACCC CT CCCT		
		A C_ A_		
GAM3794	TCF7	3' CTGTCATCGGAAGGAACGGGGC	85783	_ G A
		CTG GT GGAA GAACGGGGC		
		GAC TA CCTT CTTGCCCG		
		AG G C		
GAM3794	TFE3	3' TGCCTGATTACAGGGGTGGGGC	85784	_____ AAAGAAC
	C	GCCTGGT GGG GGGGCC		
		CGGACTA CCC CCCC		
		ATGT CA_____		
GAM3794	THBD	5' TGCCTGGTGGGAAGGG	85785	AAGAAC
		TGCCTGGTGGGA GGGG		
		ACGGACCACCCT TCCC		

GAM3794	TNR	3' CCTTGGTGGGAAAGGAGG	85786	_ AAC
		CCT GGTGGGAAAG GGGG		
		GGA CCACCCTTC CTCC		
		A _____		
GAM3794	UPF3B	5' GCTTGGCCGGAACGGGG	85787	C G AAGA
		GC TGGT GGA ACGGGG		
		CG ACCG CCT TGCCCC		
		A G _____		
GAM3794	UPF3B	5' GCTTGGCCGGAACGGGG	85787	C G AAGA
		GC TGGT GGA ACGGGG		
		CG ACCG CCT TGCCCC		
		A G _____		
GAM3794	ALTE	3' TGCCTGGAGCTGAGTGGGG	85788	TG AAA AC
		TGCCTGG GG GA GGGG		

ACGGACC TC CT CCCC
 — GA_ CA
 GAM3794 ARHGDIG 3' TGCCGGCAAAGGGTGGGGC 85789 TGGT G AAC
 TGCC GG AAAG GGGGC
 ||| || ||| ||||
 ACGG CC TTTC CCCC
 — G CCA
 GAM3794 C1orf2 5' GCCTGGTGGGGAGAGGC 85790 AAA AC
 GCCTGGTGGG GA GGGGC
 ||||| || ||||
 CGGACCACCC CT CTCCG
 — —
 GAM3794 C1orf2 5' GCCTGGTGGGGAGAGGC 85790 AAA AC
 GCCTGGTGGG GA GGGGC
 ||||| || ||||
 CGGACCACCC CT CTCCG
 — —
 GAM3794 C20orf29 3' TGCCTGGTGGGAACGGG 85791 AAGA
 TGCCTGGTGGGA ACGGG
 ||||| ||||
 ACGGACCACCCT TGCCC
 —
 GAM3794 DJ37E16.5 3' ACCAGGAAAGGGTGGGGC 85792 TGGT AAC
 GCC GGGAAAG GGGGC
 || ||||| ||||
 TGG TCCTTTC CCCC
 — CCA
 GAM3794 DKFZP434J193 5' TGTCTGGTGGGATGGGC 85793 C AAGAACG
 TG CTGGTGGGA GGGC
 || ||||| ||||
 AC GACCACCCT CCG
 A A____
 GAM3794 DKFZP586G1122 3' TGA CTGGTGGGAGGGGAC 85794 C AAGAAC
 TG CTGGTGGGA GGGGC
 || ||||| ||||
 AC GACCACCCT CCCTG
 T C____
 GAM3794 DKFZP761D0211 3' TGCCTGGGGCACGGG 85795 T GAAAGA
 TGCCTGG GG ACGGG
 ||||| || ||||
 ACGGACC CC TGCCCC
 — G____
 GAM3794 DNAJA3 3' TGCTGGTGGGGCCTGGGGGCC 85796 C AAAGAAC
 TGC TGGTGGG GGGGCC
 || ||||| ||||
 ACG ACCACCC CCCC
 — CGGAC____
 GAM3794 FLJ12660 3' TGCCTGGTGGGAAGGC 85797 AAGAACG
 TGCCTGGTGGGA GGGC
 ||||| ||||

ACGGACCACCCT TCCG

GAM3794 FLJ13102 3' TGTGTGGTGGGAGAGGG 85798 CC AA AC
TG TGGTGGGA GA GGG
|| ||||| || |||
AC ACCACCCT CT CCC
AC _ _

GAM3794 FLJ14810 3' GCCTGGTAGGATGGGGC 85799 AAGAAC
GCCTGGTGGGA GGGGC
||||||| ||||
CGGACCATCCT CCCCCG

A _
GAM3794 FLJ31978 3' TGTCTGATGAGCGGGGC 85800 C AAAGAA
TG CTGGTGGG CGGGGC
|| ||||| ||||
AC GACTACTC GCCCCG
A C _

GAM3794 H-L(3)MBT 3' TGCCTGGTGGGGCAACACGGG 85801 AA A
TGCCTGGTGGG AG ACGGG
||||||| || ||||
ACGGACCACCC TT TGCCC
CG G

GAM3794 HCGIV.9 5' CCTGGCGAGGGCGGGGC 85802 AAAGAA
CCTGGTGGG CGGGGC
||||||| ||||
GGACCGCTC GCCCCG
CC _

GAM3794 HYA22 5' GCCTGGTGGGGGAGAGGGGAGC 85803 AA A _ |||
GGGGCCG GTGGG AGA CGGGGCC G
|||| ||| ||||| |
CACCC TCT GCCCCG C
CC CCCCTC |||

GAM3794 IMAGE3451454 3' TGTCTGGATGGAAACGGGGCC 85804 C _ AAGA
TG CTGG TGGGA ACGGGGCC
|| ||| |||| |||||
AC GACC ACCTT TGCCCCGG
A T _

GAM3794 IRF7 3' TGCCTGGTGCGGGGACTCTGGG 85805 _ AAGAAC
GCC TGCCTGGT GGGA GGGGCC
|||||| ||| |||||
ACGGACCA CCCT CCCCCG
CGC GAGA _

GAM3794 KIAA0053 3' CCTGGTGGGGTGGCAGAATGGG 85806 AA _ C
G CCTGGTGGG AGAA GGGG
|||||| ||| ||||
GGACCACCC TCTT CCCC
CACCG A

GAM3794 KIAA0082 3' GCCTGGCACTGGGATGGGGCC 85807 _ AAGAAC
GCCTGGT GGGA GGGGCC
|||| ||| |||||

CGGACCG CCCT CCCC GG
TGA A _____
GAM3794 KIAA0326 3' TGCCTGGTGTGGGGAGAAC 85808 _ AA
TGCCTGGTG GG AGAAC
||||||| || |||||
ACGGACCAC CC TCTTG
A CC
GAM3794 KIAA0513 5' TGCCTGGAGGGGAGGC 85809 T AAAGAAC
TGCCTGG GGG GGGGC
||||||| || |||||
ACGGACC CCC CTCCG
T _____
GAM3794 KIAA0513 3' CTGGTGGGGAAGGGGC 85810 AAA C
CTGGTGGG GAA GGGGC
||||||| || |||||
GACCACCC CTT CCCC G

GAM3794 KIAA0773 3' TGTGTGGTGGGGGAGGGGAC 85811 CC AA AAC
TG TGGTGGG AG GGGGC
|| ||||| || |||||
AC ACCACCC TC CCCTG
AC CC _____
GAM3794 KIAA1322 3' TGCCTGGCGGGAGAGGC 85812 AAGAAC
TGCCTGGTGGGA GGGGC
||||||| |||||
ACGGACCGCCCT CTCCG

GAM3794 KIAA1530 5' TGCCTGGTGGGATGAGGCGAGG 85813 AAGAA _
GCC TGCCTGGTGGGA CG GGGCC
||||||| || |||||
ACGGACCACCCT GC CCCGG
ACTCC T
GAM3794 KIAA1872 3' CCTTGGTGGGAGGTATTGACGG 85814 _ AAGA____
GG CCT GGTGGGA ACGGGG
|| ||||| |||||
GGA CCACCCT TGCCCC
A CCATAAC
GAM3794 KIAA1908 5' TGCCTGGCGGGGAGGGCGAGGC 85815 AA AA
C TGCCTGGTGGG AG CGGGGCC
||||||| || |||||
ACGGACCGCCC TC GCTCCGG
C_ CC
GAM3794 LNIR 3' TGCATGGTGGGAGAGA 85816 C AAGAAC
TGC TGGTGGGA GGGG
|| ||||| |||||
ACG ACCACCCT CTCT
T _____
GAM3794 MAD4 3' TGCTGGTGGGAAGGGCAAGGCC 85817 C A AA
TGC TGGTGGGAA G CGGGGCC
|| ||||| || |||||

ACG ACCACCCTT C GTTCCGG
 _ _ CC
 GAM3794 MMS19L 3' TGTCTGTGGGAAAGGCAG 85818 C G AA
 TG CTG TGGGAAAG CGG
 || ||| ||||| |||
 AC GAC ACCCTTTC GTC
 A _ C_
 GAM3794 NTN4 5' CCTCGGGAGGGAACGGGGCC 85819 GG AA
 CCT TGGGA GAACGGGGCC
 ||| |||| |||||
 GGA GCCCT CTTGCCCCGG
 _ CC
 GAM3794 PP1628 3' TGCTGGTGGGGGAAGG 85820 C AAA ACG
 TGC TGGTGGG GA GGG
 ||| ||||| || |||
 ACG ACCACCC CT TCC
 _ C_ _
 GAM3794 R32184_3 3' GCACACGCGGGGAGGGCGGGGC 85821 CTG_ AA AA
 C GC GTGGG AG CGGGGCC
 || |||| || |||||
 CG CGCCC TC GCCCCGG
 TGTG C_ CC
 GAM3794 SIMRP7 3' TGCTGGAACAGGGAGTGGGGC 85822 C T_ AAGAAC
 TGC TGG GGGG GGGGC
 ||| ||| ||| |||||
 ACG ACC CCCT CCCC
 _ TTGT CA_
 GAM3794 SNURF 3' TGCCTGGTGGAGGGG 85823 AAAGAAC
 TGCCTGGTGGG GGGG
 ||||| |||
 ACGGACCACCT CCCC

 GAM3794 TNFAIP3 3' TGCTTGGTAGGAGAGGAGGAAC 85824 C A AAC
 C TGC TGGTGGGA AG GGGGCC
 ||| ||||| || |||||
 ACG ACCATCCT TC CTTGG
 A C CT_
 GAM3794 UBCE7IP5 3' TGCTGGTGGGAAGCAGG 85825 C AGAA
 TGC TGGTGGGAA CGGG
 ||| ||||| |||
 ACG ACCACCCTT GTCC
 _ C_
 GAM3794 LOC142913 5' TGCCTGGTGTGGGGGTGC 85826 _ AAAGAAC _
 TGCCTGGTG GG GGG GC
 ||||| || ||| ||
 ACGGACCAC CC CCC CG
 A _ _ A
 GAM3794 LOC144289 3' TGCCTGGTGGAAAGAGGAA 85827 G AC
 TGCCTGGTGG AAAGA GGGG
 ||||| |||| |||

ACGGACCACC TTTCT CCTT

GAM3794 LOC146988 3' CCTGGTGGGGGAGAGGAGAGGC 85828 AA AC_
CCTGGTGGG AGA GGGGC
||||||| ||| ||||
GGACCACCC TCT CTCCG
CC CCT

GAM3794 LOC155376 5' CTGGTGGGAGAGGGA 85829 AA AC
CTGGTGGGA GA GGGG
||||||| || ||||
GACCACCCT CT CCCT

GAM3794 LOC158158 5' GCCCTCCCTGGAAGGACGGGGC 85830 GGTG_ A A
C GCCT GGAA GA CGGGGCC
||| ||| || |||||
CGGG CCTT CT GCCCCGG
AGGGA C _

GAM3794 LOC164714 3' TGCCGGTGGGAGGCCCTGGCC 85831 T AAGAACGG
TGCC GGTGGGA GGCC
||| ||||| |||
ACGG CCACCCT CCGG
_ CCGGGA_

GAM3794 LOC199986 3' TGGGTGCTGGGAAGGAACGGGG 85832 CC G A
C TG TG TGGGAA GAACGGGGC
|| || ||||| |||||
AC AC ACCCTT CTTGCCCG
CC G C

GAM3794 LOC199989 3' TGCAGCGGGAGGGGCGGGGCC 85833 CT AAGAA
TGC GGTGGGA CGGGGCC
|| ||||| |||||
ACG TCGCCCT GCCCCGG
_ CCCC_

GAM3794 LOC203611 5' TGCCTGGTGGGACAGCTTGGGC 85767 A AACG
TGCCTGGTGGGA AG GGGC
||||||| || |||
ACGGACCACCCT TC CCGG
G GAA_

GAM3794 LOC204820 3' TGCCTGGTGGGCAGGGAGGCC 85834 AAAGAAC
TGCCTGGTGGG GGGGCC
||||||| |||||
ACGGACCACCC CTCCGG
GTCC_

GAM3794 LOC221849 5' TGCCGGTGGGGAAGCCAAAGGC 85835 T A AAC
TGCC GGTGGG AAG GGGC
||| ||||| || ||||
ACGG CCACCC TTC TTCCG
_ C GGT

GAM3794 LOC253532 5' CTGGTGGGAGAGGGA 85829 AA AC
CTGGTGGGA GA GGGG
||||||| || |||

GACCACCCT CT CCCT

GAM3794 LOC254099 5' TGTCTGGTGGGTGGGAGGC 85836 C AAAGAAC
TG CTGGTGGG GGGGC
|| ||||| ||||
AC GACCACCC CTCCG
A ACC_

GAM3794 LOC254875 5' CTGGTGGGAGAGGGA 85829 AA AC
CTGGTGGGA GA GGGG
||||||| || ||||
GACCACCCT CT CCCT

GAM3794 LOC256158 5' TGCTGGTGGGAGCAGGGC 85837 C AAA A
TGC TGGTGGG GA CGGGGC
||| ||||| || |||||
ACG ACCACCC CT GTCCCG

GAM3794 LOC91050 3' GCCTGGTGGGGAGGGC 85838 AAAGAAC
GCCTGGTGGG GGGGC
||||||| ||||
CGGACCACCC TCCCG
C_

GAM3795 LOC204010 3' TATTTTCTGTCAACCTTATTT 85841 A _
TATT TTT TCAACCTTATTT
|||| ||| |||||||||
ATAA AGA AGTTGGAATAAA
A C

GAM3796 IKBKB 3' GCAGTGCCACGGAGGGCTGC 85844 _ TGT
GCA CCCGCG AGGGCTGC
||| ||||| |||||||
CGT GGGTGC TCCCGACG
CAC C_

GAM3796 JPH2 3' CCCCTGCAGGCTGCAT 85845 GCG G
CCC TGTAGG CTGCAT
||| ||||| |||||
GGG ACGTCC GACGTA
G_ _

GAM3796 MMP2 3' GCAGCCCAAAGCAGGGCTGC 85846 _ CGT
GCA CCCG GTAGGGCTGC
||| ||||| |||||||
CGT GGGT CGTCCCGACG
C TT_

GAM3796 ARHGEF11 3' GCGTGCGCGTGTACACACAT 85847 ACC GG T
GC CGCGTGTA GC GCAT
|| ||||| || ||||
CG GCGCACAT TG TGTA
CAC G_ _

GAM3796 BAIAP1 5' GCGCCCGCGAGCTTTGTTTGCA 85848 A T AGGGC_
T GC CCCGCG GT TGCAT
|| ||||| || |||||

CG GGGCGC CG ACGTA
 C T AAACAA
 GAM3796 DKFZP434K1772 5' GCACCCGCGGCACAGCTGC 85849 T G
 GCACCCGCG GTA GGCTGC
 ||||| |||||
 CGTGGGCGC CGT TCGACG
 _ G
 GAM3796 DKFZP564C196 3' CCTATGAGGGCTGCAT 85850 GC T
 CC GTG AGGGCTGCAT
 || |||||
 GG TAC TCCCGACGTA
 A _
 GAM3796 FLJ10079 3' GCCCCTCAGGGCTGCAT 85851 A GCGTG
 GC CCC TAGGGCTGCAT
 || |||||
 CG GGG GTCCCGACGTA
 _ A _
 GAM3796 FLJ11362 5' AAGCCTCATGCAGGGCTG 85852 ACCCG
 AAGC CGTGTAGGGCTG
 ||| |||||
 TTCG GTACGTCCCGAC
 GA _
 GAM3796 FLJ31528 3' GCTTCGTGTGTAGGAAGCA 85853 ACC C CT
 GC CG GTGTAGGG GCA
 || ||||| |||
 CG GC CACATCCT CGT
 AA _ A T _
 GAM3796 KIAA0544 3' GCACCTCCCAGCAGGCTGCAT 85854 CGCGT G
 GCACC GTAGG CTGCAT
 |||| |||||
 CGTGG CGTCC GACGTA
 AGGGT _
 GAM3796 KIAA1155 3' AAGACCCAGGGCTGC 85855 C GCGTGT
 AAG ACCC AGGGCTGC
 |||| |||||
 TTC TGGG TCCCGACG
 _ _
 GAM3796 PEPP3 3' AAGCATCTCCACTGAGGCTGCA 85856 C _ G TA
 T AAGCA CCGC TG GGGCTGCAT
 |||| |||||
 TTCGT GGTG AC TCCGACGTA
 AGA _ _
 GAM3796 SFRS12 5' ACCGTTCTGTGTTGGCTGCAT 85857 CG _ AG
 ACC CGTGT GGCTGCAT
 || |||||
 TGG GCACA CCGACGTA
 CAA A _
 GAM3796 LOC122792 3' AAGCATGTGTGTGTGCGCGCGC 85858 CCCGC AGG _
 AT AAGCA GTGT GC TGCAT
 |||| ||| |||||

		TTCGT CACA CG GCGTA	
		ACACA CG_ C	
GAM3796	LOC144893 5'	GCATCCCTGCATGGCTGC 85859	_ GCG G
		GCA CCC TGTA GGCTGC	
		CGT GGG ACGT CCGACG	
		A _ _ A	
GAM3796	LOC146795 3'	AAGACCTGCACAGGTTGCA 85860	C CGC TG GC
		AAG ACC G TAGG TGCA	
		TTC TGG C GTCC ACGT	
		_ A_ GT A_	
GAM3796	LOC206360 5'	CCACCTGAGAGGGCTGCAT 85861	G T_
		CCGC TG AGGGCTGCAT	
		GGTG AC TCCCGACGTA	
		G TC	
GAM3796	LOC253289 3'	GCCCCTCCCCAGGGCTGCAT 85862	A GCGTG
		GC CCC TAGGGCTGCAT	
		CG GGG GTCCCGACGTA	
		_ AGGG_	
GAM3796	LOC91548 3'	ACGTGTCTGGGGGCTGCAT 85863	A_
		GCGTGT GGGCTGCAT	
		TGCACA CCGACGTA	
		GACC	
GAM3796	LOC91917 3'	GCAGTACCTGAACTGGGCTGCA 85864	CCC G TA_
	T	GCA GC TG GGGCTGCAT	
		CGT TG AC CCGACGTA	
		CA_ G TTGA	
GAM3797	CKB 3'	TAGTTTATTTTCAGCATCA 85867	ATCGAT
		TAGTTTATTTCA TATCA	
		ATCAAATAAAGT GTAGT	
		C_	
GAM3797	MAIL 3'	TAGTTTATTTAAAACCATCAG 85868	CAATC
		TAGTTTATTT GATTATCAG	
		ATCAAATAAA TTGGTAGTC	
		TT_	
GAM3798	CYP1A1 3'	TAGAGAAGGGAGACCAA 85871	ACGCAA A
		TAGAGG AG GAGACCAA	
		ATCTCT TC CTCTGGTT	
		_ _ _ C	
GAM3798	HDGF 3'	TAGAGAGGCATAGAGAGACCA 85872	AC A
		TAGAGG GCA AGAGAGACCA	

		ATCTCT CGT TCTCTCTGGT	
		C_ A	
GAM3798	POLG	5' GAAGACGTGGAGAGAGAC 85873	CAA
		GAGGACG AGAGAGAC	
		CTTCTGC TCTCTCTG	
		ACC	
GAM3798	ARS2	5' TAGAGGACCGAAGAGAG 85874	GCA
		TAGAGGAC AAGAGAG	
		ATCTCCTG TTCTCTC	
		GC_	
GAM3798	FLJ12688	3' TAGAGGACAGTGAAAAA 85875	CAAA
		TAGAGGACG GAGAGA	
		ATCTCCTGT CTTTT	
		CA_	
GAM3798	KIAA0469	3' GAGGACGCAAGAGCCA 85876	AAG A
		GAGGACGCA AGAG CCA	
		CTCCTGCGT TCTC GGT	
		— —	
GAM3798	RLUCL	3' CAGAGGACGCAGGGACCA 85877	AAGA A
		TAGAGGACGCA G GACCA	
		GTCTCCTGCGT C CTGGT	
		— C	
GAM3798	LOC120071	3' GGGGCAGAGAGAGACCA 85878	AC A
		GG GCA AGAGAGACCA	
		CC CGT TCTCTCTGGT	
		C_ C	
GAM3798	LOC143287	3' TAGGGGGCGCAAAGAAGAGA 85879	A A _
		TAG GG CGCAAAGA GAGA	
		ATC CC GCGTTTCT CTCT	
		C C T	
GAM3798	LOC146328	5' GAGGCGCAGAGAGAC 85880	A AA
		GAGG CGCA GAGAGAC	
		CTCC GCGT CTCTCTG	
		— —	
GAM3798	LOC220018	5' GGAGGCAGAGAGACCA 85881	C AA
		GGA GCA GAGAGACCA	
		CCT CGT CTCTCTGGT	
		C _	
GAM3799	ACHE	3' AGAGAGGAGGAGAAAAGAA 85884	_ CA
		AGA AGGAGGAGAAA AGAA	

			TCT TCCTCCTCTTT TCTT		
			C —		
GAM3799	ADD1	3'	AAAGGAGGGGATAAAGGAAGA 85885	A	AACAA
			GAAGGAGG GA GAAGA		
			TTTCCTCC CT CTTCT		
			C ATTTT		
GAM3799	ADD1	3'	AAAGGAGGGGATAAAGGAAGA 85885	A	AACAA
			GAAGGAGG GA GAAGA		
			TTTCCTCC CT CTTCT		
			C ATTTT		
GAM3799	AP1M1	3'	GAAGGAAGACAAGAAG 85886	GAAA	
			GAAGGAGGA CAAGAAG		
			CTTCCTTCT GTTCTTC		
GAM3799	ARPC2	5'	AGGGGAAGGAGAAACAAG 85887	AA	
			AG GGAGGAGAAACAAG		
			TC CTTCCTCTTTGTTC		
			CC		
GAM3799	ASTN	3'	AGAAGGAGAGGGTACAGAGGA 85889	G	AAACA A
			AGAAGGAG AG AGA GA		
			TCTTCCTC TC TCT CT		
			_ CCATG C		
GAM3799	ASTN	3'	GAAAGAGGAGGCCAAAAAA 85888	AAA	
			GAAGGAGGAG CAAGAAG		
			CTTTCTCCTC GTTTTTT		
			CG_		
GAM3799	BAZ1B	3'	AGAAGGGGAGATTTCAGGAA 85890	A	AA A
			AGAAGG GGAGA CA GAA		
			TCTTCC CCTCT GT CTT		
			_ AA C		
GAM3799	BGN	3'	GAGGAGGAGGAACAGAA 85891	A	A A
			GA GGAGGAG AACA GAA		
			CT CCTCCTC TTGT CTT		
			_ C _		
GAM3799	BIG1	5'	AGGAGGAGGAGAGGAAG 85892	A	AACAA
			AG AGGAGGAGA GAAG		
			TC TCCTCCTCT CTTT		
			C C_		
GAM3799	CANX	3'	GAGGGAGAAGAAATCACAGA 85893	A	_ _
			GA GGAGGAGAAA CA AGA		

			CT CCTCTTCTTT GT TCT		
			C A G		
GAM3799	CAPN1	3'	GGAGGAGAGGGGACAGGAGGA 85894	A__	A A
			GGAGGAGA ACA GA GA		
			CCTCCTCT TGT CT CT		
			CCCC C C		
GAM3799	CARPX	3'	AGAAGGAGAGAGAAGCAAGAAG 85895	_	A
			AGAAGGAG GAGAA CAAGAAG		
			TCTTCCTC CTCTT GTTCTTC		
			T C		
GAM3799	CHST6	3'	AGAGGAGGAGGGGCAAGA 85896	A	AAA
			AGA GGAGGAG CAAGA		
			TCTCCTCCTC GTTCT		
			_ CCC		
GAM3799	CKTSF1B1	3'	AGGAGGAGGAGGAAAGGAG 85897	A	_ CA
			AG AGGAGGAG AAA AG		
			TC TCCTCCTC TTT TC		
			C C CC		
GAM3799	CORT	3'	GAAGGAGGAGAGGAAAGA 85898	AAC	
			GAAGGAGGAGA AAGA		
			CTTCCTCCTCT TTCT		
			CCT		
GAM3799	CTF1	3'	GAAGGAGGGAGAGCAAGAAAA 85899	_	AA
			GAAGGAGG AGA CAAGAAGA		
			CTTCCTCC TCT GTTCTTTT		
			C C_		
GAM3799	CX3CR1	3'	GAAGGAGGAGGCAATGGGGAAT 85900	AAA	GAA_
			GAAGGAGGAG CAA GAAT		
			CTTCCTCCTC GTT CTTA		
			C_ ACCC		
GAM3799	DACH	5'	AGACGGAGGAGAAGCGAGA 85901	A	ACA
			AGA GGAGGAGAA AGA		
			TCTCCTCCTCTT TCT		
			G CGC		
GAM3799	DACH	5'	AGAAGGGGGAGAAAAGGAG 85902	A	CA A
			AGAAGG GGAGAAA AG AG		
			TCTTCC CCTCTTT TC TC		
			C _ C		
GAM3799	DDX20	5'	AGAGGGAGGAGAGGAAAGA 85903	A	AAC
			AGA GGAGGAGA AAGA		

			TCT CCTCCTCT TTCT		
			C CCT		
GAM3799	DLG5	3'	AGATGGAGGAGAAACGAGA 85904	A	A
			AGA GGAGGAGAAAC AGA		
			TCT CCTCCTCTTTG TCT		
			A C		
GAM3799	DNM2	3'	AGGAGGAGGAGGAGGAGAGGAA 85905	A	AAACA A
	T		AG AGGAGGAG AGA GAAT		
			TC TCCTCCTC TCT CTTA		
			C CTCC_ C		
GAM3799	DSC1	5'	AGTAGGAGGAGCAACGGGAGAA 85906	A	A AA A
	T		AG AGGAGGAG AAC GA GAAT		
			TC TCCTCCTC TTG CT CTTA		
			A G CC _		
GAM3799	DSC1	5'	AGTAGGAGGAGCAACGGGAGAA 85906	A	A AA A
	T		AG AGGAGGAG AAC GA GAAT		
			TC TCCTCCTC TTG CT CTTA		
			A G CC _		
GAM3799	DYRK1B	3'	AAAAGGGGGAGAGGGGCCCAAG 85907	A	AA_____
			AGAAGG GGAGA CAAG		
			TTTTCC CCTCT GTTC		
			C CCCCCG		
GAM3799	EN2	3'	AGGAGGAGGAGGAGAAGA 85908	A	AAACA
			AG AGGAGGAG AGAAGA		
			TC TCCTCCTC TCTTCT		
			C C_____		
GAM3799	EN2	3'	AGAAGGAGGAGGAGGAAG 85909		AAACAA
			AGAAGGAGGAG GAAG		
			TCTTCCTCCTC CTTC		
			CTC_____		
GAM3799	ESRRG	3'	GAAGGATGAGAAAAGAGAGGAA 85910	G	CA A
	T		GAAGGA GAGAAA AGA GAAT		
			CTTCCT CTCTTT TCT CTTA		
			A TC C		
GAM3799	EXTL2	3'	AGAAGGAAGAGGAGAAG 85911		AAACA
			AGAAGGAGGAG AGAAG		
			TCTTCCTTCTC TCTTC		
			C_____		
GAM3799	EXTL2	3'	AGAAGGAGGAATAAGA 85912		AAAC
			AGAAGGAGGAG AAGA		

			TCTTCCTCCTT TTCT			
			A__			
GAM3799	FBXL11	3'	AGAGAGAGGGGGAACAAGGAGA 85913	AG	AGA	A
			AGA GAGG AACAAAG AGA			
			TCT CTCC TTGTTC TCT			
			CT CCC C			
GAM3799	FCER1G	3'	AGAAGGGTGGGACAAGAGA 85914	A_	A AA	A
			AGAAGG GG GA CAAGA GA			
			TCTTCC CC CT GTTCT CT			
			CA _ _ _			
GAM3799	FGF12	3'	GAAGGAAGGGAAGGGGAAG 85915	A	ACAA	
			GAAGGAGG GAA GAAG			
			CTTCCTTC CTT CTTC			
			C CCC_			
GAM3799	FMR2	3'	AGGAGGAGGATGGAAAGAGAAT 85916	A	GAAAC	A
			AG AGGAGGA AAGA GAAT			
			TC TCCTCCT TTCT CTTA			
			C ACCT_ _			
GAM3799	FOX E3	3'	GAGGGAGAAGAAATGAGA 85917	A	CA	
			GA GGAGGAGAAA AGA			
			CT CCTCTTCTTT TCT			
			C AC			
GAM3799	FOX F1	3'	GAAGGAGGGGGACCTCAGCAGA 85918	A_	AACA	A
	AT		GAAGGAGG GA AG AGAAT			
			CTTCCTCC CT TC TCTTA			
			CC GGAG G			
GAM3799	GAS7	3'	AGAAGGAGCGGGAAGCAAA 85919	GA_	A	
			AGAAGGAG GAA CAAG			
			TCTTCCTC CTT GTTT			
			GCC C			
GAM3799	GAS7	3'	AGAAGGAGCGGGAAGCAAA 85919	GA_	A	
			AGAAGGAG GAA CAAG			
			TCTTCCTC CTT GTTT			
			GCC C			
GAM3799	GJA5	3'	AGAGGGAGGAGAAGCCAAG 85920	A	A_	
			AGA GGAGGAGAA CAAG			
			TCTCCTCCTCTT GTTC			
			C CG			
GAM3799	HLALS	3'	AGAGGAAGGAGAACTGGAAAAG 85921	A	ACA_	
	A		AGA GGAGGAGAA AGAAGA			

			TCT CTCCTCTT TTTCT		
			C GACC		
GAM3799	HMGB3	3'	AGAGTGAGGAGAACACGAGA	85922	AG _ A
			AGA GAGGAGAA AC AGA		
			TCT CTCCTCTT TG TCT		
			CA G C		
GAM3799	IL2RG	3'	AGAGGGAGGGAGGAAGAA	85923	A A AACAA
			AGA GGAGG GA GAAGAA		
			TCT CCTCC CT CTTCTT		
			C _ C _		
GAM3799	KCNJ16	3'	AGAAGGAGAAAGGGAAG	85924	CAA
			AGGAGGAGAAA GAAG		
			TCTTCCTCTTT CTTC		
			CC_		
GAM3799	KRTHB1	3'	GAAGGGGAGAGGCAGGAAG	85925	A AA A
			GAAGG GGAGA CA GAAG		
			CTTCC CCTCT GT CTTC		
			_ CC C		
GAM3799	LAMC1	3'	AGAAGGAAGAGGGGCAGGAGA	85926	AAACA A
			AGAAGGAGGAG AG AGA		
			TCTTCCTTCTC TC TCT		
			CCCG_ C		
GAM3799	LGR6	3'	GAAGAGAGGGGAAGAGAAGAAT	85927	_ A ACA
			GAAG GAGG GAA AGAAGAAT		
			CTTC CTCC CTT TCTTCTTA		
			T C C _		
GAM3799	LRP4	3'	AGGAGGAGGAGGACAAG	85928	A AA
			AG AGGAGGAG ACAAG		
			TC TCCTCCTC TGTTC		
			C C _		
GAM3799	MAPK10	5'	GAAGAAGGAGAAACAGGA	85929	A
			GAAGGAGGAGAAACA GA		
			CTTCTTCCTCTTTGT CT		
			C		
GAM3799	MAPT	3'	GGAGGGGGAAGAAAAAGAAT	85930	A_ AC
			GGAGG GAA AAGAAGAAT		
			CCTCC CTT TTTTCTTA		
			CC CT		
GAM3799	MAPT	3'	GGAGGGGGAAGAAAAAGAAT	85930	A_ AC
			GGAGG GAA AAGAAGAAT		

			CCTCC CTT TTTTCTTA		
			CC CT		
GAM3799	MAPT	3'	GGAGGGGGAAGAAAAAGAAT 85930	A_	AC
			GGAGG GAA AAGAAGAAT		
			CCTCC CTT TTTTCTTA		
			CC CT		
GAM3799	MAPT	3'	GGAGGGGGAAGAAAAAGAAT 85930	A_	AC
			GGAGG GAA AAGAAGAAT		
			CCTCC CTT TTTTCTTA		
			CC CT		
GAM3799	MAZ	3'	AGGAGCAGGAGAAACAAA 85931	A	G
			AG AG AGGAGAAACAAG		
			TC TC TCCTCTTTGTTT		
			C G		
GAM3799	MCC	3'	GAAAGAGGAGAAACGAGA 85932		A
			GAAGGAGGAGAAAC AGA		
			CTTTCTCCTCTTTG TCT		
			C		
GAM3799	MSI1	3'	AAAGGAGGGGAAATCTGAA 85933	A	CAA
			GAAGGAGG GAAA GAA		
			TTTCCTCC CTTT CTT		
			C AGA		
GAM3799	MYEOV	3'	AGGAAGAGGAGAGGGTAGGAGA 85934	A	AACA A
			AG AGGAGGAGA AG AGA		
			TC TTCTCCTCT TC TCT		
			C CCCA C		
GAM3799	MYO1A	3'	GGAGGAGAGAACAAGAAG 85935	_	
			GGAGGAGA AACAAGAAG		
			CCTCCTCT TTGTTCTTC		
			C		
GAM3799	NCOA3	3'	AGAAGGAGGGGGGAAAAACA 85936	_____	
			AGAAGGA GGAGAAACA		
			TCTTCCT CCTTTTGT		
			CCCC		
GAM3799	NEDD4	5'	AGGAGGAGGAGGAGAAG 85937	A	AAACA
			AG AGGAGGAG AGAAG		
			TC TCCTCCTC TCTTC		
			C C_____		
GAM3799	NID	3'	GGAGGGAGAAACCAAGGAG 85938	_	_ A
			GGAGG AGAAAC AAG AG		

		CCTCC TCTTTG TTC TC	
		C G C	
GAM3799 NKX3A	3'	AAAAGGAGGGAAGGAAGAA 85939	A ACAA
		AGAAGGAGG GAA GAAGAA	
		TTTTCCTCC CTT CTTCTT	
		_ C _	
GAM3799 NRIP1	5'	AAGGAGGAGGAGAAGAA 85940	AAACA
		AAGGAGGAG AGAAGAA	
		TTCCTCCTC TCTTCTT	
		C _	
GAM3799 PDE4D	3'	GGAGGAGAGGAATGAGAAT 85941	AAC GA
		GGAGGAGA AA AGAAT	
		CCTCCTCT TT TCTTA	
		CC_ AC	
GAM3799 PDE6D	3'	AAGGAGGAGACAAGGAG 85942	AA A
		AAGGAGGAGA CAAG AG	
		TTCCTCCTCT GTTC TC	
		_ C	
GAM3799 PHF1	3'	GAAGGATGGGAGGGGTCAGGAA 85943	_ AAA_ A
		GAAGGA GGAG CA GAA	
		CTTCCT CCTC GT CTT	
		AC CCCA C	
GAM3799 PHF1	3'	GAAGGATGGGAGGGGTCAGGAA 85943	_ AAA_ A
		GAAGGA GGAG CA GAA	
		CTTCCT CCTC GT CTT	
		AC CCCA C	
GAM3799 PIK3CD	3'	AGGAGGCTGAGGCAAGAAGAAT 85944	A_ AA
		AGGAGG GA CAAGAAGAAT	
		TCCTCC CT GTTCTTCTTA	
		GA CC	
GAM3799 PLXNA2	3'	AGAAGGAAGGGAGACAGAAA 85945	A A A
		AGAAGGAGG GA ACA GAAG	
		TCTTCCTTC CT TGT CTTT	
		C C _	
GAM3799 PMX1	5'	AGAAGGGGTGGGAGAGAAGAAT 85946	A_ ACAA
		AGAAGG GGAGA GAAGAAT	
		TCTTCC CCTCT CTTCTTA	
		CCAC _	
GAM3799 PMX1	5'	AGAAGGGGTGGGAGAGAAGAAT 85946	A_ ACAA
		AGAAGG GGAGA GAAGAAT	

TCTTCC CCTCT CTTCTTA
 CCAC _____
 GAM3799 POU2AF1 3' AGAAGGGAGGGAGGGGAAGAAT 85947 _ A AACAA
 AGAAGG AGG GA GAAGAAT
 ||||| ||| || |||||
 TCTTCC TCC CT CTTCTTA
 C _ CCC_
 GAM3799 PPP1R12B 3' GAGGGGGAAAAACAAAAGA 85948 A A A
 GA GG GGAGAAACAAGA GA
 || || ||||| ||
 CT CC CCTTTTGT TTTT CT
 C _ _
 GAM3799 PPP2R5A 3' AGGAAGAGGAGGAATGAA 85949 A AAACAA _
 AG AGGAGGAG GAA GAA
 || ||||| ||| ||
 TC TTCTCCTC CTT CTT
 C _ _ A
 GAM3799 PRKCM 5' AGGAGGAGGAGGGCGAGGAGAA 85950 A AAACA A
 AG AGGAGGAG AG AGAA
 || ||||| || |||
 TC TCCTCCTC TC TCTT
 C CCGC_ C
 GAM3799 PTK2B 3' AGAAAGAGGAGGAGTAAGA 85951 AAAC
 AGAAGGAGGAG AAGA
 ||||| |||
 TCTTTCTCCTC TTCT
 CTCA
 GAM3799 RAB33A 5' AGAGGAGGAGAGAGGGAGGAGA 85952 A AACAA_ A
 AGA GGAGGAGA AG AGA
 ||| ||||| || |||
 TCT CCTCCTCT TC TCT
 _ CTCCC C
 GAM3799 RAD23B 3' AAGGGGAAAAGACAGGGAGA 85953 A _ AGA
 AAGG GGAGAA ACA AGA
 ||| ||||| ||| |||
 TTCC CCTTTT TGT TCT
 _ C CCC
 GAM3799 RORB 5' AGAGGGAGAAGGAACAAG 85954 A A
 AGA GGAGGAG AACAAG
 ||| ||||| |||||
 TCT CCTCTTC TTGTTC
 C C
 GAM3799 RTN3 5' AGAGGGAGGGGAAATAGA 85955 A A CA
 AGA GGAGG GAAA AGA
 ||| ||||| ||| |||
 TCT CCTCC CTTT TCT
 C C A_
 GAM3799 SC5DL 3' AGAAGAGGAGGAATAAGA 85956 G A C
 AGAAG AGGAG AA AAGA
 ||||| ||||| || |||

			TCTTC TCCTC TT TTCT			
			— C A			
GAM3799	SET7	5'	AGGAGGAGGAGGAAGA	85957	A	AAACAA
			AG AGGAGGAG GAAGA			
			TC TCCTCCTC CTTCT			
			C ———			
GAM3799	SHMT2	3'	AGGAGGATGAGAAACAGGA	85958	A G A	
			AG AGGA GAGAAACA GA			
			TC TCCT CTCTTTGT CT			
			C A C			
GAM3799	SLC29A1	3'	AGAGGAGGAGGCGCAGGGGAGA	85959	A	AAACA A__
	AT		AGA GGAGGAG AG AGAAT			
			TCT CCTCCTC TC TCTTA			
			— CGCG_ CCC			
GAM3799	SLC2A2	5'	AGGAGGAGGAGCAAGGAGA	85960	AAA A	
			AGGAGGAG CAAG AGA			
			TCCTCCTC GTTC TCT			
			CTC C			
GAM3799	SLC5A1	3'	GGAGGAGGACGGACAGGAAAA	85961	AA__ A	
			GGAGGAG ACA GAAGA			
			CCTCCTC TGT CTTTT			
			CTGCC C			
GAM3799	SLC7A8	3'	GAAGGAGAGAGTAGCCAGGGAA	85962	_ AAA_ A_	
			GAAGGAG GAG CA GAA			
			CTTCCTC CTC GT CTT			
			T ATCG CC			
GAM3799	SNAP25	3'	AGAGGAGACAGGAGGAA	85963	AA A A	
			GGAGGAGA CA GA GAA			
			TCTCCTCT GT CT CTT			
			— C C			
GAM3799	SNAP25	3'	AGAGGAGACAGGAGGAA	85963	AA A A	
			GGAGGAGA CA GA GAA			
			TCTCCTCT GT CT CTT			
			— C C			
GAM3799	SNX9	3'	AGAAGAAAAATCAAGTGGGGAG	85964	_ A__	
	AAT		GGAGGAGAAA CAAG AGAAT			
			TCTTCTTTTT GTTC TCTTA			
			A ACCCC			
GAM3799	SPOCK	3'	AAAGGAGGAGAAACAGA	85965	A	
			GAAGGAGGAGAAACA GA			

TTTCCTCCTCTTTGT CT

GAM3799 SRGAP2 3' GATGGAGGAGAGGCAAGA 85966 A AA
GA GGAGGAGA CAAGA
|| ||||| ||||
CTCCTCCTCT GTTCT
A CC

GAM3799 SRRM1 3' AGAAGGAGGGGGAACAAAA 85967 AGA
AGAAGGAGG AACAAGA
||||||| |||||
TCTTCCTCC TTGTTTT
CCC

GAM3799 TAGLN2 3' GAAGAAGGAGAGACAGAA 85968 A A
GAAGGAGGAGA ACA GAA
||||||| ||| |||
CTTCTTCCTCT TGT CTT
C _

GAM3799 THBD 3' GGAGGAGAAAAGTAGGAAGAAT 85969 _AA_
GGAGGAGAAA C GAAGAAT
||||||| | |||||
CCTCCTCTTT G CTTCTTA
T ATC

GAM3799 TIRAP 3' AAGAAGAGCAGGAAGAA 85970 AAA A
AGGAGGAG CA GAAGAA
||||||| || |||||
TTCTTCTC GT CTTCTT
_ C

GAM3799 TPD52L2 3' GAAGGAGGAGGAGGAAGAAG 85971 AAAC
GAAGGAGGAG AAGAAG
||||||| |||||
CTTCCTCCTC TTCTTC
CTCC

GAM3799 TPST1 3' AAAAGAGAACAAGAGGA 85972 A A
GGAGGAGAA CAAGA GA
||||||| ||||| ||
TTTTCTCTT GTTCT CT
_ C

GAM3799 TRPC5 5' AGAAGGAGGGAGGAAGGAAG 85973 A AACAA
AGAAGGAGG GA GAAG
||||||| || |||
TCTTCCTCC CT CTTC
_ CCTTC

GAM3799 VAMP1 3' AAGGAGGAGCCCAGAGGAGA 85974 AAA _ A
AAGGAGGAG CA AG AGA
||||||| || ||| |||
TTCCTCCTC GT TC TCT
GG_ C C

GAM3799 VANGL2 3' AGAAGCGAGGAGAGAAG 85975 _ AACAA
AGAAG GAGGAGA GAAG
||||| ||||| |||

			TCTTC CTCCTCT CTTC		
			G _____		
GAM3799	VAT1	3'	AGAAGGAGGTGGGAAACAGGA	85976	A__ A
			AGAAGGAGG GAAACA GA		
			TCTTCCTCC CTTTGT CT		
			ACC C		
GAM3799	XPNPEP2	3'	AGAAGGAGGATGAATGCAAAG	85977	_ ACAA
			AGAAGGAGGA GAA GAAG		
			TCTTCCTCCT CTT TTTC		
			A ACG_		
GAM3799	XYLB	3'	AGGAGGGGGAGAGGAGAGA	85978	A A AACA A
			AG AGG GGAGA AGA GA		
			TC TCC CCTCT TCT CT		
			C C CC__ _		
GAM3799	YWHAE	3'	GAAGGAGAAGAAACAAAAGAAT	85979	A
			GAAGGAGGAGAAACAAGA GAAT		
			CTTCCTCTTCTTTGTTTT CTTA		

GAM3799	YWHAZ	3'	AGGAGGAAGAAAGAGGAAG	85980	_ CAA
			AGGAGGA GAAA GAAG		
			TCCTCCT CTTT CTTC		
			T CTC		
GAM3799	ZIC1	5'	AGGAGGAGGAGGAACAAGA	85982	A A
			AG AGGAGGAG AACAAGA		
			TC TCCTCCTC TTGTTCT		
			C C		
GAM3799	ZIC1	5'	AGGAGGAGGAGGAACAAGAGGA	85981	A A A
			AG AGGAGGAG AACAAGA GA		
			TC TCCTCCTC TTGTTCT CT		
			C C C		
GAM3799	ZIC3	5'	GAGGGAGGAGAAGGGAGGAGAA	85983	A ACA A
			GA GGAGGAGAA AG AGAA		
			CT CCTCCTCTT TC TCTT		
			C CCC C		
GAM3799	ZNF207	5'	AGAAGCAGGAGAAACGAG	85984	G A
			AGAAG AGGAGAAAC AG		
			TCTTC TCCTCTTTG TC		
			G C		
GAM3799	ADPRH	5'	GAGGAGCAAGAAGAAT	85985	AAA
			GAGGAG CAAGAAGAAT		

CTCCTC GTTCTTCTTA

GAM3799 ARFGAP1 3' GAAGGAGGAGGAACGACGA 85986 A AA_
GAAGGAGGAG AAC GA
||||||| ||
CTTCCTCCTC TTG CT
C CTG

GAM3799 ARHGEF11 3' AGGAGGAGTGGGGACGCAGAGG 85987 AA__ A_ A
A AGGAGGAG AC AGA GA
||||| || |||
TCCTCCTC TG TCT CT
ACCCC CG C

GAM3799 ATP9A 3' AGAAGGGGGAGAAATAAAA 85988 A C
AGAAGG GGAGAAA AAGA
||||| ||||| |||
TCTTCC CCTCTTT TTTT
C A

GAM3799 BMF 3' AGAAGGGAGAGGGAAACGTGA 85989 __ A AA
AGAAGG AGG GAAAC GA
||||| ||| ||||| ||
TCTTCC TCC CTTTG CT
CTC _ CA

GAM3799 C17orf31 3' AGGAAGAGGAGCAGCAGGAAG 85990 A AAA A
AG AGGAGGAG CA GAAG
|| ||||| || |||
TC TTCTCCTC GT CTTC
C GTC C

GAM3799 C5orf6 3' AGAGGGAGAAGAGCCAGGGGAG 85991 A AA A__ A
GAAT AGA GGAGGAGA CA GA GAAT
||| ||||| || || |||
TCT CCTCTTCT GT CT CTTA
C CG CCC C

GAM3799 C5orf7 3' GAGGGGGAGAAAAAGAA 85992 A A C
GA GG GGAGAAA AAGAA
|| || ||||| |||||
CT CC CCTCTTT TTCTT
C _ _

GAM3799 CACNG4 3' AGGAGGGGGAAGAAAAGAA 85993 A_ ACA
AGGAGG GAA AGAAGAA
||||| ||| |||||
TCCTCC CTT TTTCTT
CC C__

GAM3799 CDH22 3' AGAGGAGGAGGAATGGAAGA 85994 A AAACAA
AGA GGAGGAG GAAGA
||| ||||| |||
TCT CCTCCTC CTTCT
_ CTTAC_

GAM3799 CED-6 3' AGAAGAAAATATGAGAAGA 85995 ACA_
GGAGGAGAA AGAAGA
||||||| |||||

TCTTCTTTT TCTTCT
 ATAC
 GAM3799 COL4A3BP 5' AGCAGGAGGAGGGACGAAG 85996 A AA AA
 AG AGGAGGAG AC GAAG
 || ||||| || ||||
 TC TCCTCCTC TG CTTC
 G CC _
 GAM3799 CORO1A 5' AGGAGGAGGAGGAAGA 85957 A AAACAA
 AG AGGAGGAG GAAGA
 || ||||| ||||
 TC TCCTCCTC CTTCT
 C _
 GAM3799 DJ726C3.2 3' AGAGGGAGGAGAAGAGGAGGA 85997 A ACAA A
 AGA GGAGGAGAA GA GA
 ||| ||||| || ||
 TCT CCTCCTCTT CT CT
 C CTC_ C
 GAM3799 DKFZp547I224 5' AAAAGAGGGTAAGAAGAA 85998 AGAAAC
 GAAGGAGG AAGAAGAA
 ||||| |||||
 TTTTCTCC TTCTTCTT
 CA_
 GAM3799 DKFZp547M072 3' AGGAGGAGGAGGAAGA 85957 A AAACAA
 AG AGGAGGAG GAAGA
 || ||||| ||||
 TC TCCTCCTC CTTCT
 C _
 GAM3799 DKFZP586C1324 3' AGAAGGAAGGAAGGGAGA 85999 A ACA
 AGAAGGAGG GAA AGA
 ||||| ||| |||
 TCTTCCTTC CTT TCT
 _ CCC
 GAM3799 DKFZp761B0514 3' GAAGGAGGAGGAGAAA 86000 AAACA
 GAAGGAGGAG AGAAG
 ||||| ||||
 CTTCTCCTC TCTTT
 C_
 GAM3799 DKFZp761G2113 3' GGAGGAGAGGCAGGGGGAGGAA 86001 AA A_ A
 T GGAGGAGA CA GA GAAT
 ||||| || |||||
 CCTCCTCT GT CT CTTA
 CC CCCC C
 GAM3799 DNAJA4 3' AGAAGACTGGGAAACAAGAGGA 86002 A_ A A
 AT AGAAGG GG GAAACAAGA GAAT
 ||||| || ||||| ||||
 TCTTCT CC CTTTGTTCT CTTA
 GA _ C
 GAM3799 DUSP10 3' AAAAGGGGGAGAAACAAG 86003 A
 AGAAGG GGAGAAACAAG
 ||||| |||||

		TTTTCC CCTCTTTGTTC		
		C		
GAM3799	DUSP10	3' AAAAGGGGGAGAAACAAG	86003	A
		AGAAGG GGAGAAACAAG		
		TTTTCC CCTCTTTGTTC		
		C		
GAM3799	EZF-2	3' GAAGGAGGAGAGGAAGA	86004	AACAA
		GAAGGAGGAGA GAAGA		
		CTTCCTCCTCT CTTCT		
		C		
GAM3799	FBXO27	3' AGAAGAGAGGGGAGGGCAAGAA	86005	_ A AA_
		AGAAG GAGG GA CAAGAA		
		TCTTC CTCC CT GTTCTT		
		T C CCC		
GAM3799	FHX	3' GAAGGAAGAGAGAAGAA	86006	AACAA
		GAAGGAGGAGA GAAGAA		
		CTTCCTTCTCT CTTCTT		
GAM3799	FIGN	3' AGAAGGGGAGGAGATGGAGA	86007	_ AACAA
		AGAA GGAGGAGA AGA		
		TCTT CCTCCTCT TCT		
		CC ACC_		
GAM3799	FLJ00058	5' AGAAGGAGGGGAAACAGGA	86008	A A
		AGAAGGAGG GAAACA GA		
		TCTTCCTCC CTTTGT CT		
		C		
GAM3799	FLJ10468	3' AGGAGGAGGAGGAAGA	85957	A AAACAA
		AG AGGAGGAG GAAGA		
		TC TCCTCCTC CTTCT		
		C		
GAM3799	FLJ10781	3' GAAGGCGGGAGGAAGAA	86009	A_ AAACAA
		GAAGG GGAG GAAGAA		
		CTTCC CCTC CTTCTT		
		GC		
GAM3799	FLJ11078	3' GAGGGAGGAGAAAAAAGA	86010	A C
		GA GGAGGAGAAA AAGA		
		CT CCTCCTCTTT TTCT		
		C T		
GAM3799	FLJ12700	3' GAAAGAGGAGAGCAGGAA	86011	AA A
		GAAGGAGGAGA CA GAA		

		CTTTCTCCTCT GT CTT		
		C_ C		
GAM3799	FLJ12875	3' AGGAGGACGAGAGATGAAC 86012	_	AACA A
		AGGAGGA GA AGA GAAT		
		TCCTCCT CT TCT CTTG		
		G C__ A		
GAM3799	FLJ13158	3' AGAGGAAGGACAGAGGAAGA 86013	AA	A__
		GGAGGAG ACA GAAGA		
		TCTCCTT TGT CTTCT		
		CC CTC		
GAM3799	FLJ13769	3' AGGAGGAAGAGAACAGAA 86014	A	A A
		AG AGGAGGAGAA CA GAA		
		TC TCCTTCTCTT GT CTT		
		C _ _		
GAM3799	FLJ14442	3' GGAGGAGGGGGA AAAAGAA 86015	AAAC	
		GGAGGAG AAGAAGAA		
		CCTCCTC TTTTCTT		
		CCCC		
GAM3799	FLJ14442	3' AGAGGGGAGAGAGATGGAAGCA 86017	A_ _	AAC A
	GA	AGA GGAG GAGA AAG AGA		
		TCT CCTC CTCT TTC TCT		
		CC T ACC G		
GAM3799	FLJ14442	3' AGAAGGAGAGGGAACAAG 86016	G A_	
		AGAAGGAG AG AACAAG		
		TCTTCCTC TC TTGTTT		
		_ CC		
GAM3799	FLJ14594	3' AGGAGGAGGAGGAAGA 85957	A	AAACAA
		AG AGGAGGAG GAAGA		
		TC TCCTCCTC CTTCT		
		C _ _ _ _		
GAM3799	FLJ20294	5' AGAAAGAGGAGACAGGAA 86018	AA	A
		AGAAGGAGGAGA CA GAA		
		TCTTTCTCCTCT GT CTT		
		_ C		
GAM3799	FLJ20337	3' AGGAAGAGGGTTGGAAGAAT 86019	AAACAA	
		AGGAGGAG GAAGAAT		
		TCCTTCTC CTTCTTA		
		CCAACC		
GAM3799	FLJ21596	3' AGAGGGAGGGGAAAAAGAA 86020	A	A C
		AGA GGAGG GAAA AAGAA		

TCT CCTCC CTTT TTCTT
 C C _
 GAM3799 FLJ21940 3' GAGGGAGGGAGAAATGCAGGAA 86021 A _ _ A
 A GA GGAGG AGAAA CA GAAG
 || |||| |||| || ||||
 CT CCTCC TCTTT GT CTTT
 C C AC C
 GAM3799 FLJ22055 3' GATGGAGGATAGCAAGAAGAAT 86022 A GAAA
 GA GGAGGA CAAGAAGAAT
 || |||| |||| ||||
 CT CTCCT GTTCTTCTTA
 A ATC_
 GAM3799 FLJ23231 3' GATGGAGGAGAAGAAGA 86023 A AACA
 GA GGAGGAGA AGAAGA
 || |||| |||| ||||
 CT CTCCTCT TCTTCT
 A _
 GAM3799 FLJ32894 3' AGGAGGAGGAGGAAAATAAG 86024 A _ CAAG
 AG AGGAGGAG AAA AAG
 || |||| || || ||
 TC TCCTCCTC TTT TTC
 C C TA_
 GAM3799 GBTS1 3' AGAAGAGGAGGAGGCCGAGGA 86025 _ AAACAA A
 AGA AGGAGGAG GA GA
 || |||| || || ||
 TCT TCCTCCTC CT CT
 TC CGG_ C
 GAM3799 GPNMB 3' GAAGGAGAGAAAAAGAA 86026 G C
 GAAGGAG AGAAA AAGAA
 |||| |||| ||||
 CTTCTC TCTTT TTCTT
 _ _
 GAM3799 H_GS165L15.1 3' AGAGGAGGAGAGGTGAAGA 86027 A AACAA
 AGA GGAGGAGA GAAGA
 || |||| || || ||
 TCT CTCCTCT CTTCT
 _ CCA_
 GAM3799 HCDI 3' GAAAGAGGACTGGGAGAGGAAT 86028 GAAACA A
 GAAGGAGGA AGA GAAT
 |||| || || || ||
 CTTTCTCCT TCT CTTA
 GACCC_ C
 GAM3799 HIC2 3' GAAGGAGGGAAAGCGAAA 86029 A CAA
 GAAGGAGG GAAA GAAG
 |||| || || || ||
 CTTCTCC CTTT CTTT
 _ CG_
 GAM3799 HN1L 3' AGAAGGCAGGACAGATGCAAGA 86031 _ _ AA
 AGA AGAAGG AGGA GA CAAGAAGA
 |||| || || || || || ||

		TCTTCC TCCT CT GTTCTTCT		
		G GT AC		
GAM3799	HN1L	3' AGAAAGACACAGGAAGAA 86030	GAA	A
		AGGAGGA ACA GAAGAA		
		TCTTTCT TGT CTTCTT		
		G__ C		
GAM3799	HRH4	3' AGAGGTGAGGACTAAGAAGAAT 86032	A A_ _	
		GGAGG GA AC AAGAAGAAT		
		TCTCC CT TG TTCTTCTTA		
		A CC A		
GAM3799	IL14	3' AGGAGGAGGAGAAGCGCAAGGA 86033	A	A__ A
	G	AG AGGAGGAGAA CAAG AG		
		TC TCCTCCTCTT GTTC TC		
		C CGC C		
GAM3799	ITGA10	3' GAGGAGGAGGGAAGCAGA 86034	A	AAAC A
		GA GGAGGAG AAG AGA		
		CT CCTCCTC TTC TCT		
		_ CC_ G		
GAM3799	KIAA0057	3' AGGAGAGGGAGAAATGGGAGAA 86035	A GA	CAA A
		AG AG GGAGAAA GA GAA		
		TC TC CCTCTTT CT CTT		
		C TC ACC _		
GAM3799	KIAA0212	3' AGAAGGAAGAGGGTATAGAA 86036		AAACA
		AGAAGGAGGAG AGAA		
		TCTTCCTTCTC TCTT		
		CCATA		
GAM3799	KIAA0298	3' AGCAGGAGGAGAGGCCAGAGG 86037	A	AACA_ A
	A	AG AGGAGGAGA AGA GA		
		TC TCCTCCTCT TCT CT		
		G CCGGG C		
GAM3799	KIAA0319	3' AAAAGGAGGAGGGGCAGAAGAA 86038		AAACA
		AGAAGGAGGAG AGAAGAA		
		TTTTCCTCCTC TCTTCTT		
		CCCG_		
GAM3799	KIAA0352	3' GAAGGGGGATGAAAGGCCTGGA 86039	A _	CAAGAA
	AT	GAAGG GGA GAAA GAAT		
		CTTCC CCT CTTT CTTA		
		C A CCGGAC		
GAM3799	KIAA0444	3' GAAGGAGGGGAAATGTCAGCCA 86040	A	CA__ A_
	G	GAAGGAGG GAAA AG AG		

CTTCTCC CTTT TC TC
 C ACAG GG
 GAM3799 KIAA0563 3' AGAATGAGGAGAAGGGAGA 86041 G ACA
 AGAA GAGGAGAA AGA
 |||| ||||| ||
 TCTT CTCCTCTT TCT
 A CCC
 GAM3799 KIAA0648 3' GAAGGGGGAGAACAGA 86042 A A A
 GAAGG GGAGAA CA GA
 |||| ||||| ||
 CTTCC CCTCTT GT CT
 C _ _
 GAM3799 KIAA0759 3' GAAGGAGAGGAACAGAAAA 86043 GA A A
 GAAGGAG GAA CA GAAGA
 ||||| ||| || |||||
 CTTCTC CTT GT CTTTT
 TC _ _
 GAM3799 KIAA1054 3' AGGAGGAAGAAACGCAGGAAG 86044 _ AA_
 AGGAGGA GAAAC GAAG
 ||||| ||||| ||||
 TCCTCCT CTTTG CTTC
 T CGTC
 GAM3799 KIAA1128 3' AGAAGGAGGGAGCAGAA 86045 A AACA
 AGAAGGAGG GA AGAA
 ||||| || |||||
 TCTTCCTCC CT TCTT
 _ CG_
 GAM3799 KIAA1181 3' GAACGAGGAGAAGAGAGGAAGA 86046 G ACAA_
 GAA GAGGAGAA GAAGA
 ||| ||||| |||||
 CTT CTCCTCTT CTTCT
 G CTCTC
 GAM3799 KIAA1265 3' AGTAGGAGGAAAGAAGA 86047 A GAAAC
 AG AGGAGGA AAGAAGA
 || ||||| |||||
 TC TCCTCCT TTCTTCT
 A _ _
 GAM3799 KIAA1327 3' AGAAGAGGAATGAAGA 86048 G AAACAA
 AGAAG AGGAG GAAGA
 |||| ||||| |||||
 TCTTC TCCTT CTTCT
 _ A_
 GAM3799 KIAA1363 3' AGAGGGAGGAAAGACGAG 86049 A A A
 AGA GGAGGAGA AC AG
 ||| ||||| || ||
 TCT CCTCCTTT TG TC
 C C C
 GAM3799 KIAA1500 3' GAAGGGGTGTGCAAGAAGAAT 86050 A AGAAA
 GAAGG GG CAAGAAGAAT
 |||| || |||||

			CTTCC CC	GTTCTTCTTA		
			_ ACAC_			
GAM3799	KIAA1549	3'	AGAAGAAGGAGGAAGA	86051	A	AAACAA
			AGAAGGAGGAG	GAAGA		
			TCTTCTTCCTC	CTTCT		
GAM3799	KIAA1671	3'	AGGAGGAAGAGAAATGAG	86052	A	CA
			AG AGGAGGAGAAA	AG		
			TC TCCTTCTCTTT	TC		
			C	AC		
GAM3799	KIAA1750	3'	GAGGGAGGAAAGAAGAA	86053	A	GAAAC
			GA GGAGGA	AAGAAGAA		
			CT CCTCCT	TTCTTCTT		
			C			
GAM3799	KIAA1817	3'	GGAGGAGAAGCAAGGAAG	86054	A	_
			GGAGGAGAA	CAAG AAG		
			CCTCCTCTT	GTTC TTC		
			C	C		
GAM3799	KIAA1831	3'	GAAGGAGGGAGGCAAGCCAA	86055	A	AA AA
			GAAGGAGG	GA CAAG GA		
			CTTCCTCC	CT GTTC TT		
			_ CC	GG		
GAM3799	KIAA1878	3'	GAGGGAGAGAGAGAGAAGA	86056	A	_ AACA
			GA GGAG	GAGA AGAAGA		
			CT CTC	CTCT TCTTCT		
			C	T C__		
GAM3799	MGC10540	3'	AGGAGGAGGAGACAGAAG	86057	A	AACA
			AG AGGAGGAGA	AGAAG		
			TC TCCTCCTCT	TCTTC		
			C	G__		
GAM3799	MGC10812	3'	AGCAGGAGGAGAAAGGGAA	86058	A	CAA
			AG AGGAGGAGAAA	GAA		
			TC TCCTCCTCTTT	CTT		
			G	CC_		
GAM3799	MGC16824	5'	AGGAGGAGGAGGACGTGGAAGA	86059	A	AAACAA
	A		AG AGGAGGAG	GAAGAA		
			TC TCCTCCTC	CTTCTT		
			C	CTGCAC		
GAM3799	MGC21675	3'	AGAAAGAGGAGGAACCGGA	86060	A	AA
			AGAAGGAGGAG	AAC GA		

		TCTTTCTCCTC TTG CT	
		C GC	
GAM3799	MGC2574	3' GAAGGAGGGATGGGAGCTGAAT 86061	A AACA AA
		GAAGGAGG GA AG GAAT	
		CTTCCTCC CT TC CTTA	
		_ ACCC GA	
GAM3799	MGC3200	3' GAAGGAGGGGAAGTGTAGAAAA 86062	A ACA_
		GAAGGAGG GAA AGAAGA	
		CTTCCTCC CTT TCTTTT	
		C CACA	
GAM3799	MGC4415	3' AAGAAGGAGATCTTGAGAAG 86063	AACA_
		AAGGAGGAGA AGAAG	
		TTCTTCCTCT TCTTC	
		AGAAC	
GAM3799	MGC5338	3' GAAGGGGGAGAGAGAAAA 86064	A AACA
		GAAGG GGAGA AGAAGA	
		CTTCC CCTCT TCTTTT	
		C C__	
GAM3799	MGC5521	3' GAAGGAGGAAACCAGAA 86065	AACA
		GAAGGAGGAGA AGAA	
		CTTCCTCCTTT TCTT	
		GG__	
GAM3799	MGC5566	3' GGAAGAGGAAACATGGGAAG 86066	_ A__
		GGAGGAG AAACA GAAG	
		CCTTCTC TTTGT CTTC	
		C ACC	
GAM3799	MPHOSPH10	5' AGGAGGGTGGGAAACAAAAA 86067	A__
		AGGAGG GAAACAAGAA	
		TCCTCC CTTTGTTTTT	
		CACC	
GAM3799	NEUGRIN	3' AGAGAGCCTAAGCAAGAAGA 86068	_AG_ A
		GGAG G AA CAAGAAGA	
		TCTC C TT GTTCTTCT	
		T GGA C	
GAM3799	NFAT5	3' AAAGGAGGGAGGGAGGAAT 86069	A AACAA A
		GAAGGAGG GA GA GAAT	
		TTTCCTCC CT CT CTTA	
		_ CC__ C	
GAM3799	NFAT5	3' GAAGGGGAGAGGGAGGGAGAAT 86070	A AACAAAGA
		GAAGG GGAGA AGAAT	

			CTTCC CCTCT TCTTA		
			_ CCCTCCC		
GAM3799 NOVA2	3'	AGATGGGAGGAGAGAAAAG	86071	A_	AACA
		AGA GGAGGAGA AGAAG			
		TCT CTCCTCT TTTTC			
		AC C__			
GAM3799 NRN1	5'	AGAGGGAGGAGAGAAAGA	86072	A	AAC
		AGA GGAGGAGA AAGA			
		TCT CTCCTCT TTCT			
		C CT_			
GAM3799 OBTP	5'	AGAAGGGGAGGAGTGAAACTAG	86074	_ _	A
		AGAA GGAGGA GAAAC AG			
		TCTT CTCCT CTTTG TC			
		CC CA A			
GAM3799 OBTP	3'	AGGAGGAGGAGCAGGTGGAGAA	86073	A	AAACA_
A		AG AGGAGGAG AGAAG			
		TC TCCTCCTC TCTTT			
		C GTCCACC			
GAM3799 P450RAI-2	3'	AGGAGGAGGAGACGCTGAAGA	86075	A	AACAA
		AG AGGAGGAGA GAAGA			
		TC TCCTCCTCT CTTCT			
		C GCGA_			
GAM3799 P5326	3'	AGGAGGAAGACAGGAGGA	86076	AA A A	
		AGGAGGAG ACA GA GA			
		TCCTCCTT TGT CT CT			
		C_ C C			
GAM3799 PADI1	3'	GAAAGAGGCCAGGGAAGAAT	86077		AGAAACAA
		GAAGGAGG GAAGAAT			
		CTTTCTCC CTTCTTA			
		GGTCC_			
GAM3799 PCDH10	5'	AGGAGGAGGAGGAAGAAGA	86078	A	AAAC
		AG AGGAGGAG AAGAAGA			
		TC TCCTCCTC TTCTTCT			
		C C_			
GAM3799 PCDH10	5'	AGGAGGAGGAGGAAGAAGA	86078	A	AAAC
		AG AGGAGGAG AAGAAGA			
		TC TCCTCCTC TTCTTCT			
		C C_			
GAM3799 PDE1C	3'	GAAGAAGGAGAAGAAGGAGAAT	86079		AC A
		GAAGGAGGAGAA AAG AGAAT			

			CTTCTTCCTCTT	TTC TCTTA		
			C_ C			
GAM3799	PELI1	3'	GAAGGAGGGGAGAGAAGA	86080	A	AACA
			GAAGGAGG GA	AGAAGA		
			CTTCCTCC CT	TCTTCT		
			C C__			
GAM3799	PPM1A	5'	AGAAGGAGGAGGAAGA	86081	AAACAA	
			AGAAGGAGGAG	GAAGA		
			TCTTCCTCCTC	CTTCT		

GAM3799	PRO1598	5'	AGAATGGGAATGGGAATAAGAA	86082	__ __ A	AC
			GAAT	GAA GGA GG GAA AAGAAGAAT		
			CTT CCT CC CTT	TTCTTCTTA		
			AC TA _ A_			
GAM3799	RAB2	3'	AGGAGGAGAGGGGGTGAAAGAA	86083	AACAA__	
	T		AGGAGGAGA	GAAGAAT		
			TCCTCCTCT	TTTCTTA		
			CCCCCAC			
GAM3799	RAB3GAP	3'	AGAAGGGGAGGGAGACGA	86084	A	AAACA A
			AGAAGG GGAG	AGA GA		
			TCTTCC CCTC	TCT CT		
			_ CC__ G			
GAM3799	RAB6B	5'	AGGAGGAGGAGGAAAAAG	86085	A	AAAC
			AG AGGAGGAG	AAGAAG		
			TC TCCTCCTC	TTTTTC		
			C C__			
GAM3799	RBPM5	5'	AGGAGGAGGAGGAAGA	85957	A	AAACAA
			AG AGGAGGAG	GAAGA		
			TC TCCTCCTC	CTTCT		
			C			
GAM3799	RFX3	5'	AGGAGGAGGAGGAAGA	85957	A	AAACAA
			AG AGGAGGAG	GAAGA		
			TC TCCTCCTC	CTTCT		
			C			
GAM3799	RFX3	5'	AGGAGGAGGAGGAAGA	85957	A	AAACAA
			AG AGGAGGAG	GAAGA		
			TC TCCTCCTC	CTTCT		
			C			
GAM3799	RFX3	5'	AGGAGGAGGAGGAAGA	85957	A	AAACAA
			AG AGGAGGAG	GAAGA		
			TC TCCTCCTC	CTTCT		
			C			

			TC TCCTCCTC	CTTCT		
			C			
GAM3799	RFX3	5'	AGGAGGAGGAGGAAGA	85957	A	AAACAA
			AG AGGAGGAG	GAAGA		
			TC TCCTCCTC	CTTCT		
			C			
GAM3799	RNF24	3'	GAAGGAGGGGGAGAGGCCAAA	86086		AA_
			GAAGGA	GGAGA	CAAG	
			CTTCCT	CCTCT	GTTT	
			CCC	CCG		
GAM3799	RODH-4	5'	AGAAGGAGAAGGCAAAGA	86087		AAACAA
			AGAAGGAGGAG	GAAGA		
			TCTTCCTCTTC	TTTCT		
			CG			
GAM3799	SCAMP5	3'	AGAAGGAGGAGAAGGCAG	86088		ACA
			AGAAGGAGGAGAA	AG		
			TCTTCCTCCTCTT	TC		
			CCG			
GAM3799	SCYA13	3'	AGAAGAGGAGGCCAGAGGAGAA	86089	G	AAA _ A
	T		AGAAG	AGGAG	CA AG	AGAAT
			TCTTC	TCCTC	GT TC	TCTTA
			_	CG_	C	C
GAM3799	SCYA22	3'	GAAGGAGGCAGGGAAAGTGGAA	86090		AGAAAC AA
	T		GAAGGAGG	AAG	GAAT	
			CTTCCTCC	TTC	CTTA	
			GTCCCT	AC		
GAM3799	SMARCF1	3'	AGGAGGAGAGAGAAACAGGA	86091	A	_ A
			AG AGGAG	GAGAAACA	GA	
			TC TCCTC	CTCTTTGT	CT	
			C	T	C	
GAM3799	SMARCF1	3'	AGGAGGAGAGAGAAACAGGA	86091	A	_ A
			AG AGGAG	GAGAAACA	GA	
			TC TCCTC	CTCTTTGT	CT	
			C	T	C	
GAM3799	SMARCF1	3'	AGGAGGAGAGAGAAACAGGA	86091	A	_ A
			AG AGGAG	GAGAAACA	GA	
			TC TCCTC	CTCTTTGT	CT	
			C	T	C	
GAM3799	SNTA1	3'	AAGGAGGAGAGAGACAGGA	86092	A	_ A
			AAGGAGGAGA	ACA	GA	

			TTCCTCCTCT	TGT CT		
			CTC C			
GAM3799	SRF	3'	AGAGGGGGGAAGACAAG	86093	A A A _	
			AGA GG GG GAA ACAAG			
			TCT CC CC CTT TGTT			
			C _ _ C			
GAM3799	TNFSF13	5'	GAGGGAGGAGGAAAGCAAGCTA	86094	A _ _ AA	
	A		GA GGAGGAG AAA CAAG GA			
			CT CCTCCTC TTT GTTC TT			
			C C C GA			
GAM3799	TNKS1BP1	3'	GAAGGAGGAGAGGAAG	86095	AACAA	
			GAAGGAGGAGA GAAG			
			CTTCCTCCTCT CTTC			
			C____			
GAM3799	TP53INP1	5'	AGGTGAAAAGCAAGAAGA	86097	AG A	
			AGG GAGAA CAAGAAGA			
			TCC CTTTT GTTCTTCT			
			A_ C			
GAM3799	TP53INP1	3'	AGGAGGAAGAGAAGTAGCAAG	86096	A A__	
			AG AGGAGGAGAA CAAG			
			TC TCCTTCTCTT GTTC			
			C CATC			
GAM3799	TP53INP1	3'	AGGAGGAAGAGAAGTAGCAAG	86096	A A__	
			AG AGGAGGAGAA CAAG			
			TC TCCTTCTCTT GTTC			
			C CATC			
GAM3799	TP53TG3	3'	AGAGGAGAGAGACAGAAGAAT	86098	AACA_	
			GGAGGAGA AGAAGAAT			
			TCTCCTCT TCTTCTTA			
			CTCTG			
GAM3799	ULK2	3'	AGGAAGAGGAGAGGATAGAA	86099	A AACA	
			AG AGGAGGAGA AGAA			
			TC TTCTCCTCT TCTT			
			C CCTA			
GAM3799	VRP	5'	AGAAGGAGTAGAAGCAGA	86100	G ACA	
			AGAAGGAG AGAA AGA			
			TCTTCCTC TCTT TCT			
			A CG_			
GAM3799	ZFP100	5'	AGGAGGAGGAGGACAAG	85928	A AA	
			AG AGGAGGAG ACAAG			

		TC TCCTCCTC TGTTC		
		C C_		
GAM3799	LOC121457 5'	AGGAGGAGGGGCAGGACGAA	86101	AAA A A
		AGGAGGAG CA GA GAA		
		TCCTCCTC GT CT CTT		
		CCC C G		
GAM3799	LOC123775 3'	GGAGGAGAGAAAGAGAGA	86102	AAC _
		GGAGGAGA AAGA AGA		
		CCTCCTCT TTCT TCT		
		CT_ C		
GAM3799	LOC124895 5'	GAGGGAGGAGACAGTCTCGGAG	86103	A AACAAGA__
	AAT	GA GGAGGAGA AGAAT		
		CT CCTCCTCT TCTTA		
		C GTCAGAGCC		
GAM3799	LOC126669 3'	GAAGGAGGGAGAAACAAG	86104	_
		GAAGGAGG AGAAACAAG		
		CTTCCTCC TCTTTGTTC		
		C		
GAM3799	LOC138389 5'	GAAGGAGAGAAACAGCGA	86105	G A_
		GAAGGAG AGAAACA GA		
		CTTCCTC TCTTTGT CT		
		_ CG		
GAM3799	LOC143274 3'	GAAGGAGGCAGAGATAAGCGA	86106	_ AAC AA
		GAAGGAGG AGA AAG GA		
		CTTCCTCC TCT TTC CT		
		G CTA G_		
GAM3799	LOC143677 5'	GAAGGAGGAGGAAGCAAG	86107	_ A
		GAAGGAGGAG AA CAAG		
		CTTCCTCCTC TT GTTC		
		C C		
GAM3799	LOC145547 3'	AGGAGGAAGAGAAAGAA	86108	A ACA
		AG AGGAGGAGAA AGAA		
		TC TCCTTCTCTT TCTT		
		C _		
GAM3799	LOC145645 3'	AGGAGGAGGAGGATTGAGAGA	86109	A AAACA A
		AG AGGAGGAG AGA GA		
		TC TCCTCCTC TCT CT		
		C CTAAC _		
GAM3799	LOC145645 3'	AGAAAGAGGAGGAGGAGGAGGA	86110	AAACAA A
		AGAAGGAGGAG GA GA		

		TCTTTCTCCTC	CT CT		
		CTCCTC	C		
GAM3799	LOC145786 5'	AGAAAGGGTA	ACTATAAGAAGA	86111	A A AAC_
		AGAAGG	GG GA AAGAAGA		
		TCTTTC	CC TT TTCTTCT		
		_ A	GATA		
GAM3799	LOC146315 3'	AGAGGGAGGAGAGAAG		86112	A AACAA
		AGA	GGAGGAGA GAAG		
		TCT	CCTCCTCT CTC		
		C	_____		
GAM3799	LOC147071 3'	AGAATGAGGAGAAGGGAGA		86041	G ACA
		AGAA	GAGGAGAA AGA		
		TCTT	CTCCTCTT TCT		
		A	CCC		
GAM3799	LOC147632 5'	AGGAGGAGGAGAAGGAGA		86113	A ACA
		AG	AGGAGGAGAA AGA		
		TC	TCCTCCTCTT TCT		
		C	CC_		
GAM3799	LOC148113 3'	AGAAGAAGGAGGGGCAAAA		86114	AAA
		AGAAGGAGGAG	CAAGA		
		TCTTCTTCCTC	GTTTT		
		CCC			
GAM3799	LOC148195 5'	AGGAGGAGGAGGGGACAAG		86116	A AA_
		AG	AGGAGGAG ACAAG		
		TC	TCCTCCTC TGTC		
		C	CCC		
GAM3799	LOC148195 5'	AGAAGGAGGAGTAGAGGAGA		86115	AAACA A
		AGAAGGAGGAG	AG AGA		
		TCTTCCTCCTC	TC TCT		
		ATC_	C		
GAM3799	LOC148195 5'	AGAAGGAGGAGGAGGAGAAG		86117	AAACA
		AGAAGGAGGAG	AGAAG		
		TCTTCCTCCTC	TCTTC		
		CTCC_			
GAM3799	LOC148195 5'	AGGAGGAGAAGAAGAA		86118	AACA
		AGGAGGAGA	AGAAGAA		
		TCCTCCTCT	TCTTCTT		

GAM3799	LOC148696 5'	GAATGAGGAGAATCAGAA		86119	G ACA
		GAA	GAGGAGAA AGAA		

CTT CTCCTCTT TCTT
 A AG_
 GAM3799 LOC149911 3' AGCAGGAGGAAGAGGAAGA 86120 A AAACAA
 AG AGGAGGAG GAAGA
 || ||||| ||||
 TC TCCTCCTT CTTCT
 G CTC____
 GAM3799 LOC150051 3' AGAAGAAGGAGGAATCAG 86121 A CA
 AGAAGGAGGAG AA AG
 ||||| || ||
 TCTTCTTCCTC TT TC
 C AG
 GAM3799 LOC150067 5' AGGAGGAGGAGGAAGA 85957 A AAACAA
 AG AGGAGGAG GAAGA
 || ||||| ||||
 TC TCCTCCTC CTTCT
 C _____
 GAM3799 LOC150498 3' GAAGGAGAAGAAACAAAGAAT 86122 GA
 GAAGGAGGAGAAACAA AGAAT
 ||||| ||||
 CTTCTCTTCTTTGTT TCTTA

 GAM3799 LOC151195 5' GGAGGCAAGAAGAAT 86123 AGAAA
 GGAGG CAAGAAGAAT
 |||| |||||
 CCTCC GTTCTTCTTA

 GAM3799 LOC151736 5' AGGAGGAGAGGGAACAAGCTTC 86124 ____ A____
 AGA AGGAGGAGA AACAAG AGA
 ||||| |||| ||
 TCCTCCTCT TTGTTC TCT
 CCC GAAG
 GAM3799 LOC152286 5' AGAAGGGGGGAGCAGAAAGAAT 86125 A AAA AG
 AGAAGG GGAG CA AAGAAT
 |||| |||| || |||||
 TCTTCC CCTC GT TTCTTA
 C ____ CT
 GAM3799 LOC152905 5' AGAGGGAGGGGAAATAGA 85955 A A CA
 AGA GGAGG GAAA AGA
 || |||| |||| ||
 TCT CCTCC CTTT TCT
 C C A_
 GAM3799 LOC153077 3' AGAAGGAAGGGGAAAAGAAT 86126 AGAAACA
 AGAAGGAGG AGAAGAAT
 ||||| |||||
 TCTTCCTTC TTTTCTTA
 CCCC____
 GAM3799 LOC154877 3' GAGGGAAGGAGATGGCCAGAGA 86127 A _ AA__ _
 AG GA GGA GGAGA CA AGAAG
 || |||| || |||||

	CT CCT CCTCT GT TCTTC		
	C T ACCG C		
GAM3799 LOC157273 3'	AGGAGAAGGAGAAGCAAA 86128	A	A
	AG AGGAGGAGAA CAAG		
	TC TCTTCCTCTT GTTT		
	C C		
GAM3799 LOC158267 3'	AGAAGGAGAGGAAACAGGAGGA 86129	GA	A A
	AGAAGGAG GAAACA GA GA		
	TCTTCCTC CTTTGT CT CT		
	TC C C		
GAM3799 LOC159090 5'	AGAAGGATGGAGGGAAAACAAG 86130	-	---
	AGAAGGA GGAG AAACAAG		
	TCTTCCT CCTC TTTGTTC		
	A CCT		
GAM3799 LOC161003 5'	AGAGGAGAAAGTATGAGAGA 86131	CAA_	_
	GGAGGAGAAA GA AGA		
	TCTCCTCTTT CT TCT		
	CATA C		
GAM3799 LOC161784 5'	GAAGGAGAAGAATGAGA 86132	ACA	
	GAAGGAGGAGAA AGA		
	CTTCCTCTTCTT TCT		
	AC_		
GAM3799 LOC164295 5'	AGAGGGAGGAGAGAAGA 86133	A	AACAA
	AGA GGAGGAGA GAAGA		
	TCT CCTCCTCT CTTCT		
	C		
GAM3799 LOC166682 5'	AGGAAGAGAAAACAGCGGAAG 86134	-	A---
	AGGAGGAGAAA CA GAAG		
	TCCTTCTCTTT GT CTTC		
	T CGCC		
GAM3799 LOC196047 3'	AGGAGGAAGAGGGAAATGAAGA 86135	A	AAACAA
AT	AG AGGAGGAG GAAGAAT		
	TC TCCTTCTC CTTCTTA		
	C CCTTA		
GAM3799 LOC196812 3'	AGAAGGAGGAGTGGCCACCAGA 86136	AAA_	AGA
	AGAAGGAGGAG CA AGA		
	TCTTCCTCCTC GT TCT		
	ACCG GG_		
GAM3799 LOC201173 3'	AGAATGAGGAGAAGGGAGA 86041	G	ACA
	AGAA GAGGAGAA AGA		

		TCTT CTCCTCTT TCT			
		A CCC			
GAM3799	LOC201220 3'	AGAATGAGGAGAAGGGAGA	86041	G	ACA
		AGAA GAGGAGAA AGA			
		TCTT CTCCTCTT TCT			
		A CCC			
GAM3799	LOC219688 5'	AGGAGGAGGAGGAAGA	85957	A	AAACAA
		AG AGGAGGAG GAAGA			
		TC TCCTCCTC CTTCT			
		C _____			
GAM3799	LOC220002 5'	AGAAGAAGGAGAAGTCACAAA	86137		_____
		AGAAGGAGGAGAA ACAAG			
		TCTTCTTCCTCTT TGTTT			
		CAG			
GAM3799	LOC221490 5'	AGCAGGAGGAGGAACAGA	86138	A	A A
		AG AGGAGGAG AACA GA			
		TC TCCTCCTC TTGT CT			
		G C _			
GAM3799	LOC221882 5'	AGAAGGAGAGAGGAGAGGA	86139		_ AAACA A
		AGAAGGAG GAG AGA GA			
		TCTTCCTC CTC TCT CT			
		T C____ C			
GAM3799	LOC221935 3'	GAAGGAGGGGAAGGAAG	86140	A	ACAA
		GAAGGAGG GAA GAAG			
		CTTCCTCC CTT CTTC			
		C C____			
GAM3799	LOC253943 3'	GGAGGAGGGAAGAAGAAT	86141		AAAC
		GGAGGAG AAGAAGAAT			
		CCTCCTC TTCTTCTTA			
		CC____			
GAM3799	LOC254532 5'	AGGAGAAGGAGAAGCAAG	86142	A	A
		AG AGGAGGAGAA CAAG			
		TC TCTTCCTCTT GTTC			
		C C			
GAM3799	LOC255158 3'	AGAAGGAAGAGGACAATGGA	86143		AA GAA
		AGAAGGAGGAG ACAA GA			
		TCTTCCTTCTC TGTT CT			
		C_ AC_			
GAM3799	LOC255621 3'	AGAAGGAAGGGAAAATTTAAGA	86144	A	CAAG
	AT	AGAAGGAGG GAAA AAGAAT			

TCTTCCTTC CTTT TTCTTA
 C TAAA
 GAM3799 LOC255743 3' AGAAGAGGAGAGAAGA 86145 G AACAA
 AGAAG AGGAGA GAAGA
 ||||| ||||| |||||
 TCTTC TCCTCT CTTCT

 — ———
 GAM3799 LOC257459 3' AGGAGGAGGAGAAAGGAG 86146 A CA
 AG AGGAGGAGAAA AG
 || ||||| ||
 TC TCCTCCTCTTT TC
 C CC
 GAM3799 LOC257459 3' AGGAGGAGGAGAAAGGAGGGGA 86147 A CA AA
 AG AGGAGGAGAAA AG GA
 || ||||| || ||
 TC TCCTCCTCTTT TC CT
 C CC CC
 GAM3799 LOC51067 3' AAAAGGAGAGCAGGAAG 86148 AA A
 AGGAGGAGA CA GAAG
 ||||| || |||||
 TTTTCCTCT GT CTTC
 C_ C
 GAM3799 LOC51072 5' AGGAGGAGGAGGAAGA 85957 A AAACAA
 AG AGGAGGAG GAAGA
 || ||||| |||||
 TC TCCTCCTC CTTCT
 C ———
 GAM3799 LOC51644 3' AGAATGAAAAAGAATAGGAAG 86149 _ ACA
 AGAA GGAGGAGAA GAAG
 ||||| ||||| |||||
 TCTT CTTTTTCTT CTTC
 A ATC_
 GAM3799 LOC56932 3' AGACTGGGGGAGCAGGAAGA 86150 A_ A AAA A
 AGA GG GGAG CA GAAGA
 ||| || |||| || |||||
 TCT CC CCTC GT CTTCT
 GA C _ C
 GAM3799 LOC56961 5' AGAAGGAAGAGGGGGGCAAAG 86151 AAACAA
 AGAAGGAGGAG GAAG
 ||||| ||||| |||||
 TCTTCCTTCTC TTTC
 CCCCCG
 GAM3799 LOC90139 3' AGCAGGAGGAGATTAGAGGA 86152 A AACA A
 AG AGGAGGAGA AGA GA
 || ||||| ||| ||
 TC TCCTCCTCT TCT CT
 G AA_ C
 GAM3799 LOC90141 3' AGAGGGTAGGGGGCAAGAAGA 86153 A _ AGAAA
 AGA GG AGG CAAGAAGA
 ||| || ||| |||||

TCT CC TCC GTTCTTCT
 C A CCC__
 GAM3799 LOC90378 3' AGAGGGAGGAGAGAAAAG 86154 A AACAA
 AGA GGAGGAGA AGAAG
 ||| ||||| ||||
 TCT CCTCCTCT TTTTC
 C C__
 GAM3799 LOC90408 5' AGGAGGAAGAGAAGAAC 86155 AAACA
 AGGAGGAG AGAAGAAT
 ||||| |||||
 TCCTCCTT TCTTCTTG
 C__
 GAM3799 LOC90624 3' AGATAAAAGAGAAACAAGAAGA 86156 AG
 AT AGA GAGGAGAAACAAGAAGAAT
 ||| |||||
 TCT TTTCTCTTTGTTCTTCTTA
 AT
 GAM3799 LOC90632 3' AGAAGGAGGAGCAGGTAGGGAA 86157 AAACA AA
 AT AGAAGGAGGAG AG GAAT
 ||||| || |||
 TCTTCCTCCTC TC TTTA
 GTCCA CC
 GAM3799 LOC91523 3' AGGAGTGAGGAGGCAGGAA 86158 A _ AAA A
 AG AG GAGGAG CA GAA
 || || ||||| || |||
 TC TC CTCCTC GT CTT
 C A C__ C
 GAM3799 LOC92078 5' AGGAGGAAGGGAGCAGGCCAGA 86159 A _ AAACA_
 AG AG AGGA GGAG AGAAG
 || ||| ||| ||||
 TC TCCT CTCCTC TCTTC
 C TC GTCCGG
 GAM3799 LOC92299 5' AGGGGGAGGAGAGAAGA 86160 AA AACAA
 AG GGAGGAGA GAAGA
 || ||||| ||||
 TC CCTCCTCT CTTCT
 CC
 GAM3800 LOC153205 5' CTCAAGCTTCATTAAAGTGAT 86163 T_ C
 TTTA TTTTATTAAAG GAT
 ||| ||||| |||
 GAGT GAAGTAATTTC CTA
 TC A
 GAM3800 LOC257336 5' TACATTTATTTTTTTCAAAG 86164 CA
 TACATTTATTTT TTAAAG
 ||||| |||||
 ATGTAAATAAAA AGTTTC
 AA
 GAM3801 ERBB2IP 3' TTAAAGACTCTGGAAGTGTTGA 86167 CA AAC_
 TTAAAGGCTC GGGA TGA
 ||||| ||| |||

		AATTTCTGAG CCTT ACT	
		A_ CACA	
GAM3801	GNA15	3' TCAAAGGAGGGAACTGA 86168	CTCC
		TTAAAGG AGGGAACTGA	
		AGTTTCC TCCCTTTGACT	

GAM3801	GPD2	3' TTAAAAGCTAGACTGA 86169	CCAG AA
		TTAAAGGCT GGA CTGA	
		AATTTTCGA TCT GACT	

GAM3801	ITK	3' TTAAAGGGTCATTAAGTGAAT 86170	C CAGGGA
		TTAAAGG TC AACTGAAT	
		AATTTCC AG TTGACTTA	
		C TAA_____	
GAM3801	NCALD	3' AGGGGCAGGGAACTGAAT 86171	CTC
		AGG CAGGGAACTGAAT	
		TCC GTCCCTTTGACTTA	
		CC_	
GAM3801	DCLRE1A	3' TTAAGGGTCCCAGGGAGACC 86172	A CT A
		TTAA GG CCAGGGA ACT	
		AATT CC GGTCCCT TGG	
		C AG C	
GAM3801	FRAG1	3' TAAAGGCCAGAACTG 86173	CCAG
		TAAAGGCT GGAACTG	
		ATTTCCGG TCTTTGAC	

GAM3801	KCNK13	3' TTAAAGGCCTGAAGCTGAA 86174	CCAGG A
		TTAAAGGCT GAA CTGAA	
		AATTTCCGG CTT GACTT	
		A_____ C	
GAM3801	KIAA0349	3' TTAAAAGCTCAAGAACTG 86175	CA
		TTAAAGGCTC GGGAACTG	
		AATTTTCGAG TTCTTTGAC	

GAM3801	KIAA0349	3' TTAAAAGCTAAAGAACTG 86176	CC
		TTAAAGGCT AGGGAACTG	
		AATTTTCGA TTTCTTTGAC	

GAM3801	KIAA1243	3' AGGGTCCAGGAAGCCTGA 86177	C AA
		AGG TCCAGGGA CTGA	

		TCC AGGTCCTT GACT		
		C CG		
GAM3801	MGC3040	3' AAAGCTCCAGGGCCG	86178	AAA
		AAGGCTCCAGGG CTG		
		TTTCGAGGTCCC GGC		
		—		
GAM3801	LOC143888	3' TTAAAGGCTGCGGCTGAA	86179	CCA GAAA
		TTAAAGGCT GG CTGAA		
		AATTTCCGA CC GACTT		
		CG_ —		
GAM3801	LOC152719	3' AAGGTCCAGGAAACCTG	86180	C A
		AAGG TCCAGGGAA CTG		
		TTCC AGGTCCTTT GAC		
		— G		
GAM3801	LOC154860	3' TAAAGGTTGGAGAAACTG	86181	CTCCA
		TAAAGG GGGAAACTG		
		ATTTCC CTCTTTGAC		
		AAC_		
GAM3801	LOC199678	3' AGCTTTGGAAACTGAAT	86182	CCAG
		GGCT GGAAACTGAAT		
		TCGA CCTTTGACTTA		
		AA_		
GAM3801	LOC92299	3' AAGACAAGGGAAACTGA	86183	TCC
		AAGGC AGGGAAACTGA		
		TTCTG TCCCTTTGACT		
		T_		
GAM3802	HIP1	5' GCGTGTTTTTCTTTACAGC	86186	A C T
		GCGT TTTTTTCTT AC GT		
		CGCA AAAAAGGAA TG CG		
		C A T		
GAM3802	IGF1	3' GTATTTTTTCTCTTTGTT	86187	CAC
		GTATTTTTTCTT TGTT		
		CATAAAAAAGAG ACAA		
		AA_		
GAM3802	MBD4	3' CGTATTTTTTTTGGATTGTTGT	86188	CTTCAC
	C	CGTATTTTTT TGTTGTC		
		GCATAAAAAA ACAACAG		
		AACCTA		
GAM3802	DKFZP434G072	5' TCCCCTCTTCACTGTTGTC	86189	
		TTTTTTCTTCACTGTTGTC		

AGGGGAGAAGTGACAACAG

GAM3802 FLJ10539 3' GCGATTTTTCTTCAATATT 86190 T C
GCG ATTTTTCTTCA TGTT
||| ||||| |||
CGC TAAAAAGAAGT ATAA
— T
GAM3802 KIAA0644 3' GTATTTTTTTCACATTTGT 86191 CT TG
GTATTTTT TCAC TTGT
||||| ||| |||
CATAAAAA AGTG AACA
— TA
GAM3802 LOC153525 5' GTATTTTTTCTTCATATT 86192 C
GTATTTTTCTTCA TGTT
||||| ||| |||
CATAAAAAAGAAGT ATAA
—
GAM3802 LOC206426 3' GTCTCCTTTCTTCATTGTTGTC 86193 A C
GT TTTTTCTTCA TGTTGTC
|| ||||| |||||
CA AGGAAAGAAGT ACAACAG
G A
GAM3802 LOC93538 3' TTTTCTTTATTGTTGTC 86194 CAC
TTTTCTT TGTTGTC
||||| |||||
AAAAAGAA ACAACAG
ATA
GAM3803 ADAMTS8 5' TTTCTCCTCTGCGGCCAAG 86197 CGG G
TTTCTCCTC GGC CAAG
||||| ||| |||
AAAGAGGAG CCG GTTC
ACG —
GAM3803 EHD1 3' CACTTCTCTTCCCACAGG 86198 — —
CATTTCTC CTC CGGG
||||| ||| |||
GTGAAGAG GGG GTCC
AA T
GAM3803 ESRRB 5' CATTTCTCTTCCACCCCAGG 86199 —
CATTTCTC CTCCGGG
||||| |||||
GTAAAGAG GGGGTCC
AAGGT
GAM3803 FHL2 5' CCTCCCTCCGGGGCGCA 86200 T
TTTC CCTCCGGGGCGCA
||| ||||| |||||
GGAG GGAGGCCCCGCGT
—
GAM3803 ITGA1 3' CATCTCTCCTCTTCTCAGG 86201 —
CATTTCTCCTC CGGG
||||| ||| |||

			GTAGAGAGGAG GTCC		
			AAGA		
GAM3803	MAPK14	3'	ATTTCTCCCCAAACCAAG 86202	T	G G
			ATTTCTCC CCGGG C CAAG		
			TAAAGAGG GGTTT G GTTC		
			— —		
GAM3803	MAPK14	3'	ATTTCTCCCCAAACCAAG 86202	T	G G
			ATTTCTCC CCGGG C CAAG		
			TAAAGAGG GGTTT G GTTC		
			— —		
GAM3803	MAPK14	3'	ATTTCTCCCCAAACCAAG 86202	T	G G
			ATTTCTCC CCGGG C CAAG		
			TAAAGAGG GGTTT G GTTC		
			— —		
GAM3803	MMP25	3'	TTCTCTCCAGGGTGCAAG 86203	C	C
			TTCTC TCCGGGG GCAAG		
			AAGAG AGGTCCC CGTTC		
			— A		
GAM3803	NPAT	3'	CATTTTCCTCCAAAACA 86204	C	
			CATTT TCCTCCGGGGCG		
			GTAAA AGGAGGTTTTGT		
			—		
GAM3803	RBMX	3'	TTTCTCCTTTGCAATCAAG 86205	CCGGG	—
			TTTCTCCT GCG CAAG		
			AAAGAGGA CGT GTTC		
			AA — TA		
GAM3803	RGS3	5'	CATTTCCCCTTTCTCTGGG 86206	—	G
			CATTTCTCC TCC GGG		
			GTAAAGGGG AGG CCC		
			AA A		
GAM3803	STAT4	5'	CATTTCTCCTCCCAC 86207	GGGG	
			CATTTCTCCTCC CGC		
			GTAAAGAGGAGG GTG		
			—		
GAM3803	TEP1	3'	CATTCCTCCTCCTGGCA 86208	GG	
			CATTTCTCCTCC GGCG		
			GTAAGGAGGAGG CCGT		
			A —		
GAM3803	TGFBI	3'	CATTTCTCCAGCTGTGCAAG 86209	TCCGG	—
			CATTTCTCC GGC GCAAG		

		GTAAAGAGG TCG CGTTC	
		_____ ACA	
GAM3803 WDR4	3'	TTTCTCACTTCCCACAAG 86210	_ _ GGGG
		TTTCTC CT CC CGCAAG	
		AAAGAG GA GG GTGTTC	
		T A _____	
GAM3803 WDR4	3'	TTTCTCACTTCCCACAAG 86210	_ _ GGGG
		TTTCTC CT CC CGCAAG	
		AAAGAG GA GG GTGTTC	
		T A _____	
GAM3803 A	3'	TTTCTCCTCTGAGTTCAGCA 86211	C GC__
		TTTCTCCTC GGG GCA	
		AAAGAGGAG CTC CGT	
		A AAGT	
GAM3803 A	3'	TTTCTCCTCTGAGTTCAGCA 86211	C GC__
		TTTCTCCTC GGG GCA	
		AAAGAGGAG CTC CGT	
		A AAGT	
GAM3803 BPES	3'	CATTCTCCTTCCCAAGG 86212	_____
		CATTCTCCT CCGGGG	
		GTAAAGAGGA GGTTC	
		AG	
GAM3803 BZW2	3'	CATTCTCCCTCTGCACAAG 86213	CCGGG
		CATTCTCCT GCGCAAG	
		GTAAAGAGGG CGTGTTC	
		AGA_____	
GAM3803 C20orf39	5'	CATTCTCCTCCGGGACA 86214	
		CATTCTCCTCCGGGGCG	
		GTAAAGAGGAGGCCCTGT	
GAM3803 CALN1	3'	CATTCTCCCTTCTCTCCCAAG 86215	_____
		CATTCTCCT CCGGG	
		GTAAAGGGGA GTTC	
		AGAGAG	
GAM3803 ECE2	3'	CATTCTCCCTGATCCAGG 86216	_____
		CATTCTCC TCCGGG	
		GTAAAGAGG AGGTCC	
		GGA CT	
GAM3803 FLJ10483	5'	CTTCTCCCTCTGGGGTGCA 86217	_ C C
		TTTCTCC TC GGGG GCA	

		GAAGAGG AG CCCC CGT	
		G A A	
GAM3803	FLJ11362	3' CATTTCTCCTCGGGACA 86218	C
		CATTTCTCCTC GGGGCG	
		GTAAAGAGGAG CCCTGT	
		—	
GAM3803	FLJ13769	3' ATTCCTCCTCTGCACA 86219	CGGG
		ATTTCTCCTC GCGCA	
		TAAGGAGGAG CGTGT	
		A__	
GAM3803	FLJ20079	3' CATTTCTCTTCTTTTACAAG 86220	C CGGGG
		CATTTCTC TC CGCAAG	
		GTAAAGAG AG GTGTTC	
		A AAA__	
GAM3803	FLJ23132	3' CATTTCCCCTCCATTTGTAGG 86221	_____
		CATTTCTCCTCCG GGG	
		GTAAAGGGGAGGT TCC	
		AAACA	
GAM3803	KIAA0057	3' CATTTCTCCCCCAGTTGCA 86222	GGC
		CATTTCTCCTCCGG GCA	
		GTAAAGAGGGGGTC CGT	
		AA_	
GAM3803	KIAA0323	3' CATTTCTCCTCCCAACAGG 86223	_____
		CATTTCTCCTCC GGG	
		GTAAAGAGGAGG TCC	
		GTTG	
GAM3803	KIAA0356	3' CACTTCTCCACAGTGCA 86225	TC G
		CATTTCTCC CGG GCG	
		GTGAAGAGG GTC CGT	
		T_ A	
GAM3803	KIAA0356	3' CATTTCTCCTTCTCCTAATGGG 86224	___ _
		CATTTCTCC TCC GGG	
		GTAAAGAGG AGG CCC	
		AAG ATTA	
GAM3803	KIAA0574	3' TCTCTCCTGCAAAAGTGCA 86227	C _ C
		TTTCTCCT CGGG G GCA	
		AGAGAGGA GTTT C CGT	
		C T A	
GAM3803	KIAA0574	3' CATTTATCCTCCGCCAA 86226	C GGG G
		CATTT TCCTCC GC CAA	

		GTAAA AGGAGG CG GTT	
		T _ _	
GAM3803 KIAA0830	3'	CATTTCTCCTCTGTCAAG 86228	_____
		CATTTCTCCTC CGGG	
		GTAAAGAGGAG GTTC	
		ACA	
GAM3803 KIAA1204	5'	TTTCTCCTCAGCTTAAG 86229	CGG GC
		TTTCTCCTC GGC AAG	
		AAAGAGGAG TCG TTC	
		____ AA	
GAM3803 KIAA1276	5'	CATTTCCCTGGAGAGCG 86230	T CC
		CATTTC CCT GGGGCG	
		GTAAAG GGA TCTCGC	
		_ CC	
GAM3803 KIAA1679	3'	TTCTCCTCCACAGCGCA 86231	G
		TTTCTCCTCCG GCGCA	
		AAGGAGGAGGT TCGCGT	
		G	
GAM3803 KIAA1918	5'	CATTTCTCTTTGGGGAACA 86232	CTCC C
		CATTTCTC GGGG GCA	
		GTAAAGAG CCCC TGT	
		AAA_ T	
GAM3803 MGC11335	3'	CATTTCTCCTCAGGCCTCA 86233	CG G_
		CATTTCTCCTC GGGC CA	
		GTAAAGAGGAG TCCG GT	
		_ GA	
GAM3803 NTN4	3'	CATTTCCCCTTTAGCCAAG 86234	CCGG G
		CATTTCTCCT GGC CAAG	
		GTAAAGGGGA TCG GTTC	
		AA_ _	
GAM3803 PGRMC1	5'	TTTCTCCTCCCCGGACGC 86235	G_
		TTTCTCCTCC GGGCGC	
		AAAGAGGAGG CCTGCG	
		GG	
GAM3803 PPP1R1A	3'	CATCTCTCTTCCCACAGCA 86236	C_ G
		CATTTCTC TCCG GGCG	
		GTAGAGAG GGGT TCGT	
		AA G	
GAM3803 PRO1855	3'	CATTTCTCCTCATTCCTTCAGG 86237	_____
		CATTTCTCCTC CGGG	

		GTAAAGAGGAG	GTCC	
		TAAGGAA		
GAM3803	PTPRT	3' TTTCTCCTCCACATCCAAG	86238	GGGCG
		TTTCTCCTCCG	CAAG	
		AAAGAGGAGGT	GTTC	
		GTAG_		
GAM3803	RHOBTB3	3' CATTTCTCCCTTGCCAGCCAAG	86239	___ GG G
		CATTTCTCCT	CC GGC CAAG	
		GTAAAGAGGG	GG TCG GTTC	
		AAC	__ _	
GAM3803	RNF8	3' ATTTCTCCTTAATACAAG	86240	CCGG CG
		ATTTCTCCT	GG CAAG	
		TAAAGAGGA	TT GTTC	
		A__ AT		
GAM3803	VDAC3	3' CATTTCTCTTCACTTCCAGG	86241	___ _
		CATTTCTC	CT CCGGG	
		GTAAAGAG	GA GGTCC	
		AAGT	A	
GAM3803	ZNF317	3' ATTTCTCCTAGCGTAA	86242	CCGG C
		ATTTCTCCT	GGCG AA	
		TAAAGAGGA	TCGC TT	
		___ A		
GAM3803	LOC119146	5' TTTCTCCTGCGCTTGCGCA	86243	C GG_
		TTTCTCCT	CG GCGCA	
		AAAGAGGA	GC CGCGT	
		C	GAA	
GAM3803	LOC122769	3' CATTCTCCTCTCCAGCAAG	86244	CGGGGC
		CATTTCTCCTC	GCAAG	
		GTAAGGAGGAG	CGTTC	
		AGGT_		
GAM3803	LOC129831	3' CATTTTTCCTGACACAAG	86245	CTCC GG
		CATT	TCC GGCGCAAG	
		GTAAA	AGG CTGTGTTC	
		AA_ A_		
GAM3803	LOC146794	5' CATTTCTTCCTTTCCAGTGA	86246	_ _ _
		CATTTCT	CC TCCGG GG	
		GTAAAGA	GG AGGTC CT	
		A	AA A	
GAM3803	LOC152940	3' TTTCTCCTTCTAAAAGCA	86247	_ CG C
		TTTCTCCT	C GGG GCA	

	AAAGAGGA G TTT CGT	
	A AT _	
GAM3803 LOC164356 5'	ATTCCTCCTTTTCCATGAG 86248	___ _
	ATTTCTCC TCCG GGG	
	TAAGGAGG AGGT CTC	
	AAA A	
GAM3803 LOC165552 3'	ATTTCTCCTTCTCCGCA 86249	_ GGGG
	ATTTCTCCT CC CGCA	
	TAAAGAGGA GG GCGT	
	A AG__	
GAM3803 LOC168391 5'	CACTTCTCTTTTCGATGCCCAAG 86250	CTC GG G
	CATTTCTC CG GC CAAG	
	GTGAAGAG GC CG GTTC	
	AAA TA G	
GAM3803 LOC197273 5'	TTTCCCCTTCCAATGGGCGCAA 86251	- _
G	TTTCTCCT CCG GGGCGCAAG	
	AAAGGGGA GGT CCCGCGTTC	
	A TA	
GAM3803 LOC253955 5'	CATTTCCCCTCTGCAC 86252	CGGG
	CATTTCTCCTC GCGC	
	GTAAAGGGGAG CGTG	
	A__	
GAM3803 LOC256529 5'	CATTTCTCCACGGTTCCCGTGA 86253	_____ _
G	CATTTCTCC TCCG GGG	
	GTAAAGAGG GGGC CTC	
	TGCCAA A	
GAM3803 LOC56267 3'	TTTCTCCTTTGCAATCAAG 86205	CCGGG _
	TTTCTCCT GCG CAAG	
	AAAGAGGA CGT GTTC	
	AA__ TA	
GAM3803 LOC56270 3'	CATTTCCCTCCACACCAGCG 86254	T G__
	CATTTCCCTCCG GGCG	
	GTAAAG GGAGGT TCGC	
	_ GTGG	
GAM3803 LOC90719 3'	CATTTCTCTGCCCGCATGCA 86255	C_ GG_
	CATTTCTC TCCG GCG	
	GTAAAGAG GGGC CGT	
	AC GTA	
GAM3803 LOC92335 3'	CATCTCTCTTCTGCGGAG 86256	C _
	CATTTCTC TC CGGGG	

		GTAGAGAG AG GCCTC		
		A AC		
GAM3803	LOC92558	3' CATCTCTCCTTTGACCCTGGG	86257	___ G_
		CATTCTCTCT CC GGG		
		GTAGAGAGGA GG CCC		
		AACT GA		
GAM3803	LOC92703	3' CATTCTCTCCCTCCCCTAACA	86258	_ GG_
		CATTCTCTCC TCC GGCG		
		GTAAAGAGG AGG TTGT		
		G GGA		
GAM3804	ACVR1B	3' TACAGACACACACACACA	86261	AA_
		TACA ACACACACACA		
		ATGT TGTGTGTGTGT		
		CTG		
GAM3804	ANKH	3' TACATAACATATACAGCATATA	86262	A CACAC
		TACA AACA ACAGTATATA		
		ATGT TTGT TGTCGTATAT		
		A ATA__		
GAM3804	ARF4L	3' TACAGAGGACACACACAGCTTA	86263	AAAC A
	TA	TACA ACACACACAGT TATA		
		ATGT TGTGTGTGTGCG ATAT		
		CTCC A		
GAM3804	BAZ2A	3' TACAGGGTCACACACACACACA	86264	AA___ G
	CATA	TACA ACACACACACA TATATA		
		ATGT TGTGTGTGTGT GTGTAT		
		CCCAG _		
GAM3804	BCL11A	3' CACAAATAGCACACAGTGTAT	86265	ACACA A
		TACAAA CACACAGT TAT		
		GTGTTT GTGTGTCA ATA		
		ATC__ C		
GAM3804	CASP8AP2	3' TACAGAAACACACATACATACA	86266	_ C G
	TA	TACA AAACACACA ACA TATATA		
		ATGT TTTGTGTGT TGT ATGTAT		
		C A _		
GAM3804	COL13A1	3' TACAAACACACACACAG	86267	A
		TACAAA CACACACACAG		
		ATGTTT GTGTGTGTGTC		
		_		
GAM3804	COL13A1	3' TACAAACACACACACAG	86267	A
		TACAAA CACACACACAG		

ATGTTT GTGTGTGTGTC

GAM3804	COL13A1	3'	TACAAACACACACACAG	86267	A		
			TACAAA CACACACACAG				
			ATGTTT GTGTGTGTGTC				
GAM3804	COL13A1	3'	TACAAACACACACACAG	86267	A		
			TACAAA CACACACACAG				
			ATGTTT GTGTGTGTGTC				
GAM3804	COL13A1	3'	TACAAACACACACACAG	86267	A		
			TACAAA CACACACACAG				
			ATGTTT GTGTGTGTGTC				
GAM3804	COL13A1	3'	TACAAACACACACACAG	86267	A		
			TACAAA CACACACACAG				
			ATGTTT GTGTGTGTGTC				
GAM3804	CREBL2	3'	CATAAAACACACACAGACATA	86268	A	C	T
			CA AA ACACACACAG ATATA				
			GT TT TGTGTGTGTC TGTAT				
			A T				
GAM3804	CYP24	3'	TACACGGACACACACACA	86269	AA	_	
			TACA ACACACACACA				
			ATGT TGTGTGTGTGT				
			GCC				
GAM3804	DUOX1	3'	TACAGACATGCACACACA	86270	AA	_	
			TACA ACA CACACACA				
			ATGT TGT GTGTGTGT				
			C_ AC				
GAM3804	ERBB2IP	3'	TACAACACACATACAATA	86271	AA	C	
			TACA ACACACA ACAGTA				
			ATGT TGTGTGT TGTAT				
			— A				
GAM3804	FMR2	3'	TACAAAGCAAACACACACGC	86272	A	C	_
			TACAAA CA ACACACA GT				

			ATGTTT GT TGTGTGT CG		
			C T G		
GAM3804	FSTL1	3'	TACAAAAC TACACACACAG 86273	—	
			TACAAAAC ACACACACAG		
			ATGTTTTG TGTGTGTGTC		
			A		
GAM3804	GALR1	3'	AAACACACATCAATATA 86274	CA	
			AAACACACA CAGTATA		
			TTTGTGTGT GTTATAT		
			A_		
GAM3804	GATM	3'	TAAAAATACACATACAGTAT 86275	C C C	
			A AAAA ACACA ACAGTAT		
			A TTTT TGTGT TGTCATA		
			T A A		
GAM3804	GLDC	3'	TACAGAGATATACACAGTATAT 86276	AAACACAC	
	A		TACA ACACAGTATATA		
			ATGT TGTGTCATATAT		
			CTCTATA_		
GAM3804	H1F0	3'	TACACAAACACACACATGCA 86277	— CA	
			TACA AAACACACACA GTA		
			ATGT TTTGTGTGTGT CGT		
			G A_		
GAM3804	MAP3K8	3'	AAAACATACACAGTAT 86278	CAC	
			AAAACA ACACAGTAT		
			TTTTGT TGTGTCATA		
			A_		
GAM3804	MTMR6	3'	AAACACACAAATATAT 86279	CAC	
			AAACACACA AGTATAT		
			TTTGTGTGT TTATATA		
			—		
GAM3804	MTMR8	3'	AAAACACACATACACATATA 86280	C G	
			AAAACACACA ACA TATATA		
			TTTTGTGTGT TGT GTATAT		
			A _		
GAM3804	NDUFS2	3'	TACACGAACATACACACACA 86281	A_ _	
			TACA AAC ACACACACA		
			ATGT TTG TGTGTGTGT		
			GC TA		
GAM3804	PCDH11X	3'	TACAAAATTACACACAGT 86282	CAC	
			TACAAA ACACACAGT		

			ATGTTTT TGTGTGTCA		
			AAA		
GAM3804	PCDH11X	3'	TACAAAATTTACACACAGT	86282	CAC
			TACAAAA ACACACAGT		
			ATGTTTT TGTGTGTCA		
			AAA		
GAM3804	PCK1	3'	TACAAATACACATACACAAATA	86283	_ C T
	TA		TACAAA ACACA ACACAG ATATA		
			ATGTTT TGTGT TGTGTT TATAT		
			A A _		
GAM3804	PLAU	3'	AAACATACACACACATATA	86284	C G
			AAACA ACACACA TATATA		
			TTTGT TGTGTGT GTATAT		
			A _		
GAM3804	RAB23	3'	TAAAAACATATACACAATAT	86285	C CAC
			A AAAACA ACACAGTAT		
			A TTTTGT TGTGTTATA		
			T ATA		
GAM3804	RAB4A	3'	ACAGGACATACAGTACATA	86286	C_ C
			ACA ACA ACAGTATATA		
			TGT TGT TGTCATGTAT		
			CC A		
GAM3804	RB1	3'	AAAACAAGCACACAGTATA	86287	CA
			AAAACA CACACAGTATA		
			TTTTGT GTGTGTCATAT		
			TC		
GAM3804	RDX	3'	CACAGAGTACACACACACA	86288	AA__
			TACA ACACACACACA		
			GTGT TGTGTGTGTGT		
			CTCA		
GAM3804	ROR2	3'	CAAAATACACATGGAGTATA	86289	C CAC
			CAAAA ACACA AGTATA		
			GTTTT TGTGT TCATAT		
			A ACC		
GAM3804	RPS6KA5	3'	TAAAAACATACACATAGC	86290	C C C
			A AAAACA ACACA AGT		
			A TTTTGT TGTGT TCG		
			T A A		
GAM3804	SCO1	3'	CACAAAGTACAATCCAGTATAT	86291	AC CACA
			TACAAA ACA CAGTATAT		

			GTGTTT TGT GTCATATA		
			CA TAG_		
GAM3804	SH3BP4	3'	TACAGAAAACACACACACA 86292	___	
			TACA AAACACACACACA		
			ATGT TTTGTGTGTGTGT		
			CT		
GAM3804	SIL	3'	AAAACACACTCATACTCAATA 86293	___	A
			AAAACACAC AC CAGTA		
			TTTTGTGTG TG GTTAT		
			AGTA A		
GAM3804	SLC19A2	3'	TACAAAACACTGCATACAGTA 86294		ACA C
			TACAAAAC CA ACAGTA		
			ATGTTTTG GT TGTCAT		
			AC_ A		
GAM3804	SLC1A4	3'	TACACAACACACATGTGTGTAT 86295	A	CACA_
	A		TACA AACACACA GTATA		
			ATGT TTGTGTGT CATAT		
			G ACACA		
GAM3804	SLC20A2	3'	TACACAACAATCAATACACAGT 86296	A	___ C_
	ATAT		TACA AACA CA ACACAGTATAT		
			ATGT TTGT GT TGTGTCATATA		
			G TA TA		
GAM3804	SPF30	3'	TACAAAAAGTACACACCA 86297	C_	A
			TACAAAA ACACAC CA		
			ATGTTTT TGTGTG GT		
			TCA _		
GAM3804	STX7	3'	ACAGAATACACACACCTTA 86298	A C	AG
			ACA AA ACACACAC TA		
			TGT TT TGTGTGTG AT		
			C A GA		
GAM3804	TCF8	3'	TACAAAACACACATCACA 86299	___	
			TACAAAACACACA CACA		
			ATGTTTTGTGTGT GTGT		
			A		
GAM3804	TEM7	3'	TACAAACACACACACAAACATA 86300	A	T
			TACAAA CACACACACAG ATATA		
			ATGTTT GTGTGTGTGTT TGTAT		

GAM3804	CHCR	3'	CAAAACACTACAGTAT 86301		ACAC
			CAAAACAC ACAGTAT		

			GTTTTGTG	TGTCATA		
			A	_____		
GAM3804	CLDN1	3'	TACAAAACCACACTTACATGTA	86302	A	__ _
			TACAAAAC CACAC ACA GTA			
			ATGTTTTG GTGTG TGT CAT			
			_ AA A			
GAM3804	DKFZP434F091	3'	TGAAAACACACACCTTAGT	86303	C	AC_
			A AAAACACACAC AGT			
			A TTTTGTGTGTG TCA			
			C GAA			
GAM3804	DKFZP586D0623	3'	AAAACACACCAGCAT	86304	ACA	
			AAAACACAC CAGTAT			
			TTTTGTGTG GTCGTA			

GAM3804	EHM2	3'	ACAAAGCACACACTTGTAT	86305	A	ACA
			ACAAA CACACAC GTAT			
			TGTTT GTGTGTG CATA			
			C AA_			
GAM3804	FLJ10305	3'	TACAAGTACACACACACA	86306	A_	
			TACAA ACACACACACA			
			ATGTT TGTGTGTGTGT			
			CA			
GAM3804	FLJ10856	3'	CACAAAATACATACACATATA	86307	C C G	
			TACAAAA ACA ACACA TATA			
			GTGTTTT TGT TGTGT ATAT			
			A A _			
GAM3804	FLJ11850	3'	CAAAGCACACACACACAG	86308	_____	
			CAAA ACACACACACAG			
			GTTT TGTGTGTGTGTC			
			CG			
GAM3804	FLJ12666	3'	ACACATACACACATATA	86309	C G	
			ACACA ACACA TATATA			
			TGTGT TGTGT GTATAT			
			A _			
GAM3804	FLJ13910	3'	TACAATACACACATGCACA	86310	A	_____
			TACAA ACACACA CACA			
			ATGTT TGTGTGT GTGT			
			A AC			
GAM3804	FLJ14743	3'	CACAGAATACACACAGAATTAT	86311	A C	CAG_
	ATA		TACA AA ACACACA TATATA			

			GTGT TT TGTGTGT ATATAT		
			C A CTTA		
GAM3804	FLJ20071	3'	TACAACACACACACAG 86312	AA	
			TACA ACACACACACAG		
			ATGT TGTGTGTGTGTC		
			—		
GAM3804	FLJ20371	3'	TACAAACACACACACACACA 86313	—	G
		T	TACAAA ACACACACACA TATAT		
			ATGTTT TGTGTGTGTGT GTGTA		
			G —		
GAM3804	FLJ21276	3'	TACACAAACACACACACA 86314	—	
			TACA AAACACACACACA		
			ATGT TTTGTGTGTGTGT		
			G		
GAM3804	FLJ21302	3'	TACACAACATACACAGAAGTA 86315	A C C_	
			TACA AACA ACACA AGTA		
			ATGT TTGT TGTGT TCAT		
			G A CT		
GAM3804	GHITM	3'	AAAACACACATATAT 86316	CACAG	
			AAAACACACA TATAT		
			TTTTGTGTGT ATATA		
			—		
GAM3804	GT650	3'	CAAAACACACAATTCTATATA 86317	CACAG	
			CAAAACACACA TATATA		
			GTTTGTGTGT ATATAT		
			TAAG_		
GAM3804	HERPUD1	3'	TACAAACACACATGCAG 86318	A CA	
			TACAAA CACACA CAG		
			ATGTTT GTGTGT GTC		
			— AC		
GAM3804	HYPC	3'	ACAAAACACACGTACAT 86319	ACACA	
			ACAAAACACAC GTATAT		
			TGTTTTGTGTG CATGTA		
			—		
GAM3804	JAM1	3'	TACACAACACACACACAA 86320	A	
			TACA AACACACACACAG		
			ATGT TTGTGTGTGTGT		
			G		
GAM3804	JAM1	3'	TACACAACACACACACAA 86320	A	
			TACA AACACACACACAG		

			ATGT TTGTGTGTGTGTT		
			G		
GAM3804	JAM1	3'	TACACAACACACACACAA	86320	A
			TACA AACACACACACAG		
			ATGT TTGTGTGTGTGTT		
			G		
GAM3804	JAM1	3'	TACACAACACACACACAA	86320	A
			TACA AACACACACACAG		
			ATGT TTGTGTGTGTGTT		
			G		
GAM3804	KIAA0143	3'	TACAAAAGCACACAGT	86321	CACA
			TACAAA CACACAGT		
			ATGTTTT GTGTGTCA		
			C_		
GAM3804	KIAA0275	3'	TACAAGGACACACAAACGT	86322	A_ C A
			TACAA ACACACA AC GT		
			ATGTT TGTGTGT TG CA		
			CC T _		
GAM3804	KIAA0295	3'	TACAAAACACACAACAATA	86323	C
			TACAAAACACACA ACAGTA		
			ATGTTTTGTGTGT TGTTAT		
			-		
GAM3804	KIAA0318	3'	CACGACACATACAAAGTATA	86324	AA C C
			CA ACACA ACA AGTATA		
			GT TGTGT TGT TCATAT		
			GC A T		
GAM3804	KIAA0472	3'	ACACACACACATATATA	86325	G
			ACACACACACA TATATA		
			TGTGTGTGTGT ATATAT		
			-		
GAM3804	KIAA0820	3'	TACAAAGACACACACACA	86326	-
			TACAAA ACACACACACA		
			ATGTTT TGTGTGTGTGT		
			C		
GAM3804	KIAA0831	3'	TACAAAACACCAAATATA	86327	A CAC
			TACAAAACAC CA AGTATA		
			ATGTTTTGTG GT TTATAT		
			- -		
GAM3804	KIAA0978	3'	CAAAATACACACACTAAATATA	86328	C AGT
			CAAAA ACACACAC ATATA		

		GTTTT TGTGTGTG TATAT		
		A ATT		
GAM3804	KIAA1069	3' AAACACACACACATTATA 86329	G	
		AAACACACACACA TATA		
		TTTGTGTGTGTGT ATAT		
		A		
GAM3804	KIAA1423	3' TACAAACCTTGAACATAGTATA 86330	ACACAC	C
	TA	TACAAA ACA AGTATATA		
		ATGTTT TGT TCATATAT		
		GGAACT A		
GAM3804	KIAA1484	3' TACAGACACACACACAG 86331	AA	
		TACA ACACACACACAG		
		ATGT TGTGTGTGTGTC		
		C_		
GAM3804	KIAA1493	3' ACAAAACATGCAGTCAGTGTAT 86332	CA CA	A
	A	ACAAAACA CA CAGT TATA		
		TGTTTTGT GT GTCA ATAT		
		AC CA C		
GAM3804	KIAA1550	3' AAACACATACACATATA 86333	C	G
		AAACACA ACACA TATA		
		TTTGTGT TGTGT ATAT		
		A _		
GAM3804	KIAA1615	3' AACACACATACACACTATATA 86334	_	G
		AACACAC ACACA TATATA		
		TTGTGTG TGTGT ATATAT		
		TA G		
GAM3804	KIAA1958	3' TACACAGACACACACACATATA 86335	AA_	G
		TACA ACACACACACA TATA		
		ATGT TGTGTGTGTGT ATAT		
		GTC _		
GAM3804	MGC2817	3' TACAATATACACACATAAAGTA 86336	A_	CAC
		TACAA ACACACA AGTA		
		ATGTT TGTGTGT TCAT		
		ATA ATT		
GAM3804	MYO18B	5' TACAGACACACGCAGCACAT 86337	AAAC	A
		TACA ACACAC CAGTATAT		
		ATGT TGTGTG GTCGTGTA		
		C_ C		
GAM3804	PRDM13	3' AAAACAACACACACCACAT 86338	C	G
		AAAACA ACACACA TATAT		

			TTTTGT TGTGTGT GTGTA		
			— G		
GAM3804	RDC1	3'	TACAAAACACCACACAGATATA 86339	A	T
			TACAAAACAC CACACAG ATATA		
			ATGTTTTGTG GTGTGTC TATAT		
			— —		
GAM3804	SERPINB7	3'	AAACTACACAGCATAT 86340	ACAC	
			AAAC ACACAGTATAT		
			TTTG TGTGTCGTATA		
			A —		
GAM3804	SNRK	3'	TACAAAACATGCACAAT 86341	CACA	
			TACAAAACA CACAGT		
			ATGTTTTGT GTGTTA		
			AC —		
GAM3804	STK36	3'	AAACACACACACACATA 86342	G	
			AAACACACACACA TATA		
			TTTGTGTGTGTGT GTAT		
			—		
GAM3804	THEA	3'	ACACACACACAAAAATATA 86343	T_	
			ACACACACACAG ATATA		
			TGTGTGTGTGTT TATAT		
			TT		
GAM3804	TP53INP1	3'	AAACATACACACCTTCAT 86344	C	AG_
			AAAACA ACACAC TAT		
			TTTTGT TGTGTG GTA		
			A GAA		
GAM3804	TP53INP1	3'	AAACATACACACCTTCAT 86344	C	AG_
			AAAACA ACACAC TAT		
			TTTTGT TGTGTG GTA		
			A GAA		
GAM3804	USP25	3'	AAACATACACATAGTATA 86345	C	C
			AAACA ACACA AGTATA		
			TTTGT TGTGT TCATAT		
			A A		
GAM3804	ZNF387	3'	TACAAAACACATCAAGTA 86346	_	CAC
			TACAAAACACA CA AGTA		
			ATGTTTTGTGT GT TCAT		
			A —		
GAM3804	ZNF396	3'	CAAGATACACACAACTCAATAT 86347	A_	_A
			CAA ACACACA C CAGTATA		

	GTT TGTGTGT G GTTATAT		
	CTA T A		
GAM3804 LOC129401 3'	CATACTGCGCACAGTATATA 86348	C A__	
	CA AC CACAGTATATA		
	GT TG GTGTCATATAT		
	A ACGC		
GAM3804 LOC130507 3'	TACAAGATATCACACCAGTA 86349	AACA_ A	
	TACAA CACAC CAGTA		
	ATGTT GTGTG GTCAT		
	CTATA _		
GAM3804 LOC145693 5'	CAAGGTGCACACACAGATA 86350	AACA T	
	CAA CACACACAG ATA		
	GTT GTGTGTGTC TAT		
	CCAC _		
GAM3804 LOC147077 3'	AAAACACACAATACACTATATA 86351	C_ G	
	AAAACACACA ACA TATATA		
	TTTTGTGTGT TGT ATATAT		
	TA G		
GAM3804 LOC150368 3'	TACAAAACACTGTAGCAATA 86352	ACACA	
	TACAAAACAC CAGTA		
	ATGTTTTGTG GTTAT		
	ACATC		
GAM3804 LOC150406 3'	TACAAACACACACACACA 86353	_	
	TACAAA ACACACACACA		
	ATGTTT TGTGTGTGTGT		
	G		
GAM3804 LOC151103 3'	TACAAAACATTTACAGTA 86354	CACAC	
	TACAAAACA ACAGTA		
	ATGTTTGT TGTCAT		
	AAA__		
GAM3804 LOC151477 5'	CAGAACACACATGAGTCTATA 86355	A CAC A	
	CA AACACACA AGT TATA		
	GT TTGTGTGT TCA ATAT		
	C AC_ G		
GAM3804 LOC151614 5'	CAACACACACATGCACGCGCAT 86356	A _ A_	
A	CAA ACACACA CAC GTATA		
	GTT TGTGTGT GTG CGTAT		
	G AC CG		
GAM3804 LOC151647 3'	TACAATGCACACACAATA 86357	AACA	
	TACAA CACACACAGTA		

	ATGTT GTGTGTGTTAT		
	AC__		
GAM3804 LOC152633 5'	CACAAAGTACACACACGTA 86358	AC	A
	TACAAA ACACACAC GTA		
	GTGTTT TGTGTGTG CAT		
	CA _		
GAM3804 LOC154007 3'	TACAAAACACAACATGACAGTA 86359	_ C_	
TA	TACAAAACACA CA ACAGTATA		
	ATGTTTTGTGT GT TGTCATAT		
	T AC		
GAM3804 LOC154743 3'	TACAAACATACGCACAACAT 86360	A C A	
	TACAAA CA AC CACAGTAT		
	ATGTTT GT TG GTGTTGTA		
	_ A C		
GAM3804 LOC154792 3'	TACAAACACACACGCACACATA 86361	A A G	
	TACAAA CACACAC CA TATATA		
	ATGTTT GTGTGTG GT GTGTAT		
	_ C _		
GAM3804 LOC157621 3'	TACACAGACACACACACA 86362	AA_	
	TACA ACACACACACA		
	ATGT TGTGTGTGTGT		
	GTC		
GAM3804 LOC158014 5'	TACACAAACACACACACA 86314	_	
	TACA AAACACACACACA		
	ATGT TTTGTGTGTGTGT		
	G		
GAM3804 LOC201194 5'	ACACACACACACATATA 86363	G	
	ACACACACACA TATATA		
	TGTGTGTGTGT GTATAT		
	-		
GAM3804 LOC219673 5'	ACAAAACACAAAGTAT 86364	CACAC	
	ACAAAACACA AGTAT		
	TGTTTTGTGT TCATA		
	T__		
GAM3804 LOC220758 3'	TACAGAGATATACACAGTATAT 86276	AAACACAC	
A	TACA ACACAGTATATA		
	ATGT TGTGTCATATAT		
	CTCTATA_		
GAM3804 LOC257319 3'	CAGAACATACACACGCA 86365	A C A	
	CA AACA ACACAC GTA		

		GT TTGT TGTGTG CGT		
		C A _		
GAM3804	LOC51101	3' AAACATACACACATTATATA	86366	C G
		AAACA ACACACA TATATA		
		TTTGT TGTGTGT ATATAT		
		A A		
GAM3804	LOC90148	3' TACAAAGCAACACACAACAGCA	86367	A _ _
	T	TACAAA CA CACACA CAGTAT		
		ATGTTT GT GTGTGT GTCGTA		
		C T T		
GAM3804	LOC93356	5' AAAACACACGCACACAC	86368	A G
		AAAACACAC CACA TAT		
		TTTTGTGTG GTGT GTG		
		C _		
GAM3804	LOC93444	3' CAAAACATACACACGCA	86369	C A
		CAAAACA ACACAC GTA		
		GTTTTGT TGTGTG CGT		
		A _		
GAM3805	ADAM12	5' TCGGGCCCGGCGGCGAGCG	86372	T C C
		TTGGGCCC GC GCG AGCG		
		AGCCCGGG CG CGC TCGC		
		C C _		
GAM3805	CNGB1	3' GGGCGAGGGGCGCAGCGGGCG	86373	CCTGCC A
		GGGC GCGCAGCG GCG		
		CCCG CGCGTCGC CGC		
		CTCCC_ C		
GAM3805	FUT5	3' TTGGGCCCTGTGCCTCCCAGCG	86374	_ GCG
		TTGGGCCCT GCC CAGCG		
		AACCCGGGA CGG GTCGC		
		CA AGG		
GAM3805	GPR30	3' TTGGACCCTGCGGGGCGAGCG	86375	CGCGCA
		TTGGGCCCTGC GCGAGCG		
		AACCTGGGACG CGCTCGC		
		CCC_		
GAM3805	PACE	3' TTGGGCCCTGACGGGAGAGGCG	86376	C CGCA_
		TTGGGCCCTG CG GCG		
		AACCCGGGAC GC CGC		
		T CCTCTC		
GAM3805	RGS19	3' TTGGGTCCTGCCACCTTGAG	86377	C GCAGC
		TTGGG CCTGCCGC GAG		

AACCC GGACGGTG CTC
 A GAA__
 GAM3805 LOC124512 5' TTGGGCCCCGGGCGGGCG 86378 CC CA
 TTGGGCCCTG GCG GCG
 ||||| ||| |||
 AACCCGGGGC CGC CGC
 C_ C_
 GAM3805 LOC56961 5' CTGGGTTCTCAGCGCAGCGGGC 86379 CC GCC A
 G TTGGG CT GCGCAGCG GCG
 |||| || ||||| |||
 GACCC GA CGCGTCGC CGC
 AA GT_ C
 GAM3806 JAG1 3' AAGCCTTTTGTATCT 86382 AGC C
 AGGCCTTT TT GATCT
 ||||| || |||||
 TTCGGAAA AA CTAGA
 — —
 GAM3806 KIAA1594 3' ATAGGGCTTTTAGCTTCA 86383 A C
 ATA GGC TTTAGCTTCG
 ||| ||| ||||| |||
 TAT CCG AAATCGAAGT
 C A
 GAM3806 POF1B 3' ATAAGGCTTTTAGCTTCA 86384 C
 ATAAGGC TTTAGCTTCG
 ||||| ||||| |||
 TATTCCG AAATCGAAGT
 A
 GAM3806 LOC115749 5' CATCAACCCTTTGGCTTTGAT 86385 A G A C
 TAT AG CCTTT GCTT GAT
 ||| || |||| ||| |||
 GTA TT GGAAA CGAA CTA
 G G C A
 GAM3807 EBI2 3' TACATTGGGAGTTATTAAGA 86388 AGATC
 TACAT AGTTATTAAGA
 |||| ||||| |||
 ATGTA TCAATAATTCT
 ACCC_
 GAM3807 FLJ13262 3' TCTATGCAGATCAGGTAGGTAA 86389 CA T T_
 GA TCTA TAGATCAG TA TAAGA
 |||| ||||| || |||||
 AGAT GTCTAGTC AT ATTCT
 AC C CC
 GAM3807 HSMPP8 3' TACATAGATGTGCTAGAAGAA 86390 CA TT
 TACATAGAT GTTA AAGAA
 ||||| ||| |||||
 ATGTATCTA CGAT TTCTT
 CA C_
 GAM3807 KIAA0630 3' TCTCCATAGCCCAATATTAAGA 86391 A AT T
 A TCT CATAG CAGT ATTAAGAA
 ||| |||| ||| ||||| |||

			AGA GTATC GTTA TAATTCTT		
			G GG _		
GAM3807	MLCB	3'	TCTGTATAGACCACAGTTATT	86392	AC _
			TCT ATAGAT CAGTTATT		
			AGA TATCTG GTCAATAA		
			CA GT		
GAM3807	SNAP29	3'	TCTACCAGTTATTGAGA	86393	ATAGAT A
			TCTAC CAGTTATT AGA		
			AGATG GTCAATAA TCT		
			_____ C		
GAM3807	LOC149464	5'	TCTGCATAGAATCACTATAAGA	86394	A _ G T
	A		TCT CATAGA TCA TTAT AAGAA		
			AGA GTATCT AGT GATA TTCTT		
			C T _ _		
GAM3807	LOC196477	3'	TACATAGATCTGTTTATTAA	86395	AG_
			TACATAGATC TTATTAA		
			ATGTATCTAG AATAATT		
			ACA		
GAM3807	LOC254057	3'	CTACATAGGTTCTAAGA	86396	ATCA A
			CTACATAG GTT TTAAGA		
			GATGTATC CAA GATTCT		
			_____ _		
GAM3807	LOC51030	3'	TACATAGATTGCTTTAAGAA	86397	CA A
			TACATAGAT GTT TTAAGAA		
			ATGTATCTA CGA AATTCTT		
			A_ _		
GAM3807	LOC57117	5'	TCTGCAAAGATCAGTTAT	86398	A T
			TCT CA AGATCAGTTAT		
			AGA GT TCTAGTCAATA		
			C T		
GAM3808	ADCY8	5'	GCCGGGGGTGGCGGAGGG	86401	_A_
			GCCGGGGGTG C AGGG		
			CGGCCCCCAC G TCCC		
			C CC		
GAM3808	AP2M1	3'	GGGCTGGTGCAAAGGGAA	86402	_ _
			GGG GGTGCAA GGGAA		
			CCC CCACGTT CCCTT		
			GA T		
GAM3808	AQP2	3'	AGGAAGGGGTGCAAGGGAAG	86403	CC A
			AG GGGGGTGCAAGGG AAG		

			TC TCCCCACGTTCCC TTC		
			CT C		
GAM3808	CDX2	5'	GCCGGGGGGGCACGAAGGGAAAG 86404	T	___
			GCCGGGGG GCA AGGGAAAG		
			CGGCCCCC CGT TCCCTTTC		
			_ GCT		
GAM3808	FBXL7	3'	GCCTGTGTGCGAGGGAAAG 86405	GGGG	A
			GCC GTGC AGGGAAAG		
			CGG CACG TCCCTTTC		
			ACA_ C		
GAM3808	FGD1	5'	GCCGGGGGGCCGCTGGGGA 86406	_	AA
			GCCGGGGGT GC GGGA		
			CGGCCCCCG CG CCCT		
			G AC		
GAM3808	FOXE1	3'	TAGCAGGGGGTGCTGGGG 86407	C	AA
			TAGC GGGGGTGC GGG		
			ATCG CCCCCACG CCC		
			T AC		
GAM3808	GPC1	3'	CAGCTGGGGCACAGGAGGGAA 86408	CG	TG ___
			TAGC GGGG CA AGGGAA		
			GTCG CCCC GT TCCCTT		
			A_ GT CC		
GAM3808	GPX4	3'	TAGCCAGGGGTGGGGG 86409	CAA	
			TAGCCGGGGGTG GGG		
			ATCGGTCCCCAC CCC		
			C_		
GAM3808	GTF2I	5'	GCCGGGGGTGCCGAGGGGA 86410	AA	___
			GCCGGGGGTGC GGGA		
			CGGCCCCACG CCCT		
			GCTC		
GAM3808	GTF2I	5'	GCCGGGGGTGCCGAGGGGA 86410	AA	___
			GCCGGGGGTGC GGGA		
			CGGCCCCACG CCCT		
			GCTC		
GAM3808	HR	5'	GCCGAGTTGGGGGAAAG 86411	GG	CAA
			GCCGGG TG GGGAAAG		
			CGGCTC AC CCCTTTC		
			A_ C_		
GAM3808	HRH2	5'	GCCAGGGGGTGGGGAA 86412	_	CAA
			GCC GGGGGTG GGGAA		

		CGG CCCCCAC CCCTT		
		T —		
GAM3808	HSF4	3' TAGTCGGGGTAGTGGAGAG	86413	C — CA
		TAG CGGGG GTG AGGG		
		ATC GCCCC CAC TCTC		
		A AT C_		
GAM3808	KLHL1	5' GCTGGAGATGCGCGAGGGA	86414	C A_
		GC GGGGGTGC AGGGA		
		CG CCTCTACG TCCCT		
		A CGC		
GAM3808	MAP1A	5' TAGCCGGAGGTGCAGGG	86415	A
		TAGCCGGGGGTGCA GGG		
		ATCGGCCTCCACGT CCC		
		—		
GAM3808	MPDU1	3' CAGCCGGGCTGAGGGA	86416	G G CA
		TAGCCGG G TG AGGGA		
		GTCGGCC C AC TCCCT		
		_ G _		
GAM3808	NF1	5' GCCGGGGGGCGGCGAGGGAA	86417	T A_
		GCCGGGGG GC AGGGAA		
		CGGCCCCC CG TCCCTT		
		_ CCGCC		
GAM3808	NPTX1	3' GCCGGAGGTGCTGGCAGGGA	86418	A_
		GCCGGGGGTGC AGGGA		
		CGGCCTCCACG TCCCT		
		ACCG		
GAM3808	OAS3	5' CGCAGGTGCAAGGGGAAG	86419	G A
		CG GGGTGCAAGGG AAG		
		GC TCCACGTTCCC TTC		
		G C		
GAM3808	PRX	3' GCCGGGGCTCCAAGAGGGAAAG	86420	GTG _
		GCCGGGG CA AGGGAAAG		
		CGGCCCC GT TCCCTTTC		
		GAG TC		
GAM3808	PYGB	3' GGATGGCTACAAAGGGAAAG	86421	_ _ _
		GGG GG TGCAA GGGAAAG		
		CCT CC ATGTT CCCTTTC		
		A G T		
GAM3808	RANBP9	5' CAGCCGCTGAGGCAGGGGGA	86422	G_ T A_
		TAGCCG GGG GCA GGGA		

			GTCGGC CTC CGT CCCT			
			GA _ CC			
GAM3808	RARA	3'	CAGCTGGGGGTGCAGGG	86423	C	A
			TAGC GGGGGTGCA GGG			
			GTCG CCCCCACGT CCC			
			A _			
GAM3808	SGT	3'	GCCGGGAGGTCTGACTCGGAAA	86424	_	AA
			GCCGGG GGT GC GGGAA			
			CGGCCC CCA TG CCTTT			
			T GC AG			
GAM3808	SOX4	3'	GCTGGGGGTGCAGACAA	86425	C	A G
			GC GGGGGTGCA GG AA			
			CG CCCCCACGT CT TT			
			A _ G			
GAM3808	TAP2	3'	GCTGGGGAAGAGGGAAAG	86426	C	TGCA
			GC GGGGG AGGGAAAG			
			CG CCCCT TCCCTTTC			
			A TC__			
GAM3808	C20orf110	3'	GCAGGGCGAGAGGGAAAG	86427	CG	CA
			GC GGGGTG AGGGAAAG			
			CG TCCCGC TCCCTTTC			
			_ TC			
GAM3808	C20orf124	3'	GCCGGGGGTAGCATTGGA	86428	_	AG
			GCCGGGGGT GCA GGA			
			CGGCCCCCA CGT CCT			
			T AA			
GAM3808	DKFZP434N014	3'	GCTGGGGGTGCAGAGGGAA	86429	C	_
			GC GGGGGTGCA AGGGAA			
			CG CCCCCACGT TCCCTT			
			A C			
GAM3808	DKFZP434P0721	3'	TAGCAGTAGGTGGGGGAAAG	86430	CGG	CAA
			TAGC GGGTG GGGAAAG			
			ATCG TCCAC CCCTTTC			
			TCA C__			
GAM3808	DKFZP566B183	3'	GGCAGGGCAGAGGGAAAG	86431	_	T _
			GG GGG GCA AGGGAAAG			
			CC TCC CGT TCCCTTTC			
			G _ C			
GAM3808	DKFZP566G1424	3'	AGTCGGGAGTAGGGGGAA	86432	C	CAA
			AG CGGGGGTG GGGAA			

TC GCCCTCAT CCCTT
 A CC_
 GAM3808 DKFZp761G2113 3' TAGCCGGGGTGGGAAGG 86433 G CA
 TAGCCGGGG TG AGGG
 ||||| || |||
 ATCGGCCCC AC TTCC
 _ CC
 GAM3808 FKBP4 3' ACTGGGAGAGGGAAAG 86434 C TGCA
 GC GGGGG AGGGAAAG
 || ||| |||||
 TG CCCTC TCCCTTC
 A ____
 GAM3808 FLJ11181 3' CAGTTGGGGGCCAGGGAA 86435 CCG T A
 TAG GGGG GC AGGGAA
 ||| ||| || |||||
 GTC CCCC CG TCCCTT
 AA_ _ G
 GAM3808 FLJ11856 3' GGTGGCAGCATTGAGGGAAAG 86436 G _ ____
 GG GGT GCA AGGGAAAG
 || ||| || |||||
 CC CCG CGT TCCCTTC
 A T AAC
 GAM3808 FLJ14681 5' AGCCGGAACGTGCAAGGGA 86437 _
 AGCCGGGG GTGCAAGGGA
 ||||| |||||
 TCGGCCTT CACGTTCCCT
 G
 GAM3808 FLJ20986 5' GCCAGGAAGCACAGGGAA 86438 _ TG A
 GCCGGGG G CA GGGAA
 ||||| | || |||||
 CGGTCCT C GT CCCTT
 T GT _
 GAM3808 FLJ23360 5' GCGGGGGGCGCACCTAAGGGA 86439 C ____
 GC GGGGGTGCA AGGGA
 || ||||| |||
 CG CCCCCGCGT TCCCT
 C GGAT
 GAM3808 KIAA0125 3' AGTCGGTCACAGAGGGAAAG 86440 C GGGT _
 AG CGG GCA AGGGAAAG
 || ||| || |||||
 TC GCC TGT TCCCTTC
 A AG_ C
 GAM3808 KIAA0247 3' CAGCTGGGACTGGGAGGGAAAG 86441 C G CA
 TAGC GGGG TG AGGGAAAG
 ||| ||| || |||||
 GTCG CCCT AC TCCCTTC
 A G CC
 GAM3808 KIAA0255 3' GCTGGGGAGAAGAGGGAAAG 86442 C TGCA
 GC GGGGG AGGGAAAG
 || ||| |||||

		CG CCCCT TCCCTTTC		
		A CTTC		
GAM3808 KIAA0303	5'	TAGCCAGAGGAAGGGA 86443	TGC	
		TAGCCGGGGG AAGGGA		
		ATCGGTCTCC TTCCCT		
GAM3808 KIAA0427	5'	AGTCGGGGGTGGGGGAA 86444	C	CAA
		AG CGGGGGTG GGGAA		
		TC GCCCCAC CCCTT		
		A C_		
GAM3808 KIAA0590	3'	TAGCAGGGGTGCAGCCGCCAA 86445	C	_____
	GG	TAGC GGGGGTGCA AGGG		
		ATCG CCCCCACGT TTCC		
		T CGGCGG		
GAM3808 KIAA0821	5'	AGCCGGGGCTGGGGGGAA 86446	G	CAA
		AGCCGGGG TG GGGAA		
		TCGGCCCC AC CCCTT		
		G CC_		
GAM3808 KIAA1030	3'	GCCATAGCAAGGGAAAG 86447	GGGGT	
		GCCG GCAAGGGAAAG		
		CGGT CGTTCCTTTC		
		AT_		
GAM3808 KIAA1196	3'	TAGCTGGGGTGCTGGA 86448	C	AAG
		TAGC GGGGGTG C GGA		
		ATCG CCCCCACG CCT		
		A A_		
GAM3808 MDS018	3'	CAGCTGGGTTGTAGGGAAAG 86449	C	GG CA
		TAGC GGG TG AGGGAAAG		
		GTCG CCC AC TCCCTTTC		
		A A_ A_		
GAM3808 MGC16386	3'	GCCAGGGGTGCGGCAGGA 86450	AA_	
		GCCGGGGGTGC GGGAA		
		CGGTCCCCACG TCCT		
		CCG		
GAM3808 P114-RHO-GEF	3'	GCCGAGGGGCACTGGCGAGGGA 86451	_	_____ A
	A	GCCG GGGT GC AGGGAA		
		CGGC CCCC CG TCCCTT		
		T TGAC C		
GAM3808 RAB6B	5'	CAGCCGGGGCCGGGAGAG 86452	G	CA
		TAGCCGGGG TG AGGG		

			GTCGGCCCC GC TCTC			
			G CC			
GAM3808	SMCR7	3'	GCTGGGGGTGCAGCACAGAG	86453	C	_____
			GC GGGGGTGCA AGGG			
			CG CCCCCACGT TCTC			
			A CGTG			
GAM3808	TNRC4	3'	TAGCTGAGGGTGGAGGG	86454	C	CA
			TAGC GGGGGTG AGGG			
			ATCG CTCCAC TCCC			
			A C_			
GAM3808	TOMM40	3'	ACCGGGGATGGGGAA	86455		CAA
			GCCGGGGGTG GGGAA			
			TGGCCCCTAC CCCTT			

GAM3808	USP20	3'	GCTGGGAGGAAGGGAAAG	86456	C	TGC
			GC GGGGG AAGGGAAAG			
			CG CCCTC TTCCCTTTC			
			A C_			
GAM3808	LOC126364	3'	TAGTCGGGAGTGGAGGG	86457	C	CA
			TAG CGGGGGTG AGGG			
			ATC GCCCTCAC TCCC			
			A C_			
GAM3808	LOC127703	3'	GGGTTAAGTGAGGGAAAG	86458	_____	CA
			GGG GGTG AGGGAAAG			
			CCC TCAC TCCCTTTC			
			AAT _____			
GAM3808	LOC131583	3'	GCCGGGAGGTAGGGGAAAG	86459	_____	CAA
			GCCGGG GGTG GGGAAAG			
			CGGCC CCAT CCCTTTC			
			T C_			
GAM3808	LOC132864	3'	TAGCTGGGGTGAAAAG	86460	CG	C
			TAGC GGGGTG AAGGG			
			ATCG CCCCAC TTTTC			
			A_ _			
GAM3808	LOC133418	3'	TAGCCTGGTGGGGAAA	86461	GGG	CAA
			TAGCC GGTG GGGAAA			
			ATCGG CCAC CCCTTT			
			A_ _			
GAM3808	LOC145608	5'	TAGTCGGGGGTGGGGGA	86462	C	CAA
			TAG CGGGGGTG GGGA			

ATC GCCCCCAC CCCT
 A CC_
 GAM3808 LOC145761 5' AGCTGCGGTGAGGGAAAAG 86463 CGGG CA
 AGC GGTG AGGGAAAAG
 ||| ||| |||||
 TCG CCAC TCCCTTTC
 ACG_ _
 GAM3808 LOC146268 3' TAGCCGAGAAAGGGAAA 86465 GTGC
 TAGCCGGGG AAGGGAAA
 ||||| |||||
 ATCGGCTCT TTCCCTTT

 GAM3808 LOC146268 3' GGTGGGAAGCAGGGAAAAG 86464 _ T_ A
 GG GGG GCA GGGAAAAG
 || ||| ||| |||||
 CC CCC CGT CCCTTTC
 A TT _
 GAM3808 LOC163412 5' CAGCTGGGGGTGCTGTGGA 86466 C AAG
 TAGC GGGGGTGC GGA
 ||| ||||| |||
 GTCG CCCCCACG CCT
 A ACA
 GAM3808 LOC199745 3' AGCCGGGGGTGGCAGAAG 86467 _ AG
 AGCCGGGGGTG CA GG
 ||||| || ||
 TCGGCCCCAC GT TC
 C CT
 GAM3808 LOC200583 5' TAGCTGGGGGCGCTGGGG 86468 C AA
 TAGC GGGGGTGC GGG
 ||| ||||| |||
 ATCG CCCCCGCG CCC
 A AC
 GAM3808 LOC200734 3' TAGCCAGGGGTTGGGGGGAA 86469 GCAA
 TAGCCGGGGGT GGGAA
 ||||| |||||
 ATCGGTCCCA CCCTT
 ACCC
 GAM3808 LOC219347 3' GCTGGGACTGAAGGGAAAAG 86470 C G C
 GC GGGG TG AAGGGAAAAG
 || ||| || |||||
 CG CCCT AC TTCCCTTTC
 A G _
 GAM3808 LOC220020 5' ACTGGAAGAGGAGGGAAAAG 86471 C TGCA
 GC GGGG AGGGAAAAG
 || ||| |||||
 TG CCTTC TCCCTTTC
 A TCC_
 GAM3808 LOC254314 5' TAGCCAGGGGCCTAGTGAGGGA 86472 GCA_
 TAGCCGGGGGT AGGGA
 ||||| |||||

		ATCGGTCCCCG	TCCCT		
		GATCAC			
GAM3808	LOC255098	3'	TAGCCTGGTGGGGAAA	86461	GGG CAA
			TAGCC GGTG GGGAAA		
			ATCGG CCAC CCCTTT		
			A__ __		
GAM3808	LOC257152	3'	TAGCCAGGGGTAGGGGG	86473	CAA
			TAGCCGGGGGTG GGG		
			ATCGGTCCCCAT CCC		
			CC_		
GAM3808	LOC57118	5'	GCCGGGGGCGCGCTGGGGA	86474	AA__
			GCCGGGGGTGC GGA		
			CGGCCCCCGCG CCCT		
			CGAC		
GAM3808	LOC90719	3'	CAGCTGGGGGTGAGGA	86475	C CAA
			TAGC GGGGGTG GGA		
			GTCG CCCCCAC TCCT		
			A __		
GAM3808	LOC90785	3'	TAGCTGGGAGTGCAGGTGA	86476	C A _
			TAGC GGGGGTGCA GG GA		
			ATCG CCCTCACGT CC CT		
			A _ A		
GAM3808	LOC91960	3'	AGCTGAGTGCAAGGGA	86477	CGG
			AGC GGGTGCAAGGGA		
			TCG CTCACGTTCCCT		
			A__		
GAM3808	LOC92230	5'	TAGCCGGGGGTGCGTAACAACAG	86478	____ G
			TAGCCGGGGGT GCAA GG		
			ATCGGCCCCCA TGTT TC		
			GCAT G		
GAM3808	LOC93273	3'	CAGCACAGTGCAAGGGAA	86479	CGGG
			TAGC GGTGCAAGGGAA		
			GTCG TCACGTTCCCTT		
			TG__		
GAM3809	LIPA	3'	AAAGTTATCATTTTCTTGGA	86482	A ACCG
			AAAGTTAT CATTT TTGGA		
			TTTCAATA GTAAA AACCT		
			_ AG__		
GAM3809	PTGFRN	3'	AAGTTATATACTCCAAGTTTGG	86483	C ACCG_
	A		AAGTTATA ATTT TTGGA		

		TTCAATAT TGAG AACCT	
		A GTTCA	
GAM3809	TRAF1	3' GTTATACATTGCTCAGTGG 86484	TAC T
		GTTATACATT CG TGG	
		CAATATGTAA GT ACC	
		CGA C	
GAM3809	FRSB	3' AAGCTATAATTGTTGGA 86485	C TACC
		AAGTTATA ATT GTTGGA	
		TTCGATAT TAA CAACCT	
		— ———	
GAM3809	SLC26A8	3' AGTTATACATTTTATTTGA 86486	ACCG
		AGTTATACATTT TTGG	
		TCAATATGTAAA AACT	
		ATA_	
GAM3809	SLC26A8	3' AGTTATACATTTTATTTGA 86486	ACCG
		AGTTATACATTT TTGG	
		TCAATATGTAAA AACT	
		ATA_	
GAM3809	LOC196985	3' AAAGTTATATTTTATGGCTGTT 86487	CATTTACC_
		GGA AAAGTTATA GTTGGA	
		TTTCAATAT CAACCT	
		AAAATACCGA	
GAM3809	LOC201910	3' AAAGTTATACCATTTCTGGA 86488	ATTTACCG
		AAAGTTATAC TTGGA	
		TTTCAATATG GACCT	
		GTAA_	
GAM3810	RCN2	3' TAATATTTTGTGCTCAATACG 86491	C_
		T TAATATTT G TCGATACGT	
		ATTATAAA C AGTTATGCA	
		A AACG	
GAM3811	GALNT7	3' CATCACAGTTGTTTTTTT 86494	T
		CGTCACAGTT TTTTTT	
		GTAGTGTCAA AAAAAAA	
		C	
GAM3811	GPRK5	3' TCTTGAGTCACATTTTTTTTTT 86495	CAC G
		TCT GTCACA TTTTTTTTTT	
		AGA CAGTGT AAAAAAAAAA	
		ACT _	
GAM3811	HNF3B	3' CTCACAAAAGTTTTTTTTT 86496	TCAC
		CTCACG AGTTTTTTTTT	

		GAGTGT TCAAAAAAAAAA	
		TT__	
GAM3811 HOXA3	3'	TCGCGTTTACAGATTTTTTTTTT 86497	A C_ _
TC		TC CGT ACAG TTTTTTTTTTC	
		AG GCA TGTC AAAAAAAAAAAG	
		C AA T	
GAM3811 HOXB3	5'	TCTCCCGGACCTGTTTTTTTTT 86498	A TC A_
T		TCTC CG AC GTTTTTTTTT	
		AGAG GC TG CAAAAAAAAA	
		G C_ GA	
GAM3811 IRS1	3'	GTCACAGTGCATTTTTTTTTT 86499	__
		GTCACAGT TTTTTTTTT	
		CAGTGTCA AAAAAAAAAA	
		CGT	
GAM3811 KLRG1	3'	TCTCACATTAGCATTTTTTTTTT 86500	CACA
T		TCTCACGT GTTTTTTTTT	
		AGAGTGTA TAAAAAAAAA	
		ATCG	
GAM3811 MLLT3	3'	TCTACAACAGTTTTTTTTTT 86501	C TC
		TCT ACG ACAGTTTTTTTTTT	
		AGA TGT TGTCAAAAAAAAAA	
		__	
GAM3811 OLFM1	3'	TCACATACACGAAGTTTTTTTTT 86502	_ __
TTC		TCACGT CAC AGTTTTTTTTTC	
		AGTGTA GTG TCAAAAAAAAAAAG	
		T CT	
GAM3811 PHYH	3'	TCACCTTTACTGTTTTTTTTTT 86503	GTC_ A
C		TCAC AC GTTTTTTTTTC	
		AGTG TG CAAAAAAAAAAG	
		AAAA A	
GAM3811 SHOC2	3'	TCACCTTTGCCAGTTTTTTTTTT 86504	GTCA_
C		TCAC CAGTTTTTTTTTC	
		AGTG GTCAAAAAAAAAAAG	
		AAACG	
GAM3811 SOX11	3'	TCAGTTCACAGTTTTTTTTTT 86505	CG
		TCA TCACAGTTTTTTTTTT	
		AGT AGTGTCAAAAAAAAAA	
		CA	
GAM3811 SOX12	3'	TCACATGACGTTTTTTTTTTTC 86506	C A
		TCACGT AC GTTTTTTTTTC	


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AGTGTA TG CAAAAAAAAAAG
      C _
GAM3811 TACC1  3' TCACTCCTGGTTTTTTTTTT 86507  G ACA
      TCAC TC GTTTTTTTTTTT
      ||| || |||||
      AGTG AG CAAAAAAAAA
      _ GAC
GAM3811 ATP1B4 3' GCCAGGCAGGTTTTTTTTTTC 86508  _ _
      GTCA CAG TTTTTTTTTTC
      ||| ||| |||||
      CGGT GTC AAAAAAAAAAAG
      CC C
GAM3811 C1orf22 3' TCACAGAATGTTTTTTTTTTC 86509  ____
      TCACA GTTTTTTTTTTTC
      ||| ||| |||||
      AGTGT CAAAAAAAAAAG
      CTTA
GAM3811 CNTNAP1 3' TCTCTACGTTGCAGGTTTTTT 86510  _ CA T
      TCTC ACGT CAG TTTTTT
      ||| ||| ||| |||
      AGAG TGCA GTC AAAAAA
      A AC C
GAM3811 FLJ14129 3' TCTCAGGTTCCAATTTTTTTTTT 86511  C CA
      T      TCTCA GT CAGTTTTTTTTT
      ||| ||| |||||
      AGAGT CA GTTAAAAAAAAA
      C AG
GAM3811 FLJ20004 3' TCCCACGTCCTTGTTTTTTTTT 86512  ACA
      T      TCTCACGTC GTTTTTTTTTT
      ||||| |||||
      AGGGTGCAG CAAAAAAAAA
      GAA
GAM3811 FLJ20015 3' TCAACAACAGTTTTTTTTTT 86513  _ TC
      TCA CG ACAGTTTTTTTTTT
      ||| ||| |||||
      AGT GT TGTCAAAAAAAAAA
      T _
GAM3811 GTF2E1 3' TCTTACGTCCATGTTTTTC 86514  C A _
      TCT ACGTC CA GTTTTTT
      ||| ||| ||| |||
      AGA TGCAG GT CAAAAG
      A _ A
GAM3811 KIAA0391 3' TCTCCCGTCTTTTTTTTTT 86515  A ACAG
      TCTC CGTC TTTTTTTTTT
      ||| ||| |||||
      AGAG GCAG AAAAAAAAAA
      G ____
GAM3811 KIAA0494 3' TCATCTCACAGCCTTTTT 86516  CG
      TCA TCACAGTTTTTTT
      ||| |||||

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AGT AGTGTCTGGAAAAA
 AG
 GAM3811 KIAA1034 3' TCACTTCACTTTTTTTTTT 86517 G AG
 TCAC TCAC TTTTTTTT
 |||| ||| |||||
 AGTG AGTG AAAAAAAAAA
 A AA
 GAM3811 KIAA1340 3' CGCTCTGACAGTTTTTTTTTTC 86518 C___
 CGT ACAGTTTTTTTTTTC
 ||| |||||
 GCG TGTCAAAAAAAAAAAG
 AGAC
 GAM3811 KIAA1673 5' TCTCACGCCTTTTTTT 86519 ACAGTT
 TCTCACGTC TTTTTT
 ||||| |||||
 AGAGTGCGG AAAAAA

 GAM3811 MGC4604 3' TCTCATTCACAGTTCGACTTC 86520 CG TT
 TCTCA TCACAGTTT TTTT
 |||| ||||| |||
 AGAGT AGTGTCAG GAAG
 A_ CT
 GAM3811 PEG10 3' TCATGTCACAAGGGTTTTTC 86521 C ____
 TCA GTCACA GTTTTTT
 ||| ||||| |||||
 AGT CAGTGT CAAAAAG
 A TCC
 GAM3811 PTPRT 3' CCACGTTTATGTTTTTTTTTC 86522 CACA
 TCACGT GTTTTTTTTT
 ||||| |||||
 GGTGCA CAAAAAAG
 AATA
 GAM3811 SEMA5A 3' TCAGTCGTGTTCTTTTTTTC 86523 C ACA
 TCA GTC GTTTTTTTTTTC
 ||| ||| |||||
 AGT CAG CAAGAAAAAAG
 _ CA_
 GAM3811 TGOLN2 3' TCTCAGGTCACAGTACTTTTTT 86524 C TT
 C TCTCA GTCACAGT TTTTTTC
 |||| ||||| |||||
 AGAGT CAGTGTCA GAAAAAAG
 C T_
 GAM3811 TIEG 3' CATCTTCAGTTTTTTTTTC 86525 A_
 CGTC CAGTTTTTTTTT
 ||| |||||
 GTAG GTCAAAAAAG
 AA
 GAM3811 LOC130752 3' TCTCAGTTCAATTTTTTTTTT 86526 C CA
 TCTCA GT CAGTTTTTTTTT
 |||| || |||||

AGAGT CA GTTAAAAAAAAA
 _ A_
 GAM3811 LOC146159 5' GCCACAAGGTTTTTTTTTT 86527 ____
 GTCACA GTTTTTTTTTT
 ||||| |||||
 CGGTGT CAAAAAAAAA
 TC
 GAM3811 LOC220370 3' TCTCACGTACATTATTTT 86528 C GTT
 TCTCACGT ACA TTTT
 ||||| || |||
 AGAGTGCA TGT AAAG
 A AAT
 GAM3811 LOC90538 3' GCTGCAGTTTTTTTTTTT 86529 CA
 GT CAGTTTTTTTTTTT
 || |||||
 CG GTCAAAAAAAAAAG
 AC
 GAM3812 CNGA3 3' TCTCAGTTGTCAGCTTTTTT 86532 C CA_
 TCTCA GT CAGTTTTTTT
 ||||| || |||||
 AGAGT CA GTCGAAAAAA
 _ ACA
 GAM3812 FGB 3' TCCGTCATGGTTTTCCT 86533 A CA
 TC CGTCA GTTTTTTT
 || ||||| |||||
 AG GCAGT CAAAAGGA
 _ AC
 GAM3812 GNAI1 3' GTCCACAGGTTTTTTTTT 86534 _ _
 GTC ACAG TTTTTTTTTT
 ||| ||||| |||||
 CAG TGTC AAAAAAAAAA
 G C
 GAM3812 GPRK5 3' TCTTGAGTCACATTTTTTTTTT 86495 CAC G
 TCT GTCACA TTTTTTTTTT
 ||| ||||| |||||
 AGA CAGTGT AAAAAAAAAA
 ACT A
 GAM3812 IRS1 3' GTCACAGTGCATTTTTTTTTT 86535 _____
 C GTCACAGT TTTTTTTT
 ||||| |||||
 CAGTGTCA AAAAAAAG
 CGTAAA
 GAM3812 MUC4 3' TCTCCGTCACAGTTGGAGATCA 86536 A TTTTTT
 TCTC CGTCACAGTT TCA
 ||||| ||||| |||
 AGAG GCAGTGTCAA AGT
 _ CCTCT_
 GAM3812 NPAT 3' TCTTACATCACAAGTTTTT 86537 C _
 TCT ACGTCACA GTTTTT
 ||| ||||| |||||

				AGA TGTAGTGT CAAAAA		
				A T		
GAM3812	SHOC2	3'	TCAC	TTTGCCAGT	TTTTTTTTTT	86538 GTCA_
				TCAC	CAGTTTTTTTTT	
				AGTG	GTCAAAAAAAAA	
				AAACG		
GAM3812	SOX12	3'	TCACATGACG	TTTTTTTTTTTCA	86539	C AG
				TCACGT AC	TTTTTTTTTCA	
				AGTGTA TG	AAAAAAAAAAGT	
				C CA		
GAM3812	SP100	3'	TCTTACGTTGAAG	TTTTTTTTTCT	86540	C CAC
				TCT ACGT	AGTTTTTTTTT	
				AGA TGCA	TCAAAAAAAGA	
				A ACT		
GAM3812	CNTNAP1	3'	TCTCTACGTTGCAG	TTTTTTTTT	86510	_ CA T
				TCTC ACGT	CAG TTTTTT	
				AGAG TGCA	GTC AAAAAA	
				A AC C		
GAM3812	FLJ10719	3'	TCTCAGTTACAG	TTCTT	86541	C C
				TCTCA GT	ACAGTTTTT	
				AGAGT CA	TGTCAAGAA	
				_ A		
GAM3812	FLJ13942	3'	TCTCATTACAG	TGTTT	86542	CG T
				TCTCA TCACAG	TTT	
				AGAGT AGTGTCA	AAA	
				A_ C		
GAM3812	FLJ14129	3'	TCTCAGGTTCCA	ATTTTTTTTTT	86543	C CA
				TCTCA GT	CAGTTTTTTTTT	
				AGAGT CA	GTAAAAAAAAA	
				C AG		
GAM3812	KIAA0391	3'	TCTCCCGTCT	TTTTTTTTTTTTT	86544	A ACAG
				TCTC CGTC	TTTTTTTTT	
				AGAG GCAG	AAAAAAAAA	
				G AAAA		
GAM3812	KIAA0494	3'	TCATCTCACAG	CCTTTTTT	86516	CG
				TCA TCACAG	TTTTTTTTT	
				AGT AGTGT	CGGAAAAA	
				AG		
GAM3812	KIAA1034	3'	TCTACACATAGAG	GTTTTTTTTT	86545	_ CACA
	T			TCT CACGT	GTTTTTTTTT	

	AGA GTGTA CAAAAAAAAA	
	T TCTC	
GAM3812 KIAA1034	3' TCACTTCACTTTTTTTTTTTC 86546	G AG_
	TCAC TCAC TTTTTTTTTC	
	AGTG AGTG AAAAAAAAAAG	
	A AAA	
GAM3812 KIAA1946	3' TCACATCGACTTTTTTTTTT 86547	_ AG
	TCACGTC AC TTTTTTT	
	AGTG TAG TG AAAAAAA	
	C AA	
GAM3812 KLF12	3' TCCCATGTATTTTTTTTTTTC 86548	C CACA
	TCTCA GT GTTTTTTTTTTC	
	AGGGT CA TAAAAAAAAAAG	
	A ____	
GAM3812 LOC130752	3' TCTCAGTTCAATTTTTTTTTT 86526	C CA
	TCTCA GT CAGTTTTTTTTT	
	AGAGT CA GTTAAAAAAAAA	
	_ A_	
GAM3812 LOC150054	3' TCTCAGCTTTTTTTTTTTC 86549	C CACAG
	TCTCA GT TTTTTTTTTC	
	AGAGT CG AAAAAAAAAAG	
	_ AA_	
GAM3812 LOC169611	3' TCTCACTTTCCTTTTTTTTC 86550	GTCACAG
	TCTCAC TTTTTTTTTC	
	AGAGTG GGAAAAAAAAAG	
	AAA_	
GAM3812 LOC220370	3' TCTCACGTTACATTATTTTC 86528	C GTTTTTT
	TCTCACGT ACA TTTC	
	AGAGTGCA TGT AAAG	
	A AAT_	
GAM3812 LOC255518	3' TCATGTTTCAGTTTTTCTC 86551	C CA
	TCA GT CAGTTTTTTTT	
	AGT CA GTCAAAAAGAG	
	A AA	
GAM3813 FBXL2	3' CAACACAGACTCCGAGCTG 86554	TG_
	TAACACAG CGAGCTG	
	GTTGTGTC GCTCGAC	
	TGAG	
GAM3813 H3F3B	3' CAACACAATGAAAAGCTG 86555	C_
	TAACACAGTG GAGCTG	

		GTTGTGTTAC TTCGAC	
		TT	
GAM3813	HAGH	3' TAACACAAGCCAAGGGCTG 86556	T G ____
		TAACACAG GC A GCTG	
		ATTGTGTT CG T CGAC	
		_ G TCC	
GAM3813	MTR	3' TAACACAGTGAAATCCTG 86557	C G _
		TAACACAGTG GA CTG	
		ATTGTGTCAC TT GAC	
		T AG	
GAM3813	PDAP1	3' CAACACAGTCCGGGGCTG 86558	G A _
		TAACACAGT CG GCTG	
		GTTGTGTCA GC CGAC	
		G CC	
GAM3813	RET	3' CAACACAGCCAGAAGAGCTG 86559	GC ____
		TAACACAGT GAGCTG	
		GTTGTGTCG CTCGAC	
		GTCTT	
GAM3813	RET	3' CAACACAGCCAGAAGAGCTG 86559	GC ____
		TAACACAGT GAGCTG	
		GTTGTGTCG CTCGAC	
		GTCTT	
GAM3813	RET	3' CAACACAGCCAGAAGAGCTG 86559	GC ____
		TAACACAGT GAGCTG	
		GTTGTGTCG CTCGAC	
		GTCTT	
GAM3813	ZNF184	3' CAACACAGCAAAATGCTG 86560	C _
		TAACACAGTG GA GCTG	
		GTTGTGTCGT TT CGAC	
		T A	
GAM3813	CXYorf1	3' AACACAGTGCGCAGGCTG 86561	_ A ____
		AACACAGTG CG GCTG	
		TTGTGTCAC GC CGAC	
		C GTC	
GAM3813	KIAA0527	3' TAACACAGTCCCAATGCTG 86562	G_ _
		TAACACAGT CGA GCTG	
		ATTGTGTCA GTT CGAC	
		GG A	
GAM3813	PLAA	3' TAACACAGCTTACCAACTG 86563	_ _ G
		TAACACAGT GC AGCTG	

		ATTGTGTCG TG TTGAC		
		AA G		
GAM3813	ULK2	3' TAACACAGGTGATAACTG	86564	_ CG
		TAACACAG TG AGCTG		
		ATTGTGTC AC TTGAC		
		C TA		
GAM3813	LOC144744	3' CAACACAGTCCGGGGCTG	86558	G A_
		TAACACAGT CG GCTG		
		GTTGTGTCA GC CGAC		
		G CC		
GAM3813	LOC154930	3' CAACACAGTAAAATCCTG	86565	C G_
		TAACACAGTG GA CTG		
		GTTGTGTCAT TT GAC		
		T AG		
GAM3813	LOC200093	3' AACACAGTGGCGCAGGCTG	86561	_ A__
		AACACAGTG CG GCTG		
		TTGTGTCAC GC CGAC		
		C GTC		
GAM3813	LOC200609	5' TAACACAGTCAACTAGCTG	86566	__ G
		TAACACAGT GC AGCTG		
		ATTGTGTCA TG TCGAC		
		GT A		
GAM3813	LOC91040	3' AACACAGTGGCGCAGGCTG	86561	_ A__
		AACACAGTG CG GCTG		
		TTGTGTCAC GC CGAC		
		C GTC		
GAM3814	AK1	3' GGCAGGGTGGAGGCGCTGCGC	86569	AAGC_ _
		GGCA GGGGCGC GCGC		
		CCGT CTCCGCG CGCG		
		CCCAC A		
GAM3814	AMMECR1	5' GCGGGGCGCGCGCGCGCC	86570	_
		GCGGGGCGCGCGC CGCT		
		CGCCCCGCGCGCG GCGG		
		C		
GAM3814	AMPD3	5' GGCAGAGCGGAGCGGGGCTGCT	86571	A CGC C
		GGCA AGCGGGGCG GC GCT		
		CCGT TCGCCTCGC CG CGA		
		C CC_ A		
GAM3814	BCR	5' GCGAGGCGCGGGCGCTGCT	86573	_ C
		GCGGGGCGC GCGC GCT		

				CGCTCCGCG CGCG CGA			
				CC A			
GAM3814	BCR	5'	AGGCGGAGCGGGGCGCTCG	86572	AA	G	
			AGGC AGCGGGGCGC CG				
			TCCG TCGCCCCGCG GC				
			CC A				
GAM3814	BCR	5'	AGGCGGAGCGGGGCGCTCG	86572	AA	G	
			AGGC AGCGGGGCGC CG				
			TCCG TCGCCCCGCG GC				
			CC A				
GAM3814	BCR	5'	GCGAGGCGCGGGCGCTGCT	86573	__	C	
			GCGGGGCGC GCGC GCT				
			CGCTCCGCG CGCG CGA				
			CC A				
GAM3814	BGN	3'	GGCAGGCTGGGGAGACCGCT	86574	AA _	CGCGC	
			GGCA GC GGGG GCCGCT				
			CCGT CG CCCC TGGCGA				
			C_ A TC__				
GAM3814	CAPN2	5'	GGCCAGGGCCCCGGCGCGCTGCT	86575	AAAG	__	C
			GGC CGGGGC GCGCGC GCT				
			CCG GTCCCG CGCGCG CGA				
			__ GGC A				
GAM3814	CCND3	5'	AGGCAGGGCGGGAGTGCGGGC	86576	AA _	C C	
			AGGCA GCGGG G GCG GC				
			TCCGT CGCCC C CGC CG				
			CC T A C				
GAM3814	CD83	5'	GCTGGAGCGCTGCGCCGC	86577	_	_	
			GC GGGGCGC GCGCCGC				
			CG CCTCGCG CGCGGCG				
			A A				
GAM3814	CHAC	5'	AGGCGGAGCGCGGTGCAGACC	86578	AA	G C C	
			AGGC AGCG GG GCG GCC				
			TCCG TCGC CC CGT TGG				
			CC G A C				
GAM3814	CHAC	5'	AGGCGGAGCGCGGTGCAGACC	86578	AA	G C C	
			AGGC AGCG GG GCG GCC				
			TCCG TCGC CC CGT TGG				
			CC G A C				
GAM3814	CSNK1E	5'	AGGCGGGGCGGGCCGTGGCACC	86579	AAA	G C_	_
	TGCT		AGGC GCGGG CG GCGCC GCT				

			TCCG CGCCC GC CGTGG CGA			
			CCC G AC A			
GAM3814	DYRK1A	5'	GCGGGGCGCTCGCGCCGCT	86580	—	
			GCGGGGCGC GCGCCGCT			
			CGCCCCGCG CGCGGCGA			
			AG			
GAM3814	FACL4	5'	GGCGGAGCGGGGCGCGC	86581	AA	C
			GGC AGCGGGG GCGCGC			
			CCG TCGCCCC CGCGCG			
			CC —			
GAM3814	FACL4	5'	GGCGGAGCGGGGCGCGC	86581	AA	C
			GGC AGCGGGG GCGCGC			
			CCG TCGCCCC CGCGCG			
			CC —			
GAM3814	HIP1	5'	AGCAGAGCACTGCGTTGC	86582	—	CC
			AGCGGGGCGC GCG GC			
			TCGTCTCGTG CGC CG			
			A AA			
GAM3814	MADD	5'	GGCAGAGGGGGGCGCGCG	86583	A	C
			GGCA AG GGGGCGCGCG			
			CCGT TC CCCC GCGCGC			
			C C			
GAM3814	MADD	5'	GGCAGAGGGGGGCGCGCG	86583	A	C
			GGCA AG GGGGCGCGCG			
			CCGT TC CCCC GCGCGC			
			C C			
GAM3814	MADD	5'	GGCAGAGGGGGGCGCGCG	86583	A	C
			GGCA AG GGGGCGCGCG			
			CCGT TC CCCC GCGCGC			
			C C			
GAM3814	MAF	5'	AGGCAGGGCGGCGCGGCGTC	86584	AA	G — —
	CGCT		AGGCA GCGG GCGCG CG CCGCT			
			TCCGT CGCC CGCGC GC GGCGA			
			CC G C A			
GAM3814	MAP4K2	5'	GCGGGGCGGGGCGCCCGTGGCT	86585	C	—
			GCGGGGCG GCGCC GCT			
			CGCCCCGC CGCGG CGA			
			C GCAC			
GAM3814	MGAT1	5'	AGGCGGGGCGGGGCGGGGCGGA	86586	AAA	C_ CC
	CT		AGGC GCGGGGCG GCG GCT			

		TCCG CGCCCCGC CGC TGA		
		CCC CC C_		
GAM3814	MMP25	5' GGCCAGGGTCGCGCCGC 86587	AAAG	CG
		GGC CGGGG CGCGCCGC		
		CCG GTCCC GCGCGGCG		
		_____ A_		
GAM3814	MYO5A	5' GGCAGGGGCGGGGCGGGCGCC 86588	AAA	C_
		GGC GCGGGGCG GCGCC		
		CCG CGCCCCGC CGCGG		
		CCC CC		
GAM3814	NRXN1	5' AGCGCGGAGCGGGTGGCTGCT 86589	AAA	CGC_ C
		GGC GCGGGGCG GC GCT		
		TCG CGCCTCGC CG CGA		
		_____ CCAC A		
GAM3814	PABPC4	5' GGCAGGCCGCGGGCGCGGGGCT 86590	AAG	CGCC
		GGCA CGGGGCGCG GCT		
		CCGT GCCCGCGC CGA		
		CCG CC_		
GAM3814	PCNA	5' GGCAGAGTGGCAACAACGCCGC 86591	AA C _ C	
	T	GGC AG GG GGCG GCGCCGCT		
		CCG TC CC TTGT TGCGGCGA		
		CC A G _		
GAM3814	PDGFRB	5' GCAGGGCGAGCACAGGCT 86592	C C_	
		GCGGGGCG GCGC GCT		
		CGTCCCGC CGTG CGA		
		T TC		
GAM3814	POU3F1	3' AAGCGGGGTGGGGCGCATCC 86593	C_ _	
		AAGCGGGG GCGCG CC		
		TTCGCCCC CGCGT GG		
		ACCC A		
GAM3814	PPP3CC	5' GGCTAAGGCGGGGAACACCGCT 86594	_ A	CGC
		GGC AA GCGGGG GCGCCGCT		
		CCG TT CGCCCC TGTGGCGA		
		A C T_		
GAM3814	PPP5C	3' AGGCGCAGGCGGGGCCCCCTG 86595	AAA_	GCGCG _
	CT	AGGC GCGGGGC CC GCT		
		TCCG CGCCCCG GG CGA		
		CGTC GGG_ A		
GAM3814	REV3L	5' GGGCGGGGCGGTGTAGGCGCTG 86596	CAAA	C_ C
	CT	G GCGGGGCG GCGC GCT		

C CGCCCCGC CGCG CGA
 _____ CACATC A
 GAM3814 ROBO1 5' AGGCAGAAGCGCAGTAGTGCCG 86597 _ G CGCGC
 AGGCA AAGCG GG GCCG
 |||| |||| || ||||
 TCCGT TTCGC TC CGGC
 C G ATCA_

GAM3814 SCAP1 5' AGGCGGGACGGGGCGCGGGCC 86598 AAA C
 AGGC GCGGGGCGCG GCC
 |||| ||||| ||||
 TCCG TGCCCCGCGC CGG
 CCC C

GAM3814 SDC1 3' GGCGGAGGGGGCGCATGGCT 86599 AA C CGCC
 GGC AG GGGGCGCG GCT
 ||| ||||| ||||
 CCG TC CCCC GCGT CGA
 CC _ AC_

GAM3814 SLIT3 5' GGCGGAGCGGGGCGCTCC 86600 AA GCG
 GGC AGCGGGGCGC CC
 ||| ||||| ||||
 CCG TCGCCCCGCG GG
 CC A_

GAM3814 SORL1 5' GGCCGGGACCGCGCGCGCCGCT 86601 AAAG _
 GGC CGGG GCGCGCGCCGCT
 ||| |||| ||||| ||||
 CCG GCCC CGCGCGCGGCGA
 _ TGG

GAM3814 TGIF 5' AGGCAAGGCGGGGGTCTAGCGG 86602 A C_____ CGC
 CGCG GCAA GCGGGG GCG CG
 |||| |||| ||| ||
 CGTT CGCCCC CGC GC
 C CAGAIIT CGC

GAM3814 UBTF 5' GGCGGAGCGCGGCGCGTGGGGC 86603 AA G CGCC
 T GGC AGCG GGC GCG GCT
 ||| |||| |||| ||||
 CCG TCGC CCGCGC CGA
 CC G ACCC

GAM3814 C20orf108 5' AGGCGCAGCACCCGCGCCGCT 86604 AAA G G
 AGGC GCGG GC CGCGCCGCT
 |||| |||| ||||| ||||
 TCCG CGTC TG GCGCGGCGA
 _ G G

GAM3814 C22orf4 3' AGGCAGGTGGGGCGCGCC 86605 AA CG C
 AGGCA G GGG GCGCGCC
 |||| | ||||| ||||
 TCCGT C CCC CGCGCGG
 _ CA _

GAM3814 Cab45 3' GGCGGCGCGGGGCGCGGCCG 86606 AAA C
 GGC GCGGGGCGCG GCCG
 ||| ||||| |||| ||||

CCG CGCCCCGCGC CGGC
 CCG _
 GAM3814 CDC42BPB 3' GGC GGGGCGGGGTGGGGTAGCG 86607 AA C_____ CGC
 GCGCGC GCGGGG GCG CGC
 ||||| ||| |||
 CGCCCC CGC GCG
 CC ACCCA||IT CGC
 GAM3814 DEPC-1 5' GGC GGAGCCGGGCGCGCCCG 86608 AA G G
 GGC AGC GGGCGCGC CCG
 ||| ||| ||||| |||
 CCG TCG CCCGCGCG GGC
 CC G _
 GAM3814 DKFZP564O1863 5' AGGCAGGGCGGGGCCCTAGCGG 86609 AA _____ CGC
 CGCG GCA GCGGGGCG GCG CG
 ||| ||||| ||| ||
 CGT CGCCCCG CGC GC
 CC GG||IT CGC
 GAM3814 DZIP1 5' GCGGGTCGACTGGCGCCGCT 86610 G _ _ _
 GCGGG CG C GCGCCGCT
 ||||| ||| |||||
 CGCCC GC G CGCGGCGA
 A T AC
 GAM3814 FLJ12442 5' AGCCAGCTGGGCGCGCG 86611 AA G
 GGC AGC GGGCGCGCG
 ||| ||| ||||| |||
 TCG TCG CCCGCGCGC
 G_ A
 GAM3814 FLJ21839 3' GGCAGAGCGGGGCCGTGGGGGC 86612 A G C____
 C GGCA AGCGGGGCG CG GCC
 ||||| ||||| || |||
 CCGT TCGCCCCG GC CGG
 C _ ACCCC
 GAM3814 FLJ21916 5' AGGCGCGGGGCGGGCTCCGCCGC 86613 AAA GC_ G_
 T AGGC GCGGG GC CGCCGCT
 ||||| ||||| || |||||
 TCCG CGCCC CG GCGGCGA
 _ GCC AG
 GAM3814 GDF10 5' GGC GGGGCGGGGCGGCGCGCT 86614 AAA CGC _
 GGC GCGGGGCG GCCG CT
 ||| ||||| ||||| |||
 CCG CGCCCCGC CGGC GA
 CCC _ C
 GAM3814 KATNB1 3' GGCAAAGCTGGGCAGCTATTGC 86615 G C GCC_
 T GGCAAAGC GGGCG GC GCT
 ||||| ||||| ||| |||
 CCGTTTCG CCCGT CG CGA
 A _ ATAA
 GAM3814 KIAA0844 5' GGC GGAGCGAGGCGCGGC 86616 AA C
 GGC AGCGGGGCGCG GC
 ||| ||||| ||||| |||

CCG TCGCTCCGCGC CG
 CC _
 GAM3814 KIAA1857 3' GGCCGGGCGGGGGGCCCTGCT 86617 AAA CGC G _
 GGC GCGGGG GC CC GCT
 ||| ||||| || |||
 CCG CGCCCC CG GG CGA
 GCC C_ _ A
 GAM3814 LAT1-3TM 5' AGCGAGGATTGTGCGCGCCGCT 86618 C____
 AGCGGGG GCGCGCCGCT
 ||||| |||||
 TCGCTCC CGCGCGGCGA
 TAACA
 GAM3814 MGC16385 5' GGCAGGGCGAGGCTGCGC 86619 AA GC
 GGCA GCGGGG GCGC
 ||| ||||| |||
 CCGT CGCTCCG CGCG
 CC A_
 GAM3814 MGC19595 5' GGAAAGGTGGGGCGCGCG 86620 C C_
 GG AAAG GGGGCGCGCG
 || ||| |||||
 CC TTTC CCGCGCGCG
 _ CA
 GAM3814 MGC3047 3' AGGAAAGCGGGACCAGCCGCT 86621 C G C
 AGG AAAGCGGGG CG GCCGCT
 ||| ||||| || |||||
 TCC TTTCGCCCTG GT CGGCGA
 _ _ _
 GAM3814 MGC3279 5' AGGCGAACGGGGCGTCC 86622 AA CGCG
 AGGC AGCGGGGCG CC
 ||| ||||| ||
 TCCG TTGCCCGC GG
 C_ A____
 GAM3814 ODC-p 5' GGCCAGAGCCAGGCGCGCTGC 86623 AA_ G _
 GGC AGC GGGCGCGC GC
 ||| ||| ||||| ||
 CCG TCG TCCGCGCG CG
 GTC G A
 GAM3814 RNF10 5' AGGCGGAGCGGGGCGGC 86624 AA C
 AGGC AGCGGGGCG GC
 ||| ||||| ||
 TCCG TCGCCCCG CG
 CC _
 GAM3814 SCAP 5' GCGGAGCGCGGCGTGCGCGCT 86625 AA G C C
 GGC AGCG GGCG GCGC GCT
 ||| ||| ||| ||| |||
 CCG TCGC CCGC CGCG CGA
 CC G A _
 GAM3814 SEPT6 5' GCGGATTTAACGCGCCGCT 86626 GC____
 GCGGG GCGCGCCGCT
 ||||| |||||

CGCCT TCGCGGCGA
 AAAT
 GAM3814 STX3A 5' AGGCGGCGGCGGCGGCGCG 86627 AAA _ _ C
 CT AGGC GCGG GGCG CG GCCGCT
 |||| |||| |||| ||||
 TCCG CGCC CCGC GC CGGCGA
 C_ GC C _
 GAM3814 TUBB5 3' GGTGAAGCGGGGCTCCTAGCGG 86628 CA C_____ CGC
 CGCG AAGCGGGG GCG CG
 ||||| ||| ||
 TTCGCCCC CGC GC
 AC GAGGAIIT CGC
 GAM3814 LOC145173 5' GGAGCGGAGCTGCGCCGC 86629 A GC
 A AGCGGGGC GCGCCGC
 | ||||| |||||
 C TCGCCTCG CGCGGCG
 C A_
 GAM3814 LOC145376 5' GGCGCGGAGCGGGGCGGGGCGT 86630 AA_ C_ C
 CGCT GGC AGCGGGGCG GCG CGCT
 ||| ||||| ||| |||
 CCG TCGCCCCG CGC GCGA
 CGCC CC A
 GAM3814 LOC145989 3' AGCGAGGCGGGGTGCACGGTCT 86631 AAA C CCG
 GGC GCGGGG GCGCG CT
 ||| ||||| ||||| ||
 TCG CGCCCC CGTGC GA
 CTC A CA_
 GAM3814 LOC146108 5' AGGCGCGGGAGCTTGCGTGCTG 86632 AAA _ _ C C
 CT AGGC GCGGG GC GCG GC GCT
 |||| ||||| || |||||
 TCCG CGCCC CG CGC CG CGA
 _ T AA A A
 GAM3814 LOC150384 5' AGTAACAGCTCGCGCGCGCTGC 86633 GCAA GGG C
 T AG AGC GCGCGCGC GCT
 || ||| ||||| |||
 TC TCG CGCGCGCG CGA
 ATTG AG_ A
 GAM3814 LOC157586 5' AGGCTGGGCGGGGCGCGCG 86634 AAA
 AGGC GCGGGGCGCGCG
 |||| |||||
 TCCG CGCCCCGCGCGC
 ACC
 GAM3814 LOC200014 3' AGGCAGAGCTGGGGTGACG 86635 A _ C_
 AGGCA AGC GGGG GCG
 ||||| ||| ||| |||
 TCCGT TCG CCCC TGC
 C A AC
 GAM3814 LOC201549 5' GGCCGGAGCGGGGCGGGCGGCT 86636 AA_ C CC
 GGC AGCGGGGCG GCG GCT
 ||| ||||| ||| |||

CCG TCGCCCCGC CGC CGA
 GCC C _
 GAM3814 LOC203068 5' AGGCTGGGCGGGGCGCGCG 86634 AAA
 AGGC GCGGGGCGCGCG
 ||| |||||
 TCCG CGCCCCGCGCGC
 ACC
 GAM3814 LOC254552 5' AGGCGGGGCGGGGCGCTCA 86638 AAA G
 AGGC GCGGGGCGC CG
 ||| ||||| ||
 TCCG CGCCCCGCG GT
 CCC A
 GAM3814 LOC254552 5' GGCAGAGCGGGGCGGGGCGC 86637 AAA C_
 GGC GCGGGGCG GCGC
 || ||||| |||
 CCG CGCCCCGC CGCG
 CTC CC
 GAM3814 LOC51063 5' GGCAGCGGCGGCCTCCGCCG 86639 AA _ GCG
 GGCA GCGG GGC CGCCG
 ||| ||| || ||||
 CCGT CGCC CCG GCGGC
 _ G GAG
 GAM3814 LOC51279 3' GGCACAGGTGGGGTGTCTAGCG 86640 A C_ C_____ CGC
 GCGCGC AG GGGG GCG CGC
 || ||| ||| |||
 TC CCCC CGC GCG
 G CA ACAGAIIT CGC
 GAM3814 LOC90630 5' GGCAGAGCGGGGCGCGCA 86641 A
 GGCA AGCGGGGCGCGCG
 ||| |||||
 CCGT TCGCCCCGCGCGT
 C
 GAM3814 LOC91208 5' GGCAGAGCGGGGCGCGCA 86641 A
 GGCA AGCGGGGCGCGCG
 ||| |||||
 CCGT TCGCCCCGCGCGT
 C
 GAM3815 ESR1 3' TAGAAATGGCTGTAAATG 86644 ATTT C A
 TGGAAATGG CTG AAAT G
 ||||| ||| ||| |
 ATCTTTACC GAC TTTA C
 _ A C
 GAM3815 GNRH1 5' TGGTAAATTATACTGCAAATGG 86645 _ GGATTT A
 A TGG AAAT CTGCAAAT GA
 ||| ||| ||||| ||
 ACC TTTA GACGTTTA CT
 A ATAT_ C
 GAM3815 GRM6 3' TGGAGATACCCTGCAAGTAGA 86646 AATG _ A
 TGGA GAT TTCTGCAA TAGA
 ||| ||| ||||| |||

		ACCT CTA GGGACGTT ATCT		
		____ T C		
GAM3815	RFX2	3' TGGAGATGGGTTCTGCA	86647	A A
		TGGA ATGG TTTCTGCA		
		ACCT TACC AAGGACGT		
		C C		
GAM3815	TCN1	3' TGGAACTCCACTGCAAATGGA	86648	ATGGATT T A
		TGGAA CTGCAAAT GA		
		ACCTT GACGTTTA CT		
		GAGGT____ C		
GAM3815	TLL1	3' TGGAAATGGATTTTCTTCATAG	86649	_ GCAA
	A	TGGAAATGGATTT CT ATAGA		
		ACCTTTACCTAAA GA TATCT		
		A AG__		
GAM3815	BRAG	3' TGGGGACTGTCCCTGCAA	86650	AAAT ____
		TGG GGATT TCTGCAA		
		ACC CCTGA GGACGTT		
		____ CAG		
GAM3815	MGC20255	3' TGGAAATGTACAAGTA	86651	GATTTC A
		TGGAAATG TGCAA TA		
		ACCTTTAC ATGTT AT		
		____ C		
GAM3815	PRRG1	5' GGAGGTGGATTTCTTTCTCTAA	86652	AA GCAAA
	A	GGA TGGATTTCT TAGA		
		CCT ACCTAAAGA ATTT		
		CC AAGAG		
GAM3815	UPB1	3' TGGGAATGGACTTCTGTCA	86653	A _
		TGG AATGGATTTCTG CA		
		ACC TTACCTGAAGAC GT		
		C A		
GAM3815	ZNF282	3' GAAATGGATAACGGATAG	86654	TTCT AA
		GAAATGGAT GC ATAG		
		CTTTACCTA TG TATC		
		T__ CC		
GAM3815	LOC151124	5' GGTGGATTTCTGAACTCAG	86655	AAA CAAA
		GG TGGATTTCTG TAG		
		CC ACCTAAAGAC GTC		
		__ TTGA		
GAM3815	LOC151278	5' GATTCCTTTCTGCAAATGGA	86656	AATGGA A
		GA TTTCTGCAAAT GA		

		CT	AAAGACGTTTA	CT		
		AAAGG_	C			
GAM3815	LOC157807	5'	TGGGAATGTATTTCTGCA	86657	A	G
			TGG AATG ATTTCTGCA			
			ACC TTAC TAAAGACGT			
			C A			
GAM3815	LOC201685	3'	TGGGAATGGATTTCTGGC	86658	A	_
			TGG AATGGATTTCTG C			
			ACC TTACCTAAAGAC G			
			C C			
GAM3815	LOC221683	5'	TAGGGATGGATTTCTGCA	86659	AA	
			TGG ATGGATTTCTGCA			
			ATC TACCTAAAGACGT			
			CC			
GAM3815	LOC222234	3'	TGGAAGTAGATTTCTTCCCAGA	86660	A	GCAAA
			TGGAA TGGATTTCT TAGA			
			ACCTT ATCTAAAGA GTCT			
			C AGG_			
GAM3816	MEOX2	3'	AAGGATCATTTATTAAACACA	86663	G	_
			AAGGATCATT ATTAA CGCG			
			TTCCTAGTAA TAATT GTGT			
			A T			
GAM3816	PDE4A	3'	AAGGATTATTGATCAACG	86664	C	
			AAGGAT ATTGATTAACG			
			TTCCTA TAACTAGTTGC			
			A			
GAM3816	MGC12992	5'	AAGGAGCGGGCGCAGCGCGGTT	86665	TCATTGAT	A
		T	AAGGA TA CGCGGTTT			
			TTCCT GT GCGCCAAA			
			CGCCCGC_ C			
GAM3816	LOC221184	5'	AGGTTGTTGATCGCGGTT	86666	ATCA	TAA
			AGG TTGAT CGCGGTT			
			TCC AACTA GCGCCAA			
			AAC_ _			
GAM3817	GPC6	5'	TGCGTGGAGGTATGTGTTG	86669	_ C_	
			TGTG GGA ATGTGTTG			
			ACGC CCT TACACAAC			
			A CCA			
GAM3817	SR-BP1	3'	TGTGTGTGTGTGTGTATGTGTT	86670	AATAT	GGAC
		G	TGT TGTG ATGTGTTG			

		ACA ACAC TACACAAC		
		CACAC ACA_		
GAM3817	LOC150622 5'	TGGGATATTGTGGGGCTCTGTT 86671	TA	ACATG
	G	TG ATATTGTGGG TGTTG		
		AC TATAACACCC ACAAC		
		CC CGAG_		
GAM3817	LOC151242 3'	GTGATGTTATTTACATGTGTTG 86672	A A	GGG
		GT AT TTGT ACATGTGTTG		
		CA TA AATA TGTACACAAC		
		C C AA_		
GAM3817	LOC90155 3'	TGTATATTTAGGTATGTGTTG 86673	A G	AC
		TGTA TATT TGGG ATGTGTTG		
		ACAT ATAA ATCC TACACAAC		
		_ _ A_		
GAM3818	PSG7 3'	TGTAGTACATGTTTTATTCTGC 86676	CG C	
		TGTG ACA GTTTTATTCTGC		
		ACAT TGT CAAAATAAGACG		
		CA A		
GAM3818	SH3BP2 3'	TCTGTATGTTGTTTTATTCTGC 86677	CGACAC	
		TTTGTG GTTTTATTCTGC		
		AGACAT CAAAATAAGACG		
		ACAA_		
GAM3818	SEMA3C 3'	CAACATGTTTTATTTTGC 86678	C C	
		CGACA GTTTTATT TGC		
		GTTGT CAAAATAA ACG		
		A A		
GAM3818	LOC150135 3'	TCTGTGCGTTGTGCTTTTGTTT 86679	ACAC	A_
	TGC	TTTGTGCG GTTTT TTCTGC		
		AGACACGC CGAAA AAGACG		
		AACA AC		
GAM3818	LOC158314 5'	TTTGTGGATGTTTCATTTTGC 86680	C CAC	C
		TTTGTG GA GTTTTATT TGC		
		AAACAC CT CAAAGTAA ACG		
		_ A_ A		
GAM3819	CLDN3 3'	TTGGTGGTGGTGGTGG 86683	A A	TAC
		TTG GTGGTGGT GT GG		
		AAC CACCACCA CA CC		
		_ C _		
GAM3819	CAPN6 3'	TGAGTGGTGGTGGTGG 86684	A	TAC
		TGAGTGGTGGT GT GG		

		ACTCACCACCA CA CC	
		C ____	
GAM3819 KIAA0601	3'	GTGGCTGGGTAGTTACGGAT 86685	____
		GTGGT GGTAGTTACGGAT	
		CACCG CCATCAATGCCTA	
		AC	
GAM3819 LOC148760	3'	CTGAGTGGCATTATGG 86686	GGTA C
		TTGAGTGGT GTTA GG	
		GA CTCACCG TAAT CC	
		____ A	
GAM3819 LOC151103	3'	TATTGAGTTGTGGTGCAGTGG 86687	G A TAC
		TATTGAGT GTGGT GT GG	
		ATAACTCA CACCA CG CC	
		A _ TCA	
GAM3819 LOC203078	3'	TTGGTGGTGGTGGCGG 86688	A A TTA
		TTG GTGGTGGT G CGG	
		AAC CACCACCA C GCC	
		_ C ____	
GAM3819 LOC254181	5'	TTGGGTGGGGAGTGG A 86689	A T T TAC
		TTG GTGG GG AGT GGA	
		AAC CACC CC TCA CCT	
		C _ _ ____	
GAM3820 ABCA1	5'	TTGTGTTTGCCTCTCTTT 86692	A TG
		TTGTGTTT CGT CTTT	
		AACACAAA GCA GAAA	
		C GA	
GAM3820 CD69	3'	TTGTGTTTATTCTACTTTT 86693	CG
		TTGTGTTTA TTGCTTTT	
		AACACAAAT GATGAAAA	
		AA	
GAM3820 CERD4	3'	TGTTGCTGTCGTTGCTTTT 86694	_ TA
		TGT GTT CGTTGCTTTT	
		ACA CGA GCAACGAAAA	
		A CA	
GAM3820 SELE	3'	TGTGTTTGCATTTATGCTTTT 86695	A ____
		TGTGTTT CGT TGCTTTT	
		ACACAAA GTA ACGAAAA	
		C AAT	
GAM3820 CCR8	3'	CATTGTGTTTGATGGCTTTT 86696	AC T
		TATTGTGTTT GT GCTTTT	

		GTAACACAAA TA CGAAAA	
		C_ C	
GAM3820 CHODL	3'	TATTGTGTATGTCACTTCT 86697	TTAC TG
		TATTGTGT GT CTTT	
		ATAACACA CA GAAGA	
		TA__ GT	
GAM3820 DIO2	3'	TGTGTTTACCTGTTGGCTTTT 86698	__ _
		TGTGTTTAC GTTG CTTT	
		ACACAAATG CAAC GAAAA	
		GA C	
GAM3820 DIO2	3'	TGTGTTTACCTGTTGGCTTTT 86698	__ _
		TGTGTTTAC GTTG CTTT	
		ACACAAATG CAAC GAAAA	
		GA C	
GAM3820 DKFZP761L0424	3'	TGTGCAAACCTGTTGCTTTT 86699	TT __
		TGTGT AC GTTGCTTTT	
		ACACG TG CAACGAAAA	
		TT AA	
GAM3820 FLJ10521	3'	TTGTGTTTTTTGCTTTT 86700	ACG
		TTGTGTTT TTGCTTTT	
		AACACAAA AACGAAAA	
		A__	
GAM3820 KCNH8	3'	TGTGTTTAGATACTTTT 86701	CGT
		TGTGTTTA TGCTTTT	
		ACACAAAT ATGAAAA	
		CT_	
GAM3820 KIAA0865	3'	CTGTGTCCTGTGCTTTT 86702	ACGT
		TTGTGTTT TGCTTTT	
		GACACAGG ACGAAAA	
		AC__	
GAM3820 KIAA1254	3'	TATTTACCATACGTTGCTTTT 86703	GTGTT
		TATT TACGTTGCTTTT	
		ATAA ATGCAACGAAAA	
		ATGGT	
GAM3820 KLHL4	3'	TTGTGTTTCATGACCTTT 86704	A T
		TTGTGTTT CGT GCTTTT	
		AACACAAA GTA TGGAAA	
		_ C	
GAM3820 MGC15482	3'	TATTGTCTTCCATGCTTTT 86705	G A T
		TATTGT TTT CGT GCTTTT	

		ATAACA AAA GTA CGAAAA	
		G G _	
GAM3820	PSMD12	3' TATGCTCTATGTTGCTTTT	86706 AC_
		TGTGTTT GTTGCTTTT	
		ATACGAG CAACGAAAA	
		ATA	
GAM3820	PTPRT	3' TACTGTGCTTTTGCTTTT	86707 ACG
		TATTGTGTTT TTGCTTTT	
		ATGACACGAA AACGAAAA	
		—	
GAM3820	TUSP	5' TTGGCTTGC GTTGCTTTT	86708 T A
		TTG GTTT CGTTGCTTTT	
		AAC CGAA GCAACGAAAA	
		_ C	
GAM3820	ZFP100	3' TGTGTCCAGTGCTTTT	86709 C T
		TGTGTTTA GT GCTTTT	
		ACACAGGT CA CGAAAA	
		— —	
GAM3820	LOC126616	3' TATTGGTTTGCTGCTTT	86710 T AC
		TATTG GTTT GTTGCTTT	
		ATAAC CAAA CGACGAAA	
		— —	
GAM3820	LOC131000	3' TTGTGTTTACA ACTTTT	86711 TT
		TTGTGTTTACG GCTTTT	
		AACACAAATGT TGAAAA	
		—	
GAM3820	LOC144266	5' TTGTGTTCCCAGGCTTTT	86712 TA TT
		TTGTGTT CG GCTTTT	
		AACACAA GT CGAAAA	
		GG C_	
GAM3820	LOC152503	5' TATTGGTCTGAGGTTGCTTTT	86713 T AC_
		TATTG GTTT GTTGCTTTT	
		ATAAC CAGA CAACGAAAA	
		_ CTC	
GAM3820	LOC152897	3' TTGTGTTTTGCGCTTTT	86714 AC T
		TTGTGTTT GT GCTTTT	
		AACACAAA CG CGAAAA	
		A_ _	
GAM3820	LOC153918	3' TGTGTTTAATGCTTTT	86715 CGT
		TGTGTTTA TGCTTTT	

ACACAAAT ACGAAAA
 T__
 GAM3820 LOC201799 3' TTGTGCCATTGCTTTT 86716 TTA
 TTGTGT CGTTGCTTTT
 ||||| |||||
 AACACG GTAACGAAAA

 GAM3821 C6orf33 3' TTAAAACATGCTGGTCAAATAT 86719 T CT_ CG
 GG TTAAAACAT GCTGG GG TGG
 ||||| |||| || ||
 AATTTTGTA CGACC TT ACC
 _ AGT AT
 GAM3821 LOC63928 3' CTAAAATATTGCTGGCTG 86720 C
 TTAAAA ATTGCTGGCTG
 ||||| |||||
 GATTTT TAACGACCGAC
 A
 GAM3822 PRKCN 5' TTCCTTTCAGTCTGTACT 86723 CT T
 TTCCTTTC GTTT GTACT
 ||||| |||| ||||
 AAGGAAAG CAGA CATGA
 T_ _
 GAM3822 LOC127703 5' TATTCCTTTTGTGCTTACT 86724 CC TTTG
 TATTCCTTT TGT TACT
 ||||| || ||||
 ATAAGGAAA ACA ATGA
 A_ CGA_
 GAM3822 LOC222166 3' TCCTTTCCTGCCCTTGTA 86725 _
 TCCTTTCCTGTT TTGTA
 ||||| ||||
 AGGAAAGGACGG AACAT
 G
 GAM3823 ANK3 3' GGTTACAAATGATTGGCTTACT 86728 GC AAAA_
 GAAA GGT ACAAATGATT TGAAA
 || ||||| ||||
 CCA TGTTTACTAA ACTTT
 A_ CCGAATG
 GAM3823 CHN2 3' GGTGTCACAGCAAAATGA 86729 _ AATGAT
 GGTG CACA TAAAATGA
 |||| |||| |||||
 CCAC GTGT GTTTTACT
 A C_
 GAM3823 DAZ 3' GGTCACAATATAAAATGA 86730 G ATGAT
 GGT CACAA TAAAATGA
 || |||| |||||
 CCA GTGTT ATTTTACT
 _ AT_
 GAM3823 GLS 3' GGTCACAATTTAAAATGAA 86731 G ATGA
 GGT CACAA TTAAAATGAA
 || |||| |||||

			CCA GTGTT AATTTTACTT		
			— A —		
GAM3823	HNF3A	3'	GTGCATGAAAAATGA 86732	CAAA	TT
			GTGCA TGA AAAATGA		
			CACGT ACT TTTTACT		
			— —		
GAM3823	PDYN	3'	GGTGCACAGGAGATCTTTTGA 86733	AAT	AAAA
			GGTGCACA GATT TGA		
			CCACGTGT CTAG ACT		
			CCT AAA_		
GAM3823	TRAM	3'	GGTGACACAAGTGAGAAATG 86734	_ A	TTA
			GGTG CACAA TGA AAATG		
			CCAC GTGTT ACT TTTAC		
			T C C_		
GAM3823	CLLD8	5'	GGTCCACAAATGGATGAA 86735	G	ATTAAA
			GGT CACAAATG ATGAA		
			CCA GTGTTTAC TACTT		
			G C_		
GAM3823	DCTN4	3'	GGTCACAAAAAATGA 86736	G	TGATT
			GGT CACAAA AAAATGA		
			CCA GTGTTT TTTTACT		
			— —		
GAM3823	ELOVL2	3'	GGTACAAATGATTTATGAA 86737	CA	AAA
			GGTGCA AATGATT ATGAA		
			CCATGT TTAATAA TACTT		
			— A_		
GAM3823	FLJ20275	3'	GTGCACAAATACTAAGATG 86738	G	A
			GTGCACAAAT ATTAATG		
			CACGTGTTTA TGATT TAC		
			— C		
GAM3823	KIAA1009	3'	GGTACACAGAGACATAAAGATG 86739	AAT	_ _
			GGTGCACA GAT TAAA ATG		
			CCATGTGT CTG ATTT TAC		
			CT_ T C		
GAM3823	KIAA1881	3'	GGTGCACACGGTGACCCCTG 86740	AA_	AAAA
			GGTGCACA TGATT TG		
			CCACGTGT ACTGG AC		
			GCC GG_		
GAM3823	LOC126616	3'	AGTGTACAAATGAAATG 86741	C	TTAA
			GGTG ACAAATGA AATG		

	TCAC TGT T TACT TTAC	
	A _____	
GAM3823 LOC126917 3'	GGTGTGGATGACCAAAAGTGA 86742	CACAA _
	GGTG ATGATTA AAA TGA	
	CCAC TACTGGT TTT ACT	
	ACC_ C	
GAM3823 LOC131870 3'	AGTGCACAAAGCACAGATGAA 86743	TG TAAA
	GGTGCACAAA AT ATGAA	
	TCACGTGTTT TG TACTT	
	CG TC_	
GAM3823 LOC142948 3'	AGTGCACAGGTAACAGTGAA 86744	AA TAAAA
	GGTGCACA TGAT TGAA	
	TCACGTGT ATTG ACTT	
	CC TC_	
GAM3823 LOC143286 5'	GGTACAAATAAAAAATGAA 86745	CA TT
	GGTGCA AATGA AAAATGAA	
	CCATGT TTATT TTTTACTT	
	— —	
GAM3823 LOC145231 5'	GGTGCCGTGGAAAAATGAA 86746	ACAAA ATT
	GGTGC TG AAAATGAA	
	CCACG AC TTTTACTT	
	GC_ CT_	
GAM3823 LOC153514 3'	AGTGTACAAACAAAATGAA 86747	C GATT
	GGTG ACAAAT AAAATGAA	
	TCAC TGTTTG TTTTACTT	
	A _____	
GAM3823 LOC155434 3'	GGTGCCCTTAAATGAA 86748	ACAAATGA
	GGTGC TTAAATGAA	
	CCACG AATTTTACTT	
	GG_____	
GAM3823 LOC158724 3'	GATTGATGATTAAAATGA 86749	GCACAA
	GGT ATGATTAAAATGA	
	CTA TACTAATTTTACT	
	AC_	
GAM3823 LOC221931 3'	GGTGCACAGAAAAATGAA 86750	AAT TT
	GGTGCACA GA AAAATGAA	
	CCACGTGT CT TTTTACTT	
	— —	
GAM3823 LOC253782 3'	GTGCACAAGAAATGAA 86751	AT TTAA
	GTGCACAA GA AATGAA	

CACGTGTT CT TTACTT

GAM3823 LOC254848 5' GGTCCACGTTTTAAAATGA 86752 G AAATGA
GGT CAC TTAAAATGA
||| ||| |||||
CCA GTG AATTTTACT
G CAA__

GAM3823 LOC93206 3' GGTGCACAATAAATGGTGAA 86753 A TTAAAA
GGTGCACAA TGA TGAA
||||||| ||| |||
CCACGTGTT ATT ACTT
_ TACC__

GAM3824 FABP5 3' TGTAATAATGTTTATGATAAA 86756 T C
TGTAATAAT TTTGT GATAAA
||||||| ||||| |||||
ACATTTTA AAATA CTATTT
C _

GAM3824 ZHX1 3' TGTAATAATTTTTGGTCAA 86757 _
TGTAATAATTTTTG TCGA
||||||| ||||| |||
ACATTTTAAAAAC AGTT
C

GAM3824 KIAA0981 3' TGAAAATTTTTGCCACAAA 86758 T G
TG AAAATTTTTGTC ATAAA
|| ||||| ||||| |||||
AC TTTTAAAAACGG TGTTT

GAM3824 KIAA1615 3' GTAAAATTTTCTTATAAAAAT 86759 GTCG
GTAAAATTTTT ATAAAAT
||||||| ||||| |||
CATTTTAAAAG TATTTTAA
AA__

GAM3824 SGP28 3' TGTAATAATTTATGCAGATAAAA 86760 T C
A TGTAATAATTT TGT GATAAAAA
||||||| ||| ||||| |||
ACATTTTAAA ACG CTATTTTT
T T

GAM3824 LOC201973 3' TGCAAAATTTTTCTCAAAAAA 86761 G T
TGTAATAATTTTT TCGA AAA
||||||| ||| ||| |||
ACGTTTTAAAAA AGTT TTT
G T

GAM3825 DTNB 3' GCGGGTGGAGTGACGTCTGGCA 86764 CA AT T _
GC GCG TGGA TG TG CTGGCAGC
||| |||| || || |||||
CGC ACCT AC GC GACCGTCG
CC C_ T A

GAM3825 DTNB 3' GCGGGTGGAGTGACGTCTGGCA 86764 CA AT T _
GC GCG TGGA TG TG CTGGCAGC
||| |||| || || |||||

CGC ACCT AC GC GACCGTCG
CC C_ T A
GAM3825 FES 3' GCAGTGTGGATGCTGGTGGC 86765 ____ AT C
GCA TGA TGTTG TGGC
||| ||| |||| ||||
CGT ACCT ACGAC ACCG
CAC _ C
GAM3825 ARHGDIG 3' TGGGATGCCCTGGCAGC 86766 AAT G
TGG TGTT CTGGCAGC
||| ||| |||||
ACC ACGG GACCGTCG
CT_ G
GAM3825 FLJ20618 3' GCATAGAATTGTTCTCTGGC 86767 G_
GCATGGAATTGTT CTGGC
||||||| ||||
CGTATCTTAACAA GACCG
GA
GAM3825 KIAA0261 3' GCATGGAATTGTTAACAGC 86768 CTG
GCATGGAATTGTTG GCAGC
||||||| ||||
CGTACCTTAACAAT TGTCG

GAM3825 KIAA0459 3' CATGGATGGCTGGCAG 86769 AT TT
CATGGA TG GCTGGCAG
||||| || |||||
GTACCT AC CGACCGTC

GAM3825 MGC21621 5' GCGTCTGGGCCCTGCTGGCAG 86770 CA AA G
C GCG TGG TT TTGCTGGCAGC
||| ||| || |||||
CGC ACC GG GACGACCGTCG
AG C_ G
GAM3825 SCYB10 3' TGGAATTGTATGTAGGTAGC 86771 _ CT C
TGGAATTGT TG GG AGC
||||||| || |||
ACCTTAACA AC CC TCG
T AT A
GAM3825 LOC131873 3' GCTGGAATTGTCAGGAG 86772 A GCT C
GC TGGAATTGTT GG AG
|| ||||| || ||
CG ACCTTAACAG CC TC

GAM3825 LOC146136 5' GCGTGGAATTGTTGACTGG 86773 A _
GC TGGAATTGTTG CTGG
|| ||||| ||||
CG ACCTTAACAAC GACC
C T
GAM3825 LOC148397 3' GCACATGGGCAGGCTGGCAGC 86774 AATT T_
GCGCATGG GT GCTGGCAGC
||||| || |||||

CGTGTACC CG CGACCGTCG
 _____ TC
 GAM3825 LOC157421 5' TGGAGGGT GAGGCTGGCAGC 86775 AT_ TT
 TGA TG GCTGGCAGC
 |||| || |||||
 ACCT AC CGACCGTCG
 CCC TC
 GAM3825 LOC200317 5' GCGTTGGGGTTACCAAGGGTAG 86776 CA AATT ____ C
 C GCG TGG GTTGCT GG AGC
 ||| ||| ||||| |||||
 CGC ACC CAATGG CC TCG
 A_ C____ TTC A
 GAM3825 LOC220565 3' GCGTGGAATTGTTGACTGG 86773 A _
 GC TGGAATTGTTG CTGG
 || ||||| |||||
 CG ACCTTAACAAC GACC
 C T
 GAM3825 LOC64150 5' GCGCACGGGACGCTGGCG 86777 AATTGT A
 GCGCATGG TGCTGGC G
 ||||| ||||| |
 CGCGTGCC GCGACCG C
 CT____ C
 GAM3826 CD34 3' TCGGCAGAGAGGAGGG 86780 __ CAAAA A
 TGCG C GAGA G GAGGG
 |||| | |||| | |||||
 ACGC G CTCT C CTCCC
 C T _____
 GAM3826 ED1 5' CTGGGCGGGACGGAGCAGGG 86781 C A AAAA _
 CTG GCG GAC GAG AGGG
 ||| ||| ||| |||||
 GAC CGC CTG CTC TCCC
 C C C____ G
 GAM3826 HOXA7 3' GACTGTCCGGTGCAGAGAGGG 86782 CG AGACAAA
 GACTG CG AGAGAGGG
 |||| || |||||
 CTGAC GC TCTCTCCC
 AG CACG____
 GAM3826 HOXA7 3' GACTGTCCGGTGCAGAGAGGG 86782 CG AGACAAA
 GACTG CG AGAGAGGG
 |||| || |||||
 CTGAC GC TCTCTCCC
 AG CACG____
 GAM3826 KRTHA5 3' CTGCGCGAAGAGAGG 86783 GACAAA
 CTGCGCGA AGAGAGG
 ||||| |||||
 GACGCGCT TCTCTCC

 GAM3826 PATE 3' GACTGTAGAAAAGGAGAGG 86784 CGCG C A
 GACTG AGA AAA GAGAGG
 |||| ||| ||| |||||

		CTGAC TCT TTT CTCTCC	
		A___ _ C	
GAM3826 PDE7A	5'	CTGTCCCGAGGCCAAAAGAGAGG 86785	CG_ A
G		CTG CGAG CAAAAGAGAGGG	
		GAC GCTC GTTTTCTCTCCC	
		AGG C	
GAM3826 RAI3	3'	GACAGTGCAAGAAGAGAGG 86786	TGC CAAA
		GAC GCGAGA AGAGAGG	
		CTG CGTTCT TCTCTCC	
		TCA _____	
GAM3826 SCD	3'	CTGTGCCTCATGAGAGAGGG 86787	C GAGA AA
		CTG GC CA AGAGAGGG	
		GAC CG GT TCTCTCCC	
		A GA__ AC	
GAM3826 SF1	5'	GCGCGAGACGCACAAAGAGGG 86788	AAA_
		GCGCGAGAC AGAGAGGG	
		CGCGCTCTG TTTCTCCC	
		CGTG	
GAM3826 SFRP1	3'	CTGCCGCAGAGAGAGGG 86789	G _ CAAAA
		CTGC CG AGA GAGAGGG	
		GACG GC TCT CTCTCCC	
		_ G _____	
GAM3826 SHMT2	3'	CTGCCTGAGAGAGGAGAGGG 86790	GC CAAAA
		CTGC GAGA GAGAGGG	
		GACG CTCT CTCTCCC	
		GA CTC__	
GAM3826 SLC2A3	3'	GAGTGCGTGGGATGAGAAAGG 86791	C CGA CAAA
		GA TGCG GA AGAGAGG	
		CTACGC CT TCTTTCC	
		C ACC AC__	
GAM3826 SNX5	5'	CTGTGCGAGGAAAGAAG 86792	C ACAA
		CTG GCGAG AGAGAGG	
		GAC CGCTC TTTCTTC	
		A C_____	
GAM3826 CAMTA2	3'	GACTGCACGAGGCGCCCCAGG 86793	ACAAAAGAG
G		GACTGCGCGAG AGGG	
		CTGACGTGCTC TCCC	
		CGCGGGGG_	
GAM3826 DKFZP434I0714	3'	GACTACACTTAGGAGGGAGGG 86794	GAGACAAA A
		GACTGCGC AG GAGGG	

		CTGATGTG	TC CTCCC		
		AATCC__	C		
GAM3826	FLJ10110	5'	GACTGAGCGCGCGAGAGAGGG	86795	C AGACAAA
			GACTG GCG AGAGAGGG		
			CTGAC CGC TCTCTCCC		
			T GCGC__		
GAM3826	FLJ11186	5'	CCGCGCGGAGAGAGG	86796	A CAAAA
			CTGCGCG GA GAGAGG		
			GGCGCGC CT CTCTCC		
			— ———		
GAM3826	FLJ22390	5'	GATTGCGCGAGGAGGA	86797	C ACAAAAGA
			GA TGC GCGAG GAGGG		
			CT ACGCGCTC CTCCT		
			A ———		
GAM3826	FLJ32334	3'	GACTGCAGCCAGGAGAGAGGG	86798	_ G ACAA
			GACTGC GC AG AGAGAGGG		
			CTGACG CG TC TCTCTCCC		
			T G C__		
GAM3826	HRH3	3'	CTGCCGTGGCATTAAAGAGAGGG	86799	G AGA A_
			CTGC CG CA AAGAGAGGG		
			GACG GC GT TTCTCTCCC		
			_ ACC AA		
GAM3826	KIAA0335	3'	CTGGTGGAAGAAGAGAGGG	86800	CGC_ CAAA
			CTG GAGA AGAGAGGG		
			GAC TTCT TCTCTCCC		
			CACC ———		
GAM3826	KIAA0710	3'	TGGCAAGGATAAAAGAGGG	86801	C ACAA
			TG GCGAG AAGAGAGGG		
			AC CGTTC TTTTCTCCC		
			_ CTA_		
GAM3826	KIAA1041	5'	CTGCGGCTGGAAGAGAGAGGG	86802	_ GA CAAA
			CTGCG C GA AGAGAGGG		
			GACGC G CT TCTCTCCC		
			C AC TC__		
GAM3826	KIAA1274	3'	CTGCCGGGACAGAGAG	86803	G A AAA
			CTGC CG GACA GAGAG		
			GACG GC CTGT CTCTC		
			_ C ———		
GAM3826	KIAA1668	3'	AACTGTGAGGGAGAGAGG	86804	CGC ACAA
			GACTG GAG AGAGAGG		

			TTGAC CTC TCTCTCC		
			A__ CC__		
GAM3826	MRPS21	5'	GACGCGCGAGATGGAGCACATG 86805	T	CAAAA AG__
	G		GAC GCGCGAGA GAG GG		
			CTG CGCGCTCT CTC CC		
			_ AC__ GTGTA		
GAM3826	PTPNS1	3'	GCTGTCTCTGGGTAAAAGAGAG 86806	A	CGCGAGAC_
	GG		G CTG AAAAGAGAGGG		
			C GAC TTTTCTCTCCC		
			_ AGAGACCCA		
GAM3826	RAB11B	3'	ACGAGACAGAGGAGGG 86807	AA A	
			GCGAGACA AG GAGGG		
			TGCTCTGT TC CTCCC		
			C_ _		
GAM3826	RAB24	3'	GATAAACAGACAAAAGGGAGGG 86808	C C G	A
			GA TG GC AGACAAAAG GAGGG		
			CT AT TG TCTGTTTTCTCTCCC		
			_ T _ C		
GAM3826	LOC143903	5'	GACCGCACGGGAGGCGGGGGGG 86809	A	CAAAAGA__
	AGGG		GACTGCGCG GA GAGGG		
			CTGGCGTGCT CTCTCCC		
			C CCGCCCCC		
GAM3826	LOC149506	3'	CTGCTGGAGACAAGAGAGGG 86810	GC	AA
			CTGC GAGACA AGAGAGGG		
			GACG CTCTGT TCTCTCCC		
			AC _		
GAM3826	LOC149706	3'	CTGCTGCTCCAAGAGAGGG 86811	_	GAGACAA
			CTGC GC AAGAGAGGG		
			GACG CG TTCTCTCCC		
			A AGG__		
GAM3826	LOC150935	3'	GACTGGCAACAGGGAGGG 86812	C GA	AAA A
			GACTG GC GACA GAG GG		
			CTGAC CG TTGT CTC CC		
			_ _ CC_ _		
GAM3826	LOC152283	3'	GCTGTGATCAGGAGAGAGGG 86813	A CG	GA AA
			G CTG CGA CA AGAGAGGG		
			C GAC GCT GT TCTCTCCC		
			_ A_ A_ CC		
GAM3826	LOC219653	3'	CTGTGGTGGGAGAGAAAGGAGA 86814	CGC__	C A
	GGG		CTG GAGA AAA GAGAGGG		

				GAC	CTCT TTT CTCTCCC			
				ACCACC	C C			
GAM3826	LOC253962	5'		CTGGGGAGGTGGAAGAGAGGG	86815	CGC	ACAA	
				CTG GAG AAGAGAGGG				
				GAC CTC TTCTCTCCC				
				CC_ CACC				
GAM3826	LOC255565	5'		GCTGGTGGACAAAAGAGGGG	86816	GCGA_	A	
				GC GACAAAAGAG GGG				
				CG CTGTTTTCTC CCC				
				ACCAC _				
GAM3826	LOC85414	3'		GA	CTGGGGAGAGAGGAGAGGG	86817	CGC	CAAAA
				GA	CTG GAGA GAGAGGG			
				CTGAC CTCT CTCTCCC				
				CC_ CTC_				
GAM3826	LOC93082	5'		GA	CTGCGCGGGCACAGAGCAGG	86818	AGACAA	_
				GA	CTGCGCG AGAG AGG			
				CTGACGCGC TCTC TCC				
				CCGTG_ G				
GAM3827	ALEX2	5'		TG	GA	ACTGGATTGCTTAAG	86821	CA_
				TG	GA	ACTGGAT TTAGG		
				AC	CTTGACCTA AATTC			
				ACG				
GAM3827	FOXI1	3'		TG	GGGCTGGCATGGAGGACCTC	86822	AA	ATCATT
	T			TG	G CTGG AGGACCTCT			
				ACC GACC TCCTGGAGA				
				CC GTACC_				
GAM3827	KLK4	3'		GG	GGCTGGGACCTGGACCTCT	86823	AA	_ ATTA
				GG	CTGG ATC GGACCTCT			
				CC GACC TGG CCTGGAGA				
				CC C A_				
GAM3827	PRL	3'		TG	GAACGGATCATTAAGGACCT	86824	T	_
				TG	GAAC GGATCATTA GGACCT			
				AC	CTTG CCTAGTAAT CCTGGA			
				_ T				
GAM3827	RUNX1	3'		TG	GA	ACTAGATTGACCT	86825	CATTAG
				TG	GA	ACTGGAT GACCT		
				AC	CTTGATCTA CTGGA			
				A_				
GAM3827	SS18	3'		TG	GA	ATGGAAGGATCT	86826	C TCATT C
				TG	GA	TGGA AGGA CT		

ACCTT ACCT TCCT GA
 — ——— A
 GAM3827 FLJ10743 3' TGGAAGTGGCAGGACCC 86827 ATCAT
 TGGAAGTGG TAGGACCT
 ||||| |||||
 ACCTTGACC GTCCTGGG

———
 GAM3827 FLJ12700 3' TGGGACTCGGGGGACCTC 86828 A _ ATCATTA
 TGG ACT GG GGACCTC
 ||| ||| || |||||
 ACC TGA CC CCTGGAG
 C G C ———

GAM3827 FLJ21791 3' TGCAATTGGATTAGAACACC 86829 G C CAT _
 TG AA TGGAT TAGGAC CT
 || || ||||| ||||| ||
 AC TT ACCTA ATCTTG GG
 G A — T

GAM3827 KIAA0280 3' TGGAATGGGTAGAGGACCTCT 86830 C ATCATT
 TGGAA TGG AGGACCTCT
 ||||| ||| |||||
 ACCTT ACC TCCTGGAGA
 _ CATC_

GAM3827 KPTN 3' TGGAATGGGATCATCCCT 86831 CT AGGA
 TGGAA GGATCATT CCT
 ||||| ||||| |||
 ACCTT CCTAGTAG GGA
 AC ———

GAM3827 PDCD6IP 3' TGGAAGTGGGGCACAGCTTCT 86832 AT TA ACC
 TGGAACTGG CAT GG TCT
 ||||| ||| || |||
 ACCTTGACC GTG TC AGA
 CC _ GA_

GAM3827 PLCL2 3' TGGAAGTGGGTTAGAATGTCT 86833 ATCA CC
 TGGAACTGG TTAGGA TCT
 ||||| ||||| |||
 ACCTTGACT AATCTT AGA
 C_ AC

GAM3827 LOC129676 5' TGGGTCTTATCTTTGGGACCT 86834 AA GG A A
 TGG CT ATC TT GGACCT
 ||| || ||| || |||||
 ACC GA TAG AA CCTGGA
 CA A_ A C

GAM3827 LOC148936 5' TGGGGTCTGGAGGACCTC 86835 AA_ TCATTA
 TGG CTGGA GGACCTC
 ||| ||||| |||||
 ACC GACCT CCTGGAG
 CCA ———

GAM3827 LOC148938 5' TGGGGTCTGGAGGACCTC 86835 AA_ TCATTA
 TGG CTGGA GGACCTC
 ||| ||||| |||||

		ACC GACCT CCTGGAG	
		CCA _____	
GAM3827	LOC149606 3'	GGATTGGCTCAGACCCCT 86836	AC A TTAG
		GGA TGG TCA GACCTCT	
		CCT ACC AGT CTGGGGA	
		A_ G _____	
GAM3827	LOC222985 5'	TGGAAGTGGAAACATTCACCAG 86837	_____
		TGGAAGTGGAA TCATTAG	
		ACCTTGACCT AGTGGTC	
		TGTA	
GAM3828	RBBP9 3'	TTAGTGTAACAAATTCAA 86840	
		TTAGTGTAATAAATTTAA	
		AATCACATTGTTTAAGTT	
GAM3828	CDW92 3'	TTAGTGCAATAAGTTTAAAAAA 86841	A T
		TTAGTGTAATAA TTAA AAA	
		AATCACGTTATT AAATT TTT	
		C T	
GAM3828	KATNB1 3'	TAGTTACAAATTTAATAAAAT 86842	GTA
		TAGT ATAAATTTAATAAAAT	
		ATCA TGTTTAAATTATTTTA	
		A_	
GAM3828	KIAA1737 3'	AGTGTAATAAATTACAAA 86843	TA
		AGTGTAATAAATT ATAAA	
		TCACATTATTTAA TGTTT	
GAM3828	SDCBP 3'	TTAGTGTAATAACTTTTACA 86844	A A
		TTAGTGTAATAA TTT ATA	
		AATCACATTATT AAA TGT	
		G A	
GAM3828	LOC253943 3'	TTAGTGTTGTAAATTTAAC 86845	AA
		TTAGTGT TAAATTTAAT	
		AATCACA ATTTAAATTG	
		AC	
GAM3828	LOC255042 3'	TTAGTGTAACAGAACTCA 86846	_
		TTAGTGTAATA AATTTA	
		AATCACATTGT TTGAGT	
		C	
GAM3829	CD244 3'	CCTCTTGCTTTGGAAGATGG 86849	CTC_ C
		CCTCTTGT GGAGA GG	

GGAGAACG CTTCT CC
AAAC A
GAM3829 GATA2 3' CTTTGTCTCAGAGTAGG 86850 C AC
CT TTGTCTCGGAG GG
|| ||||| ||
GA AACAGAGTCTC CC
A AT
GAM3829 NEUROD2 3' CCTTTTGCCTCGGCAGCTGG 86851 C_ AGA _
CCT TTGTCTCGG CGGC GG
||| ||||| ||| ||
GGA AACGGAGCC GTCG CC
AA _ A
GAM3829 OLIG2 3' TCTTTTCCCGGAGGTGGTGG 86852 G AC C
TCTT TCTCGGAG GG GG
|||| ||||| |||
AGAA AGGGCCTC CC CC
A CA A
GAM3829 PCK1 3' TCCCCCTGCAACTGGGGATGGC 86853 T _ C A C
GG TCCC CTTGT CT GG GA GGCGG
|||| |||| || || |||||
AGGG GGACG GA CC CT CCGCC
_ TT C _ A
GAM3829 PCK1 3' TCCCCCTGCAACTGGGGATGGC 86853 T _ C A C
GG TCCC CTTGT CT GG GA GGCGG
|||| |||| || || |||||
AGGG GGACG GA CC CT CCGCC
_ TT C _ A
GAM3829 PCK1 3' TCCCCCTGCAACTGGGGATGGC 86853 T _ C A C
GG TCCC CTTGT CT GG GA GGCGG
|||| |||| || || |||||
AGGG GGACG GA CC CT CCGCC
_ TT C _ A
GAM3829 SIX3 3' CCCTCTTGTCTCGTGGTGG 86854 _ GAGAC C
CCCTCTTGT CTCG GG GG
||||||| ||| |||
GGGAGAACA GAGC CC CC
G A _ A
GAM3829 13CDNA73 5' CCCTGCAGCCCTCGGAGGCGGC 86855 CTT _ A
GG CCCT GTC TCGGAG CGGCGG
|||| ||| ||||| |||||
GGGA CGG AGCCTC GCCGCC
CGT G C
GAM3829 CCNI 5' TCCCTCTCGCCATAGGGCGGCG 86856 TC_ AGA
G TCCCTCTTGTGTC GG CGGCGG
||||||| || |||||
AGGGAGAGCGG CC GCCGCC
TAT C_
GAM3829 ELOVL1 3' TCCCTCTTGTGTTGTGGACAG 86857 CTCGGA
TCCCTCTTGT GACGG
||||||| |||||

			AGGGAGAACA	CTGTC		
			AACAC_			
GAM3829	FASTK	5'	TCCCTCTCCCACAGGAGGCGGC	86858	G T_ A	
	GG		TCCCTCTT TC C GGAG CGGCGG			
			AGGGAGAG GG G CCTC GCCGCC			
			_ T T C			
GAM3829	GABBR1	5'	CTCTTCTTCCCCGGGGCGGCGG	86859	G_	AGA
			CTCTT TCTCGG CGGCGG			
			GAGAA GGGGCC GCCGCC			
			GAA CC_			
GAM3829	KIAA1814	3'	TCCTTCTGGTCTCAAAGGTGG	86860	C T	AC
			TCC TCT GTCTCGGAG GG			
			AGG AGA CAGAGTTTC CC			
			A C CA			
GAM3829	MGC2306	3'	CTTTTGTCTCAGAGTAGG	86850	C	AC
			CT TTGTCTCGGAG GG			
			GA AACAGAGTCTC CC			
			A AT			
GAM3829	OS-9	5'	CTTATGCAGAGGAGACGGCGG	86861	CT CTC	
			CT TGT GGAGACGGCGG			
			GA ACG CCTCTGCCGCC			
			AT TCT			
GAM3829	RNF10	5'	TCTTGTCCATGTCTCGGAGGCGGT	86862	_____	A C
	GG		TCTTGTCT TCGGAG CGG GG			
			AGAACAG AGCCTC GCC CC			
			GTAC C A			
GAM3829	ZF5128	3'	CTCTTTCCAGAGGTGGCGG	86863	G	AC
			CTCTT TCTCGGAG GGCGG			
			GAGAA AGGGTCTC CCGCC			
			_ CA			
GAM3829	LOC126755	3'	TCCCTCTCGTCTTGGAGA	86864		C
			TCCCTCTTGTCT GGAGA			
			AGGGAGAGCAGA CCTCT			
			A			
GAM3829	LOC144559	5'	TCTTATTTCAAAACGGTGG	86865	C	C
			TCTTGT TCGGAGACGG GG			
			AGAATA AGTTTTTGCC CC			
			A A			
GAM3829	LOC150113	5'	TCCCTCTTTTCTTGGGTGCTGG	86866	G C AGACG _	
			TCCCTCTT TCT GG GC GG			

AGGGAGAA AGA CC CG CC
 A A CA__ A
 GAM3829 LOC151278 5' TCCCTGTTGTTTTGGAAATGCC 86867 C CTC CG__
 GCGG TCCCT TTGT GGAGA GCGG
 |||| ||| |||| ||||
 AGGGA AACA CCTTT CGCC
 C AAA ACGG
 GAM3829 LOC170394 5' TCCCTCTTGCTCCTCCTGGCGG 86868 CT GGAGAC
 TCCCTCTTGT C GGCGG
 ||||| || | ||||
 AGGGAGAACG G CCGCC
 AG AGGA__
 GAM3829 LOC255019 5' TCCTTCCTGTCTACGGCG 86869 C CGGAG
 TCC TCTTGTCT ACGGCG
 || ||||| ||||
 AGG AGGACAGA TGCCGC
 A _____
 GAM3829 LOC56270 5' CCTCTCGCTGGGGACGGCGG 86870 T C A
 CCTCTTG CT GG GACGGCGG
 ||||| || || |||||
 GGAGAGC GA CC CTGCCGCC
 _ C _